GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 19, 2004, 13:46:37 ; Search time 14114 Seconds
(without alignments)
17476.634 Million cell updates/sec

Title: US-09-964-956-12
Perfect score: 5691
Sequence: 1 atgaaagccatgccctggaa.....gcttagacagctgaaataaa 5691

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	19	1554	27.3	2875	9	BC009343	BC009343 Homo sapi
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ALIGNMENTS

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LOCUS AX503782 5691 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 12 from Patent WO0226826.
ACCESSION AX503782
VERSION AX503782.1 GI:23385966
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gerlach,V.L., Macdougall,J.R., Smithson,G., Millet,I., Stone,D., Gunther,E., Ellerman,K., Grosse,W.M., Alsobrook,J.P., Lepley,D.M., Burgess,C.E., Padigaru,M., Kekuda,R., Spytek,K.A., Leach,M.D. and

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            Shimkets,R.A.
  TITLE     Proteins and nucleic acids encoding same
  JOURNAL   Patent: WO 0226826-A 12 04-APR-2002;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
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ORIGIN

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  Matches 5691;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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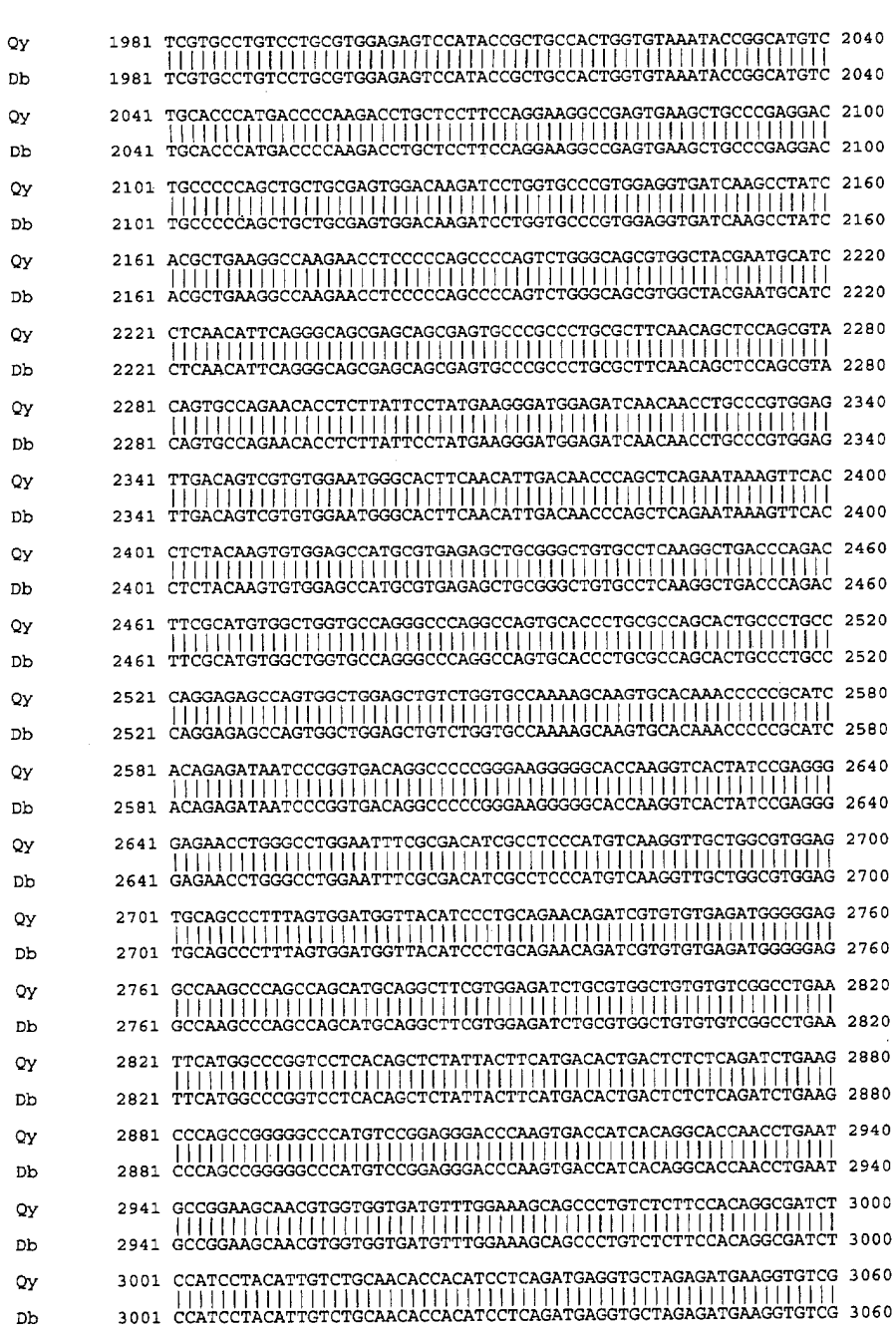
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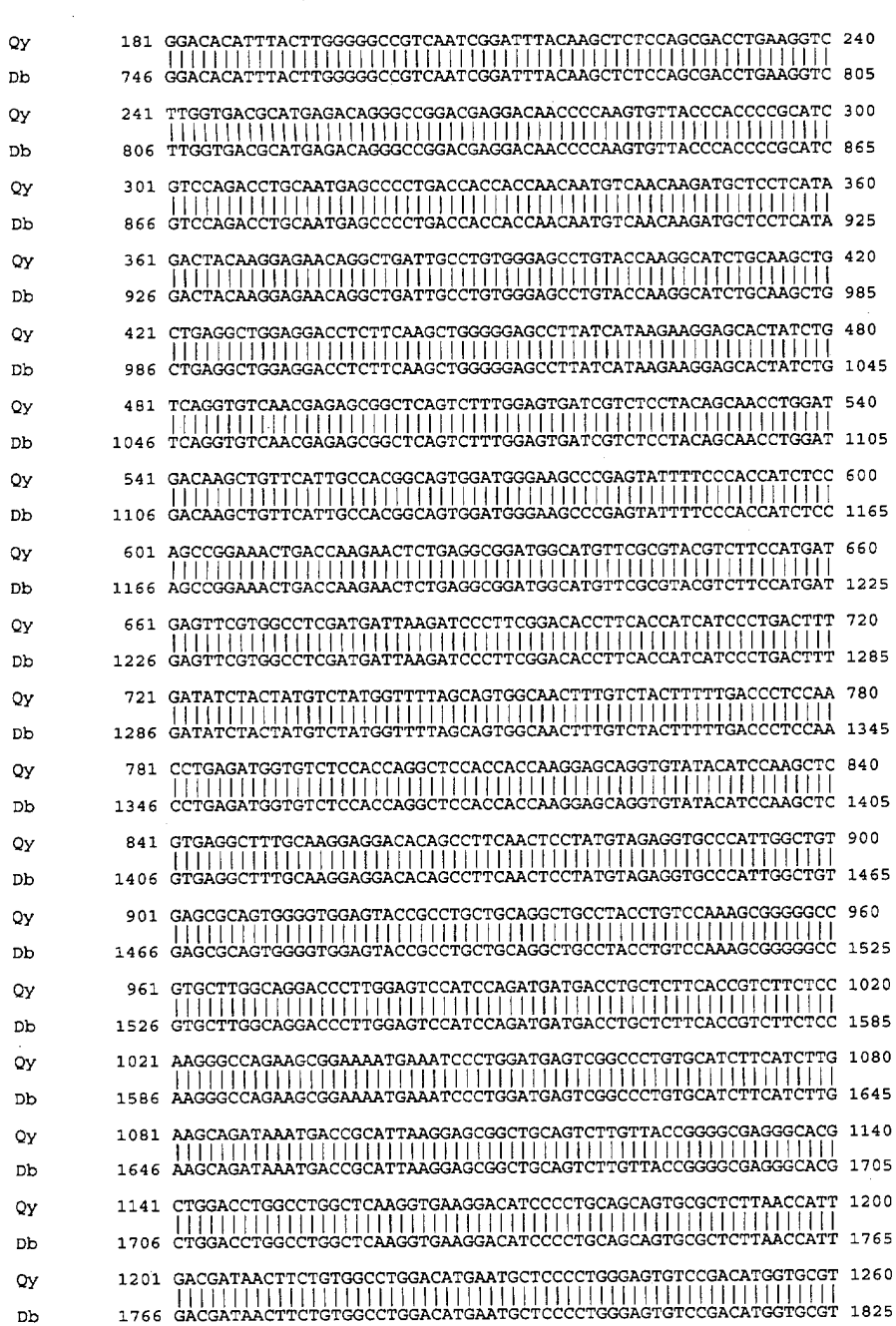
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DEFINITION Mus musculus mRNA for plexin-A4, complete cds.
ACCESSION AB073228
VERSION AB073228.1 GI:28200902
KEYWORDS .
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Suto,F., Murakami,Y., Nakamura,F., Goshima,Y. and Fujisawa,H.
TITLE Identification and characterization of a novel mouse plexin, plexin-A4
JOURNAL Mech. Dev. 120 (3), 385-396 (2003)
MEDLINE 22480023
PUBMED 12591607
REFERENCE 2 (bases 1 to 7022)
AUTHORS Suto,F. and Fujisawa,H.
TITLE Direct Submission
JOURNAL Submitted (18-OCT-2001) Fumikazu Suto, Nagoya University Graduate School of Science, Group of Developmental Neurobiology, Division of Biological Science; Chikusa-ku, Nagoya, Aichi 464-8602, Japan (E-mail:fumiwa@bio.nagoya-u.ac.jp, Tel:81-52-789-2981, Fax:81-52-789-2979)

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ORIGIN

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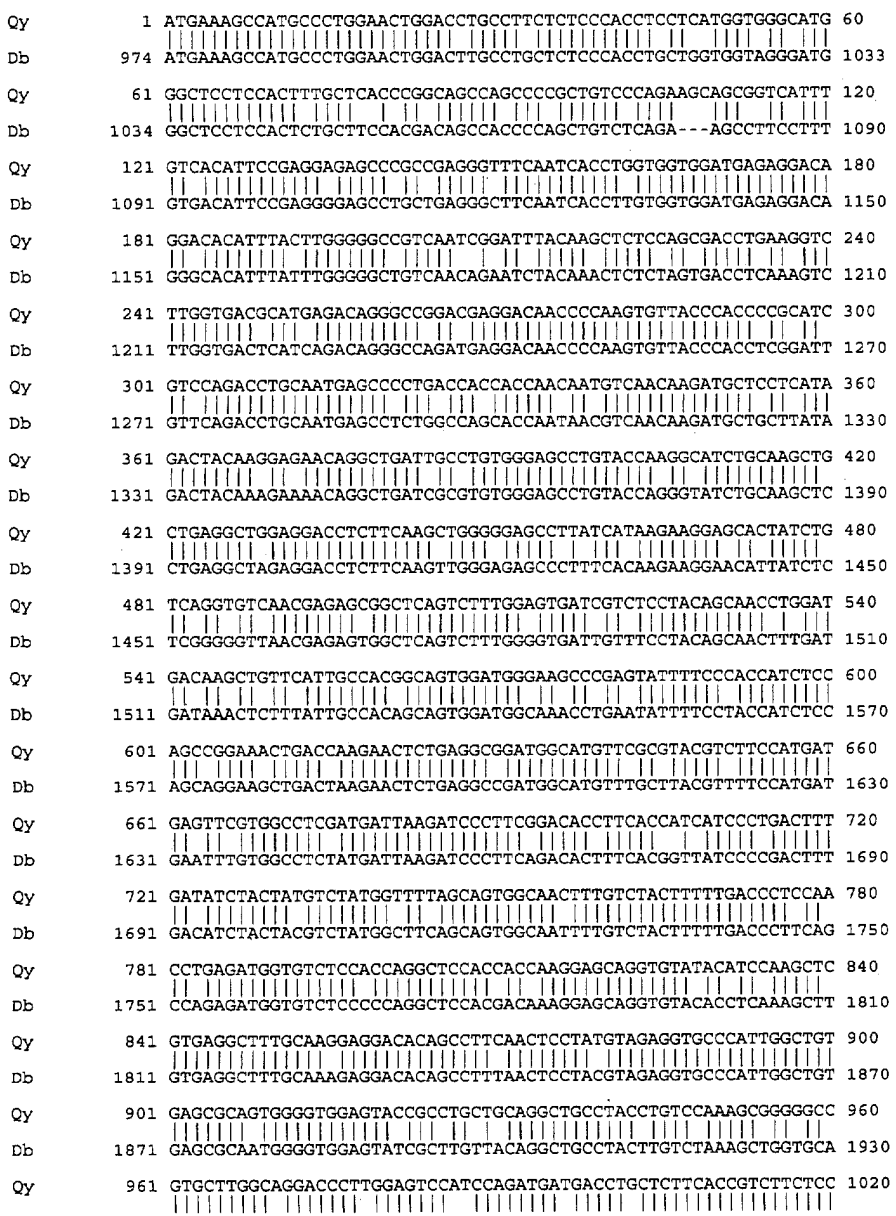

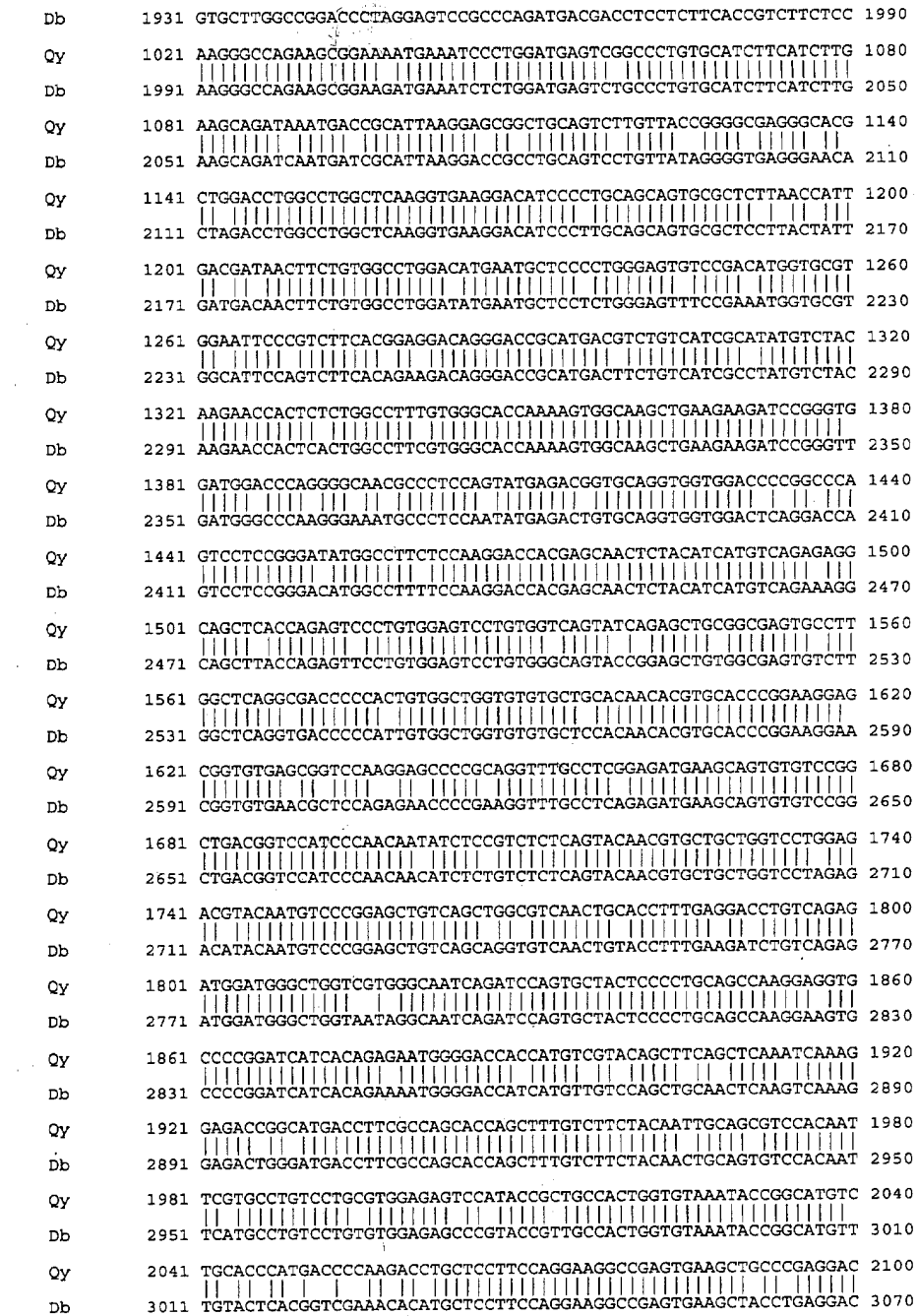

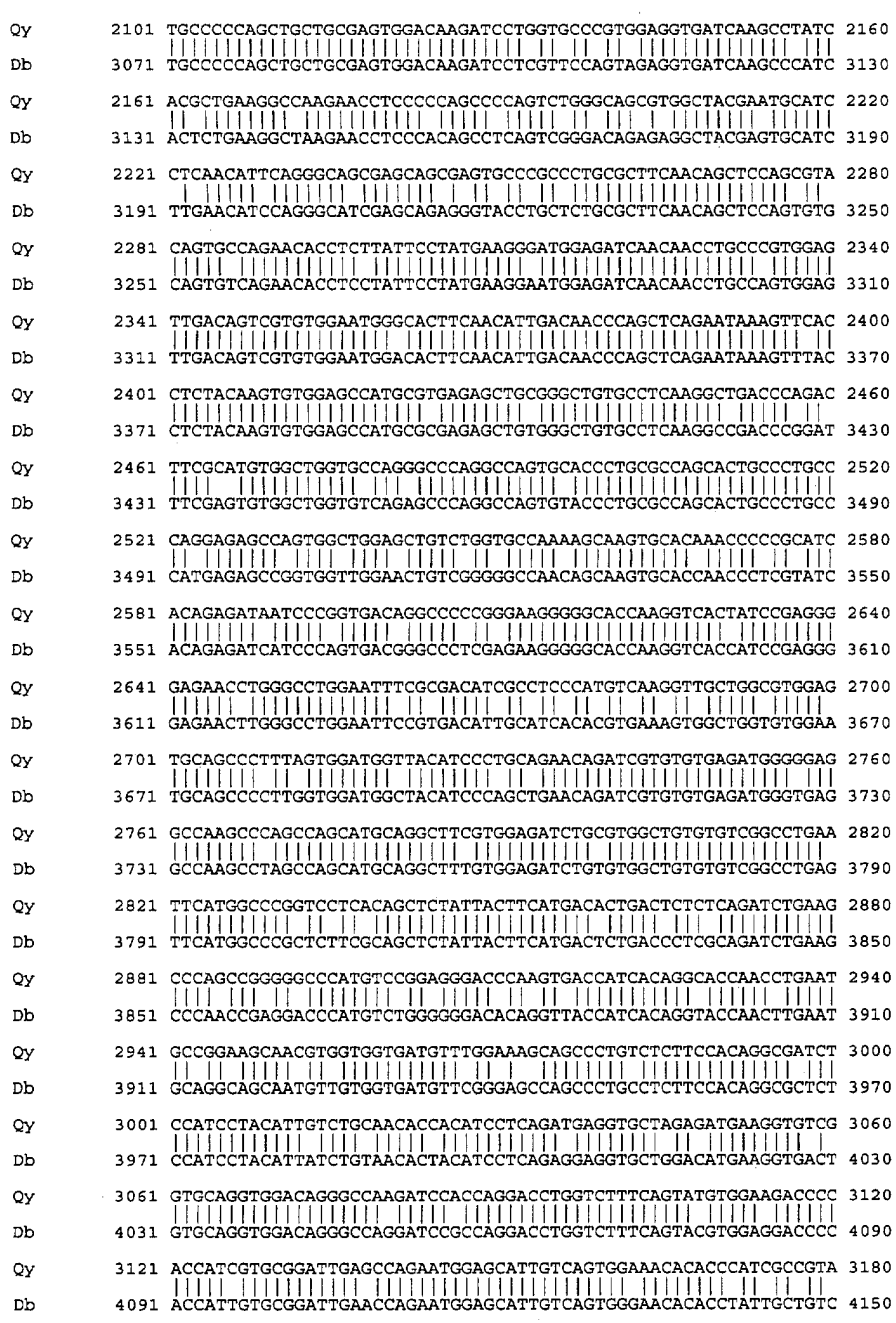
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  AUTHORS   Tang,Y.T., Liu,C., Zhou,P., Asundi,V., Zhang,J., Zhao,Q.A., Ren,F.,
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ORIGIN

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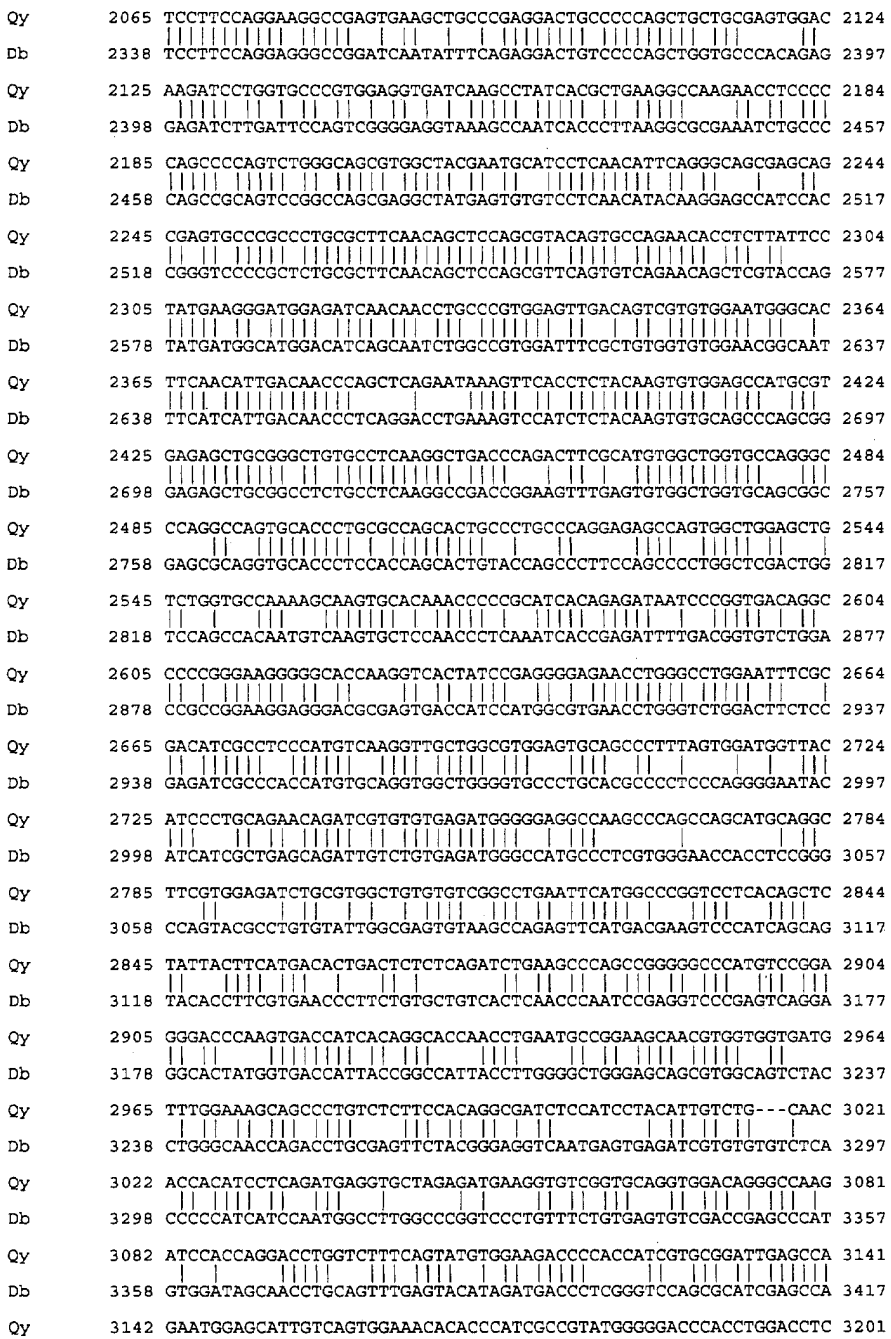
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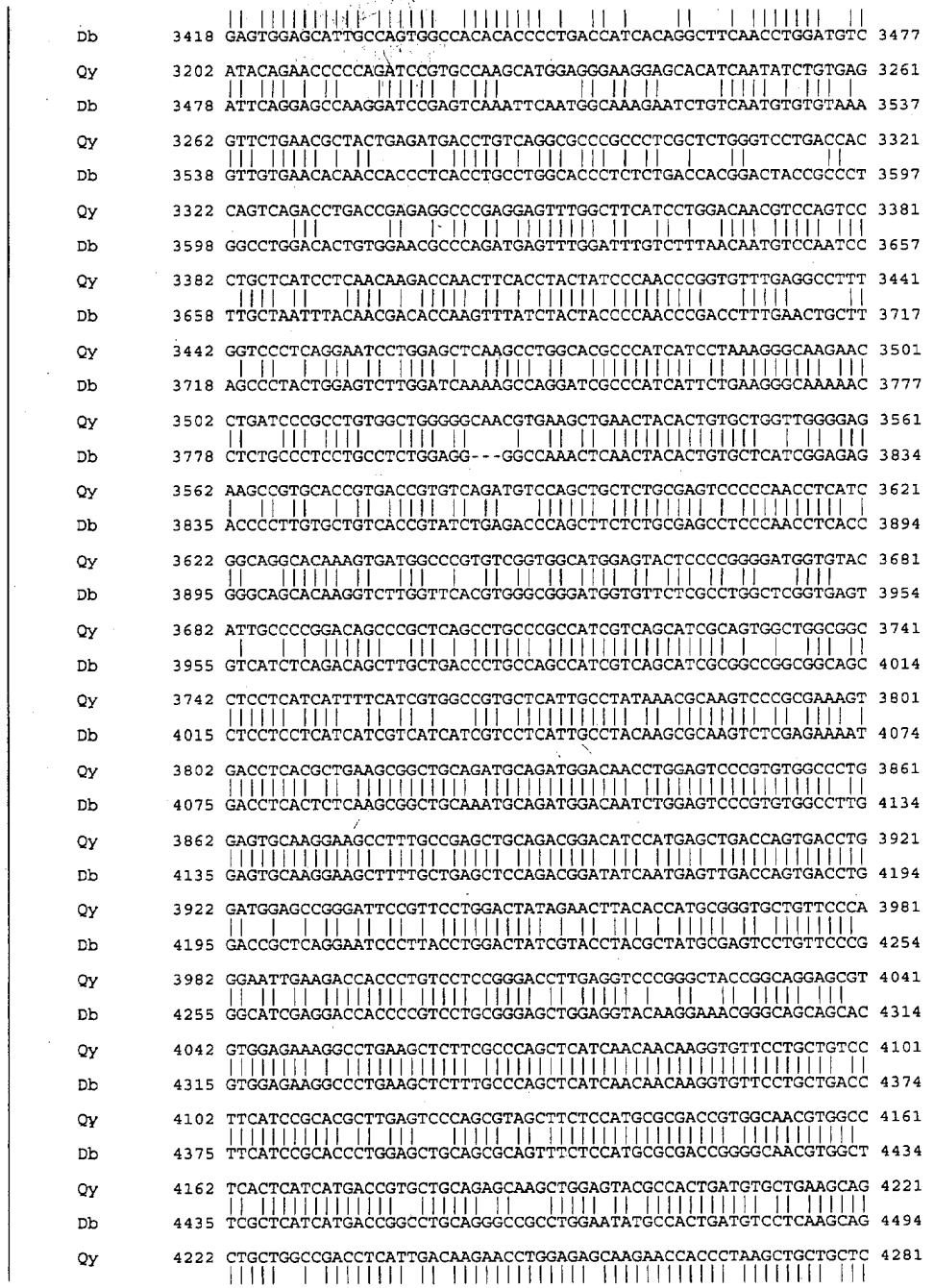
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AUTHORS Seki,N., Ohira,M., Nagase,T., Ishikawa,K., Miyajima,N.,
Nakajima,D., Nomura,N. and Ohara,O.
TITLE Characterization of cDNA clones in size-fractionated cDNA libraries
from human brain
JOURNAL DNA Res. 4 (5), 345-349 (1997)
MEDLINE 98116662
PUBMED 9455484
REFERENCE 2 (bases 1 to 6263)
AUTHORS Ohara,O.
TITLE Direct Submission
JOURNAL Submitted (08-OCT-1997) Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913,
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ORIGIN

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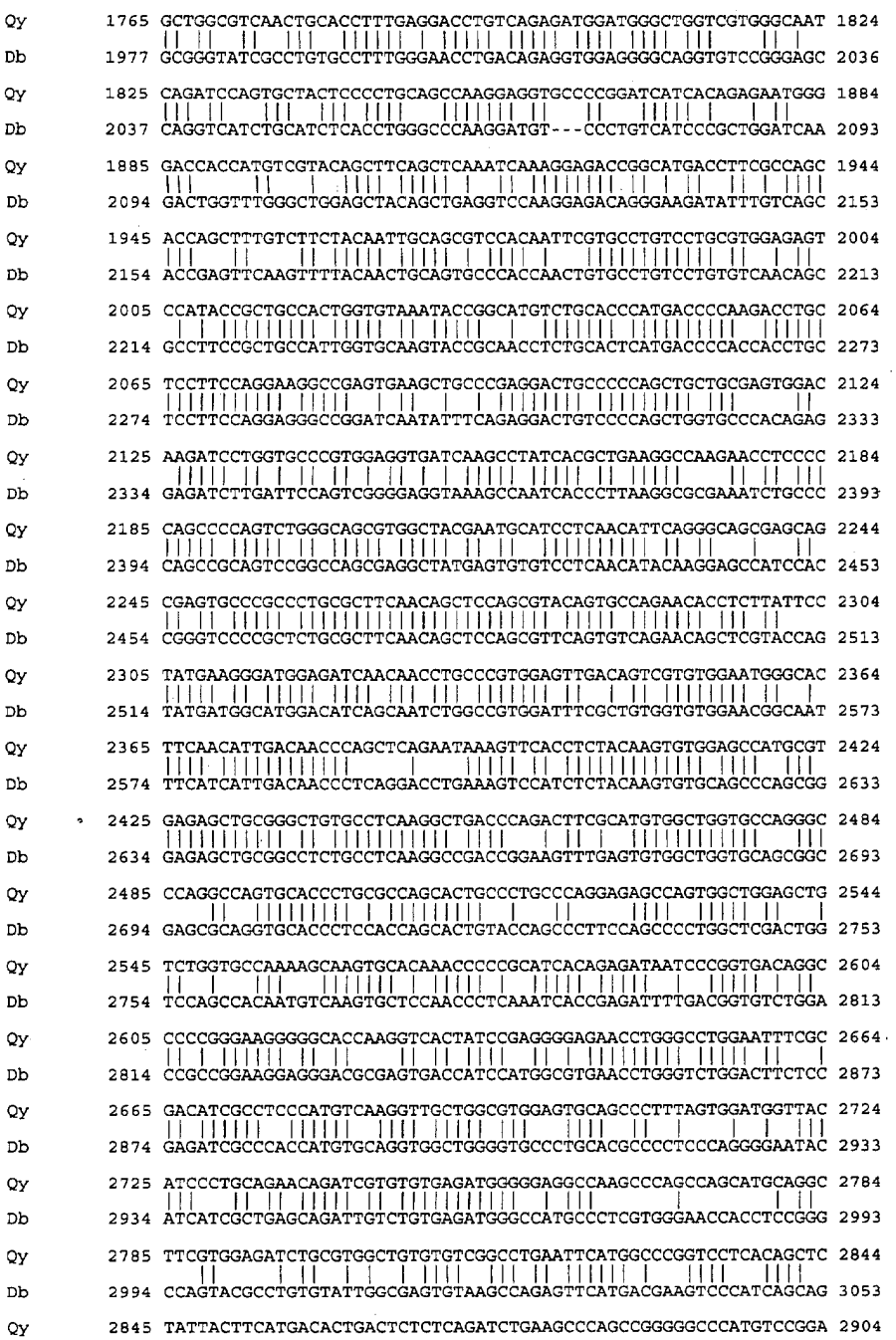
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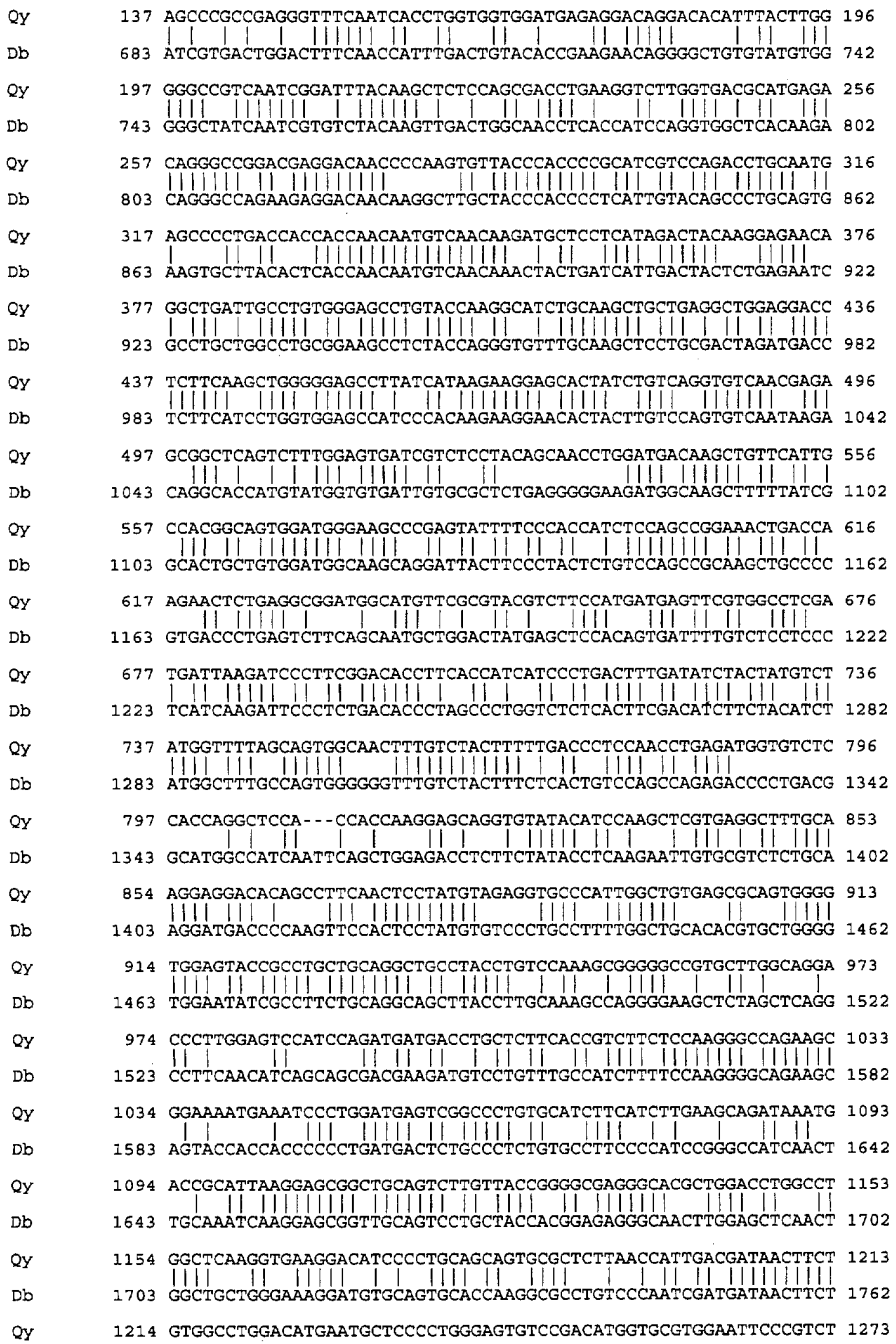
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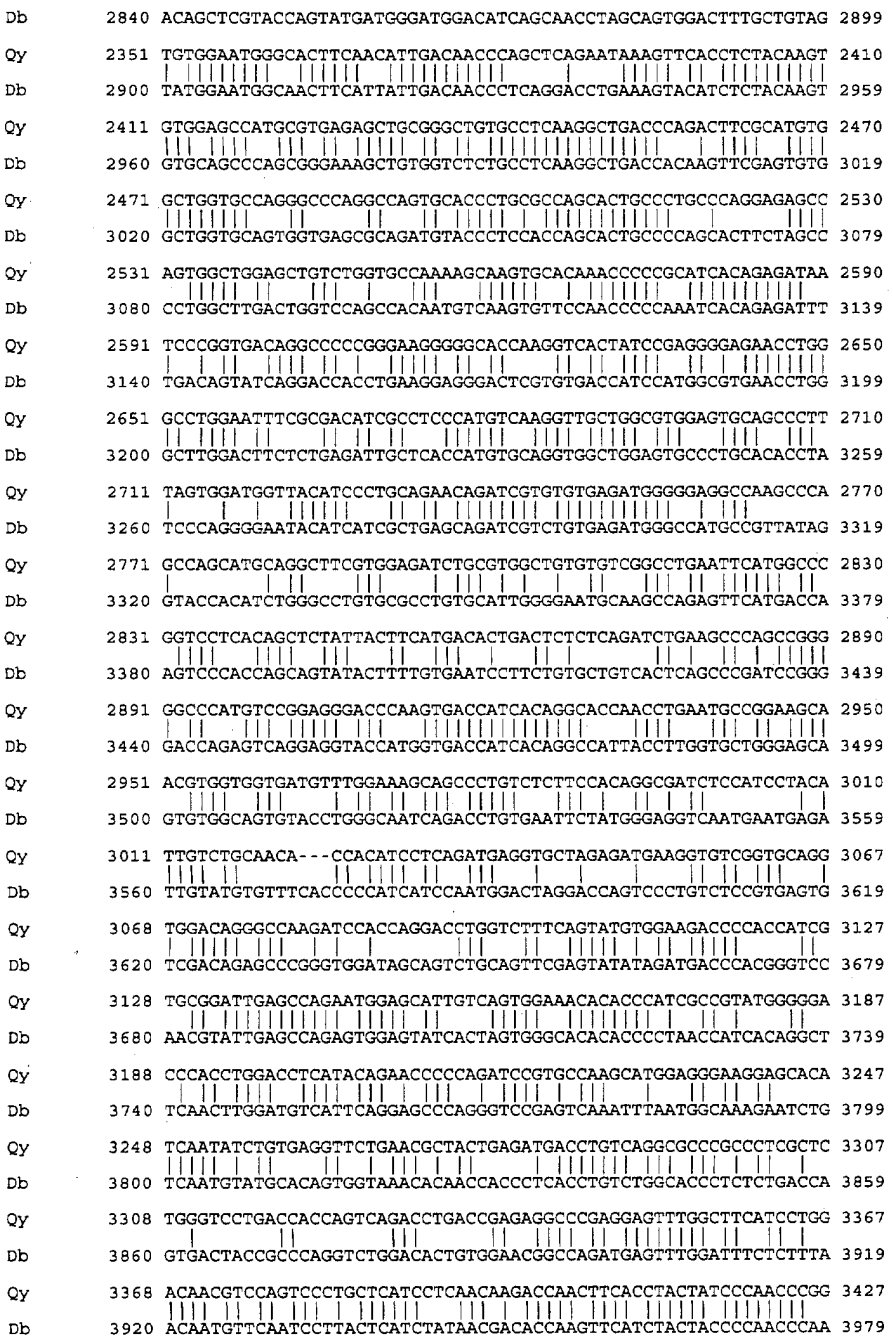
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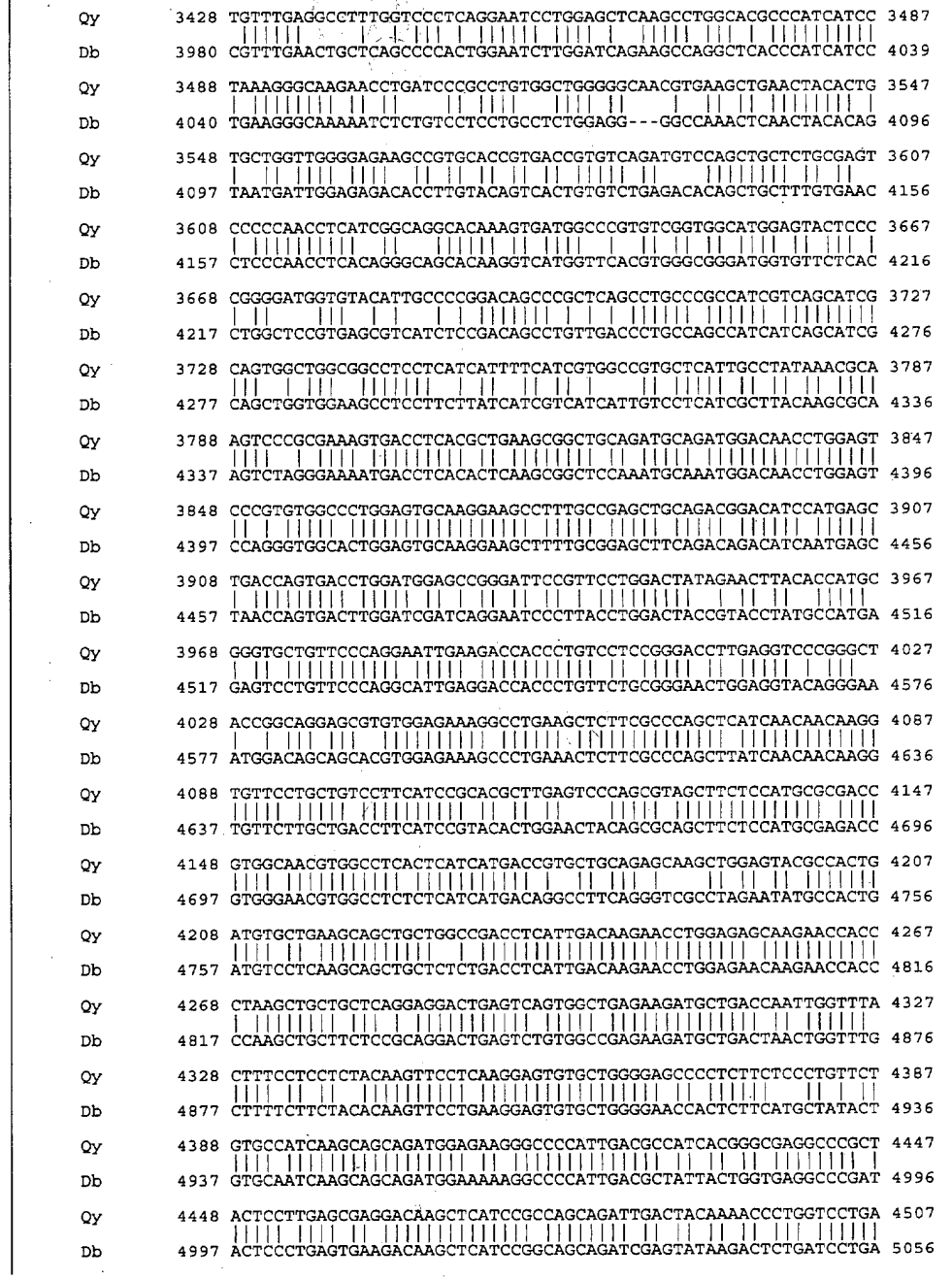
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  AUTHORS   Kameyama,T., Murakami,Y., Suto,F., Kawakami,A., Takagi,S.,
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  TITLE     Identification of plexin family molecules in mice
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  AUTHORS   Shimizu,M., Murakami,Y., Suto,F. and Fujisawa,H.
  TITLE     Determination of cell adhesion sites of neuropilin-1
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REFERENCE   3  (bases 1 to 6730)
  AUTHORS   Fujisawa,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-AUG-1996) Hajime Fujisawa, Nagoya University Graduate
            School of Science, Division of Biological Science; Furo-cho,
            Chikua-ku, Nagoya, Aichi 464-01, Japan
            (E-mail:fujisawa@bio.nagoya-u.ac.jp, Tel:052-789-2978,
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ORIGIN

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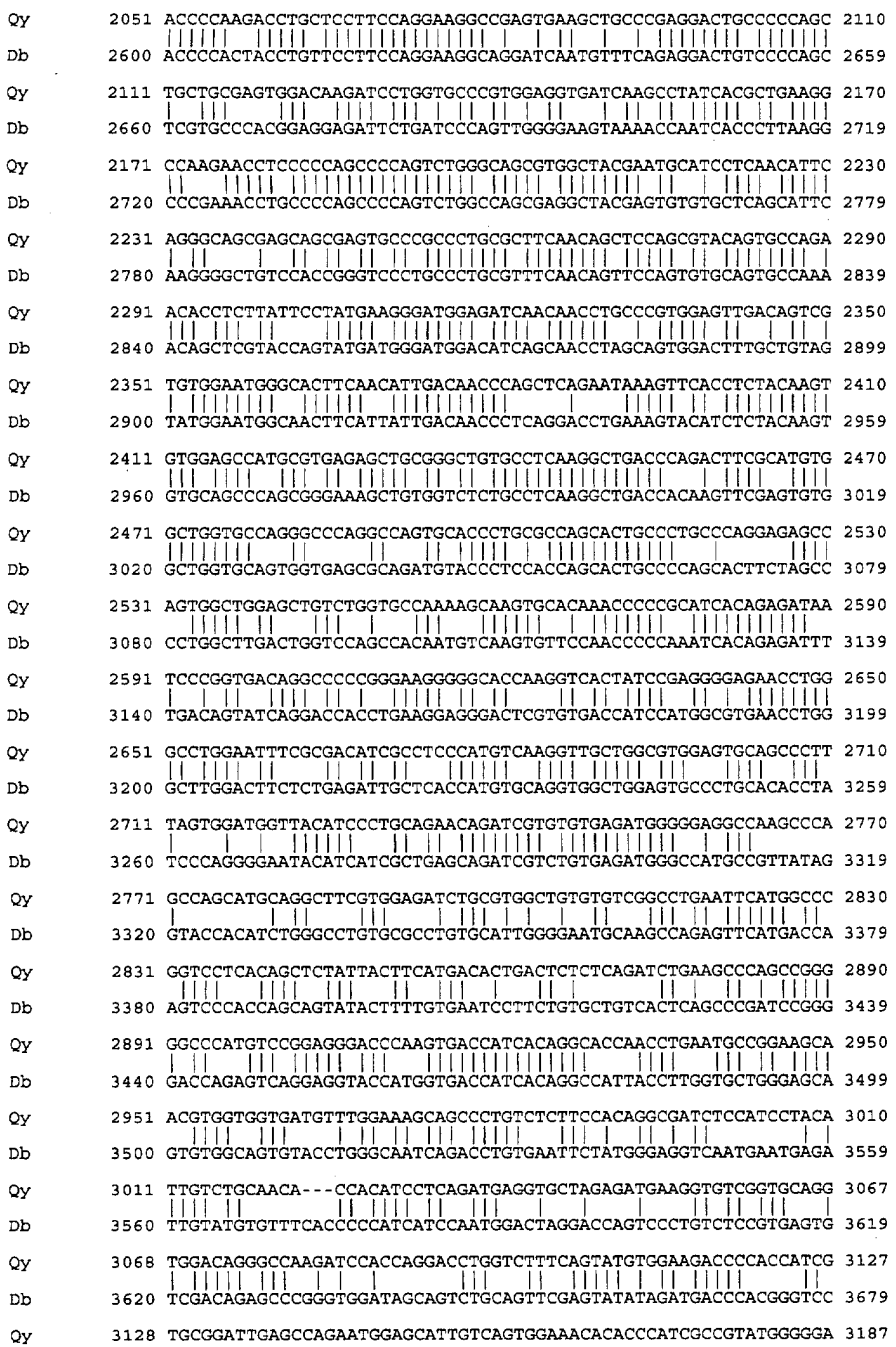

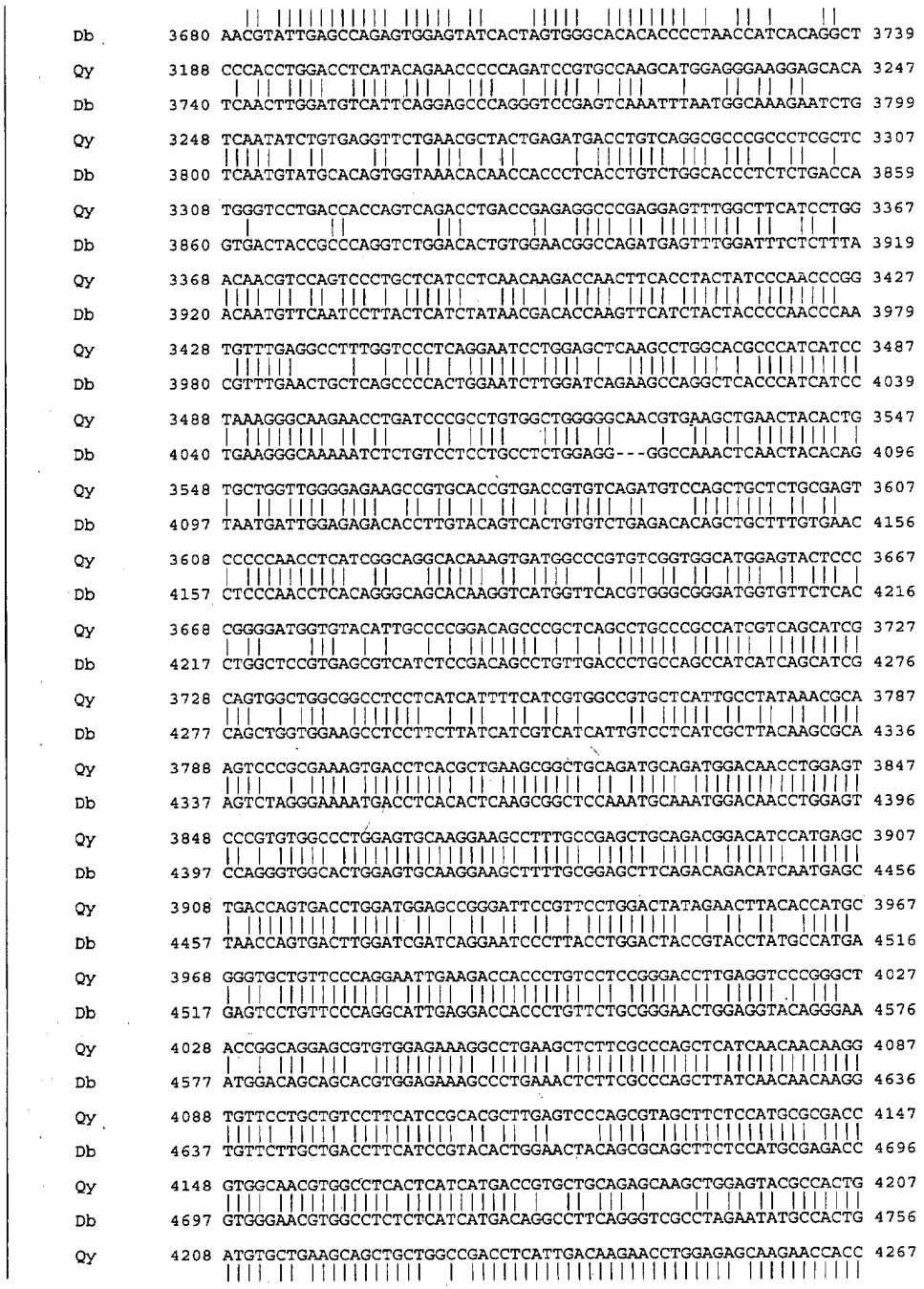

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  AUTHORS   Gururajan,R., Hafalia,A.J., Kallick,D.A., Patterson,C., Azimzai,Y.,
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            Yang,J., Zingler,K.A., Delegeane,A.M., Gietzen,K., Marcus,G.A.,
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            and Warren,B.A.
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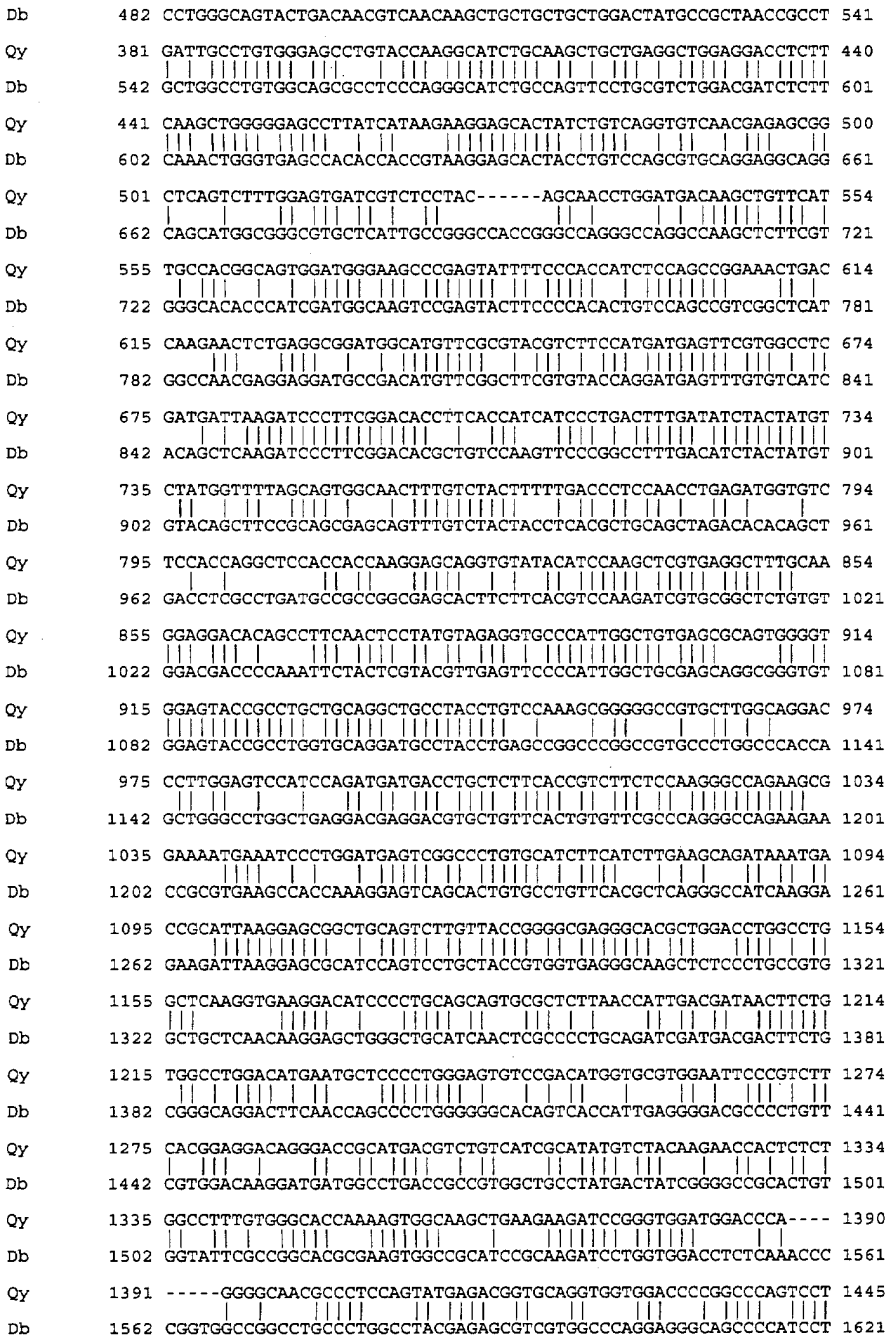
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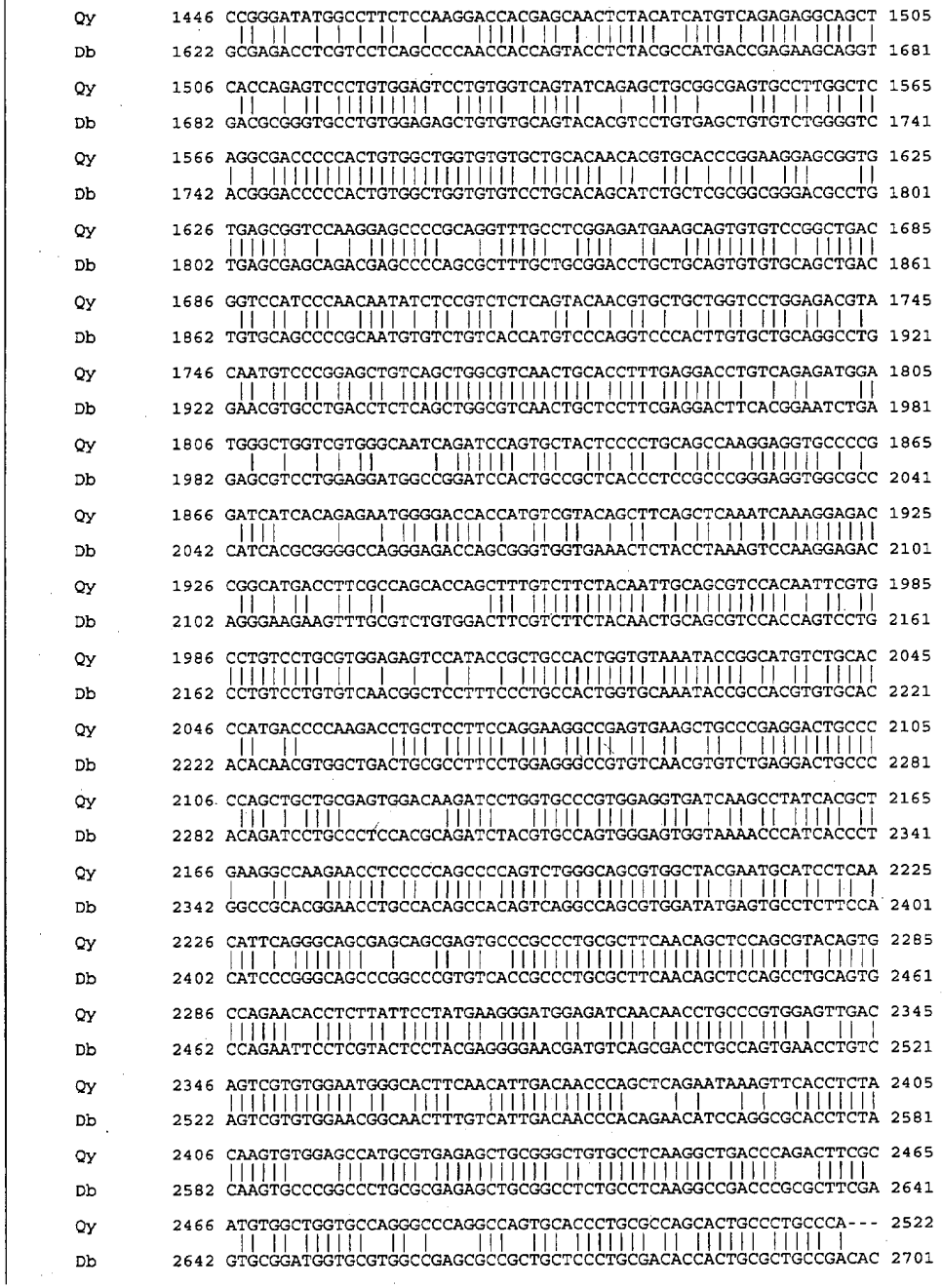
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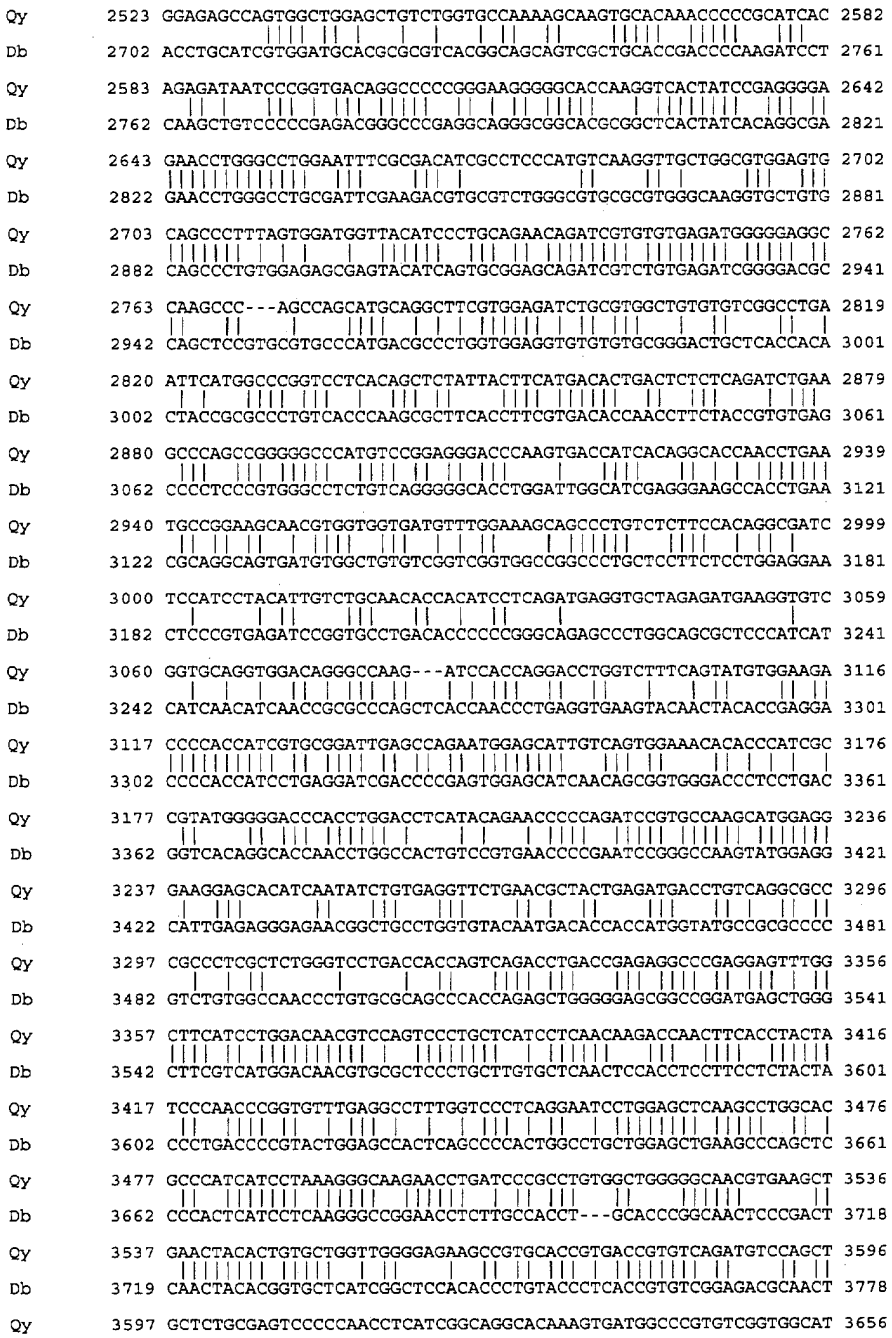
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  AUTHORS   Shimizu,M., Murakami,Y., Suto,F. and Fujisawa,H.
  TITLE     Determination of cell adhesion sites of neuropilin-1
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  AUTHORS   Fujisawa,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-AUG-1996) Hajime Fujisawa, Nagoya University Graduate
            School of Science, Division of Biological Science; Furo-cho,
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            (E-mail:fujisawa@bio.nagoya-u.ac.jp, Tel:052-789-2978,
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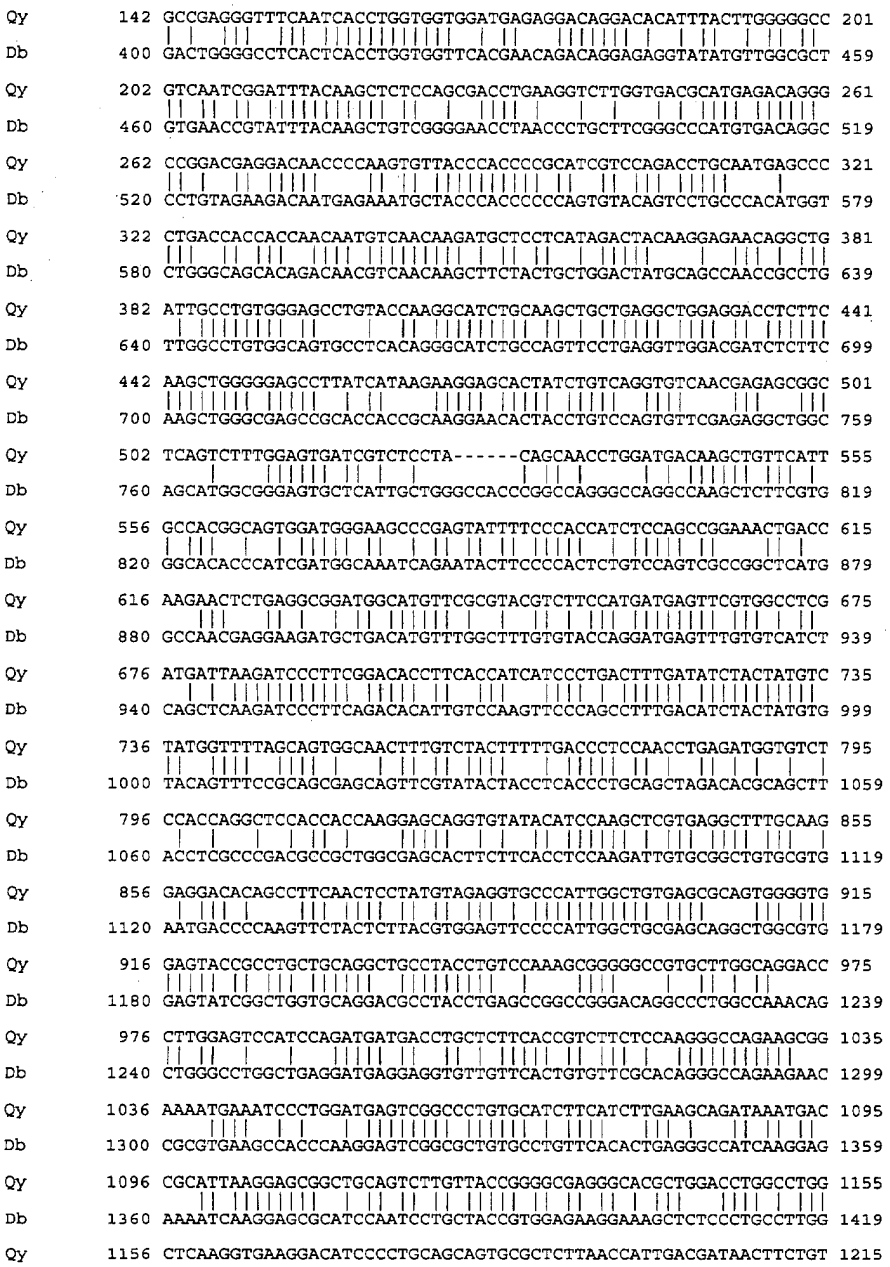

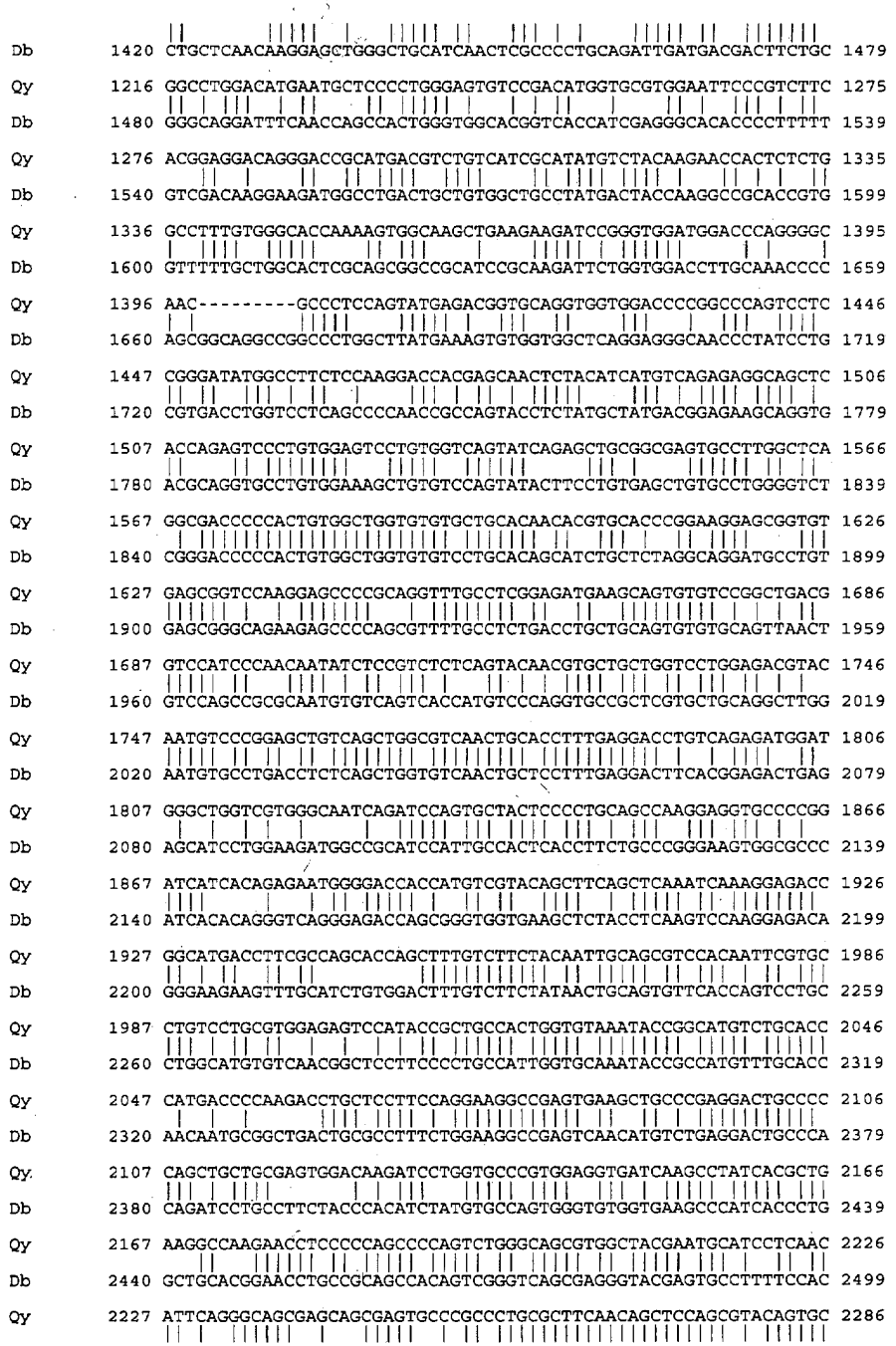

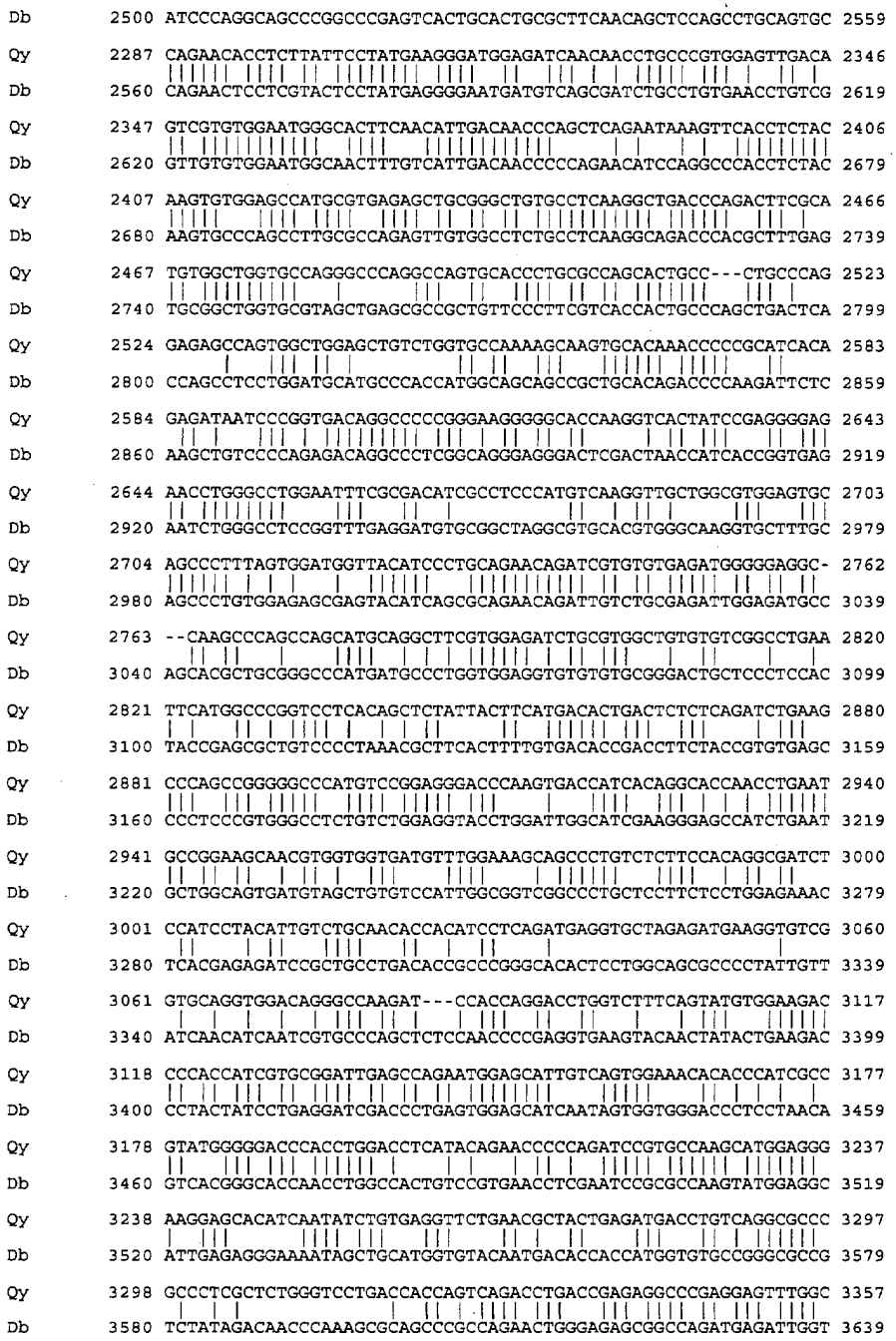
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REFERENCE   1  (bases 1 to 6039)
  AUTHORS   Maestrini,E., Tamagnone,L., Tamanini,F., Cremona,O., Gulisano,M.,
            Longati,P., Bione,S., Neel,B., Toniolo,D. and Comoglio,P.M.
  TITLE     A novel family of transmembrane proteins with homology to the
            cMet/HGF receptors
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 6039)
  AUTHORS   Toniolo,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JUN-1995) D. Toniolo, Instituto di Genetica
            Biochimica ed Evoluzionistica, CNR, Via Abbiategrasso 207, 27100
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ORIGIN

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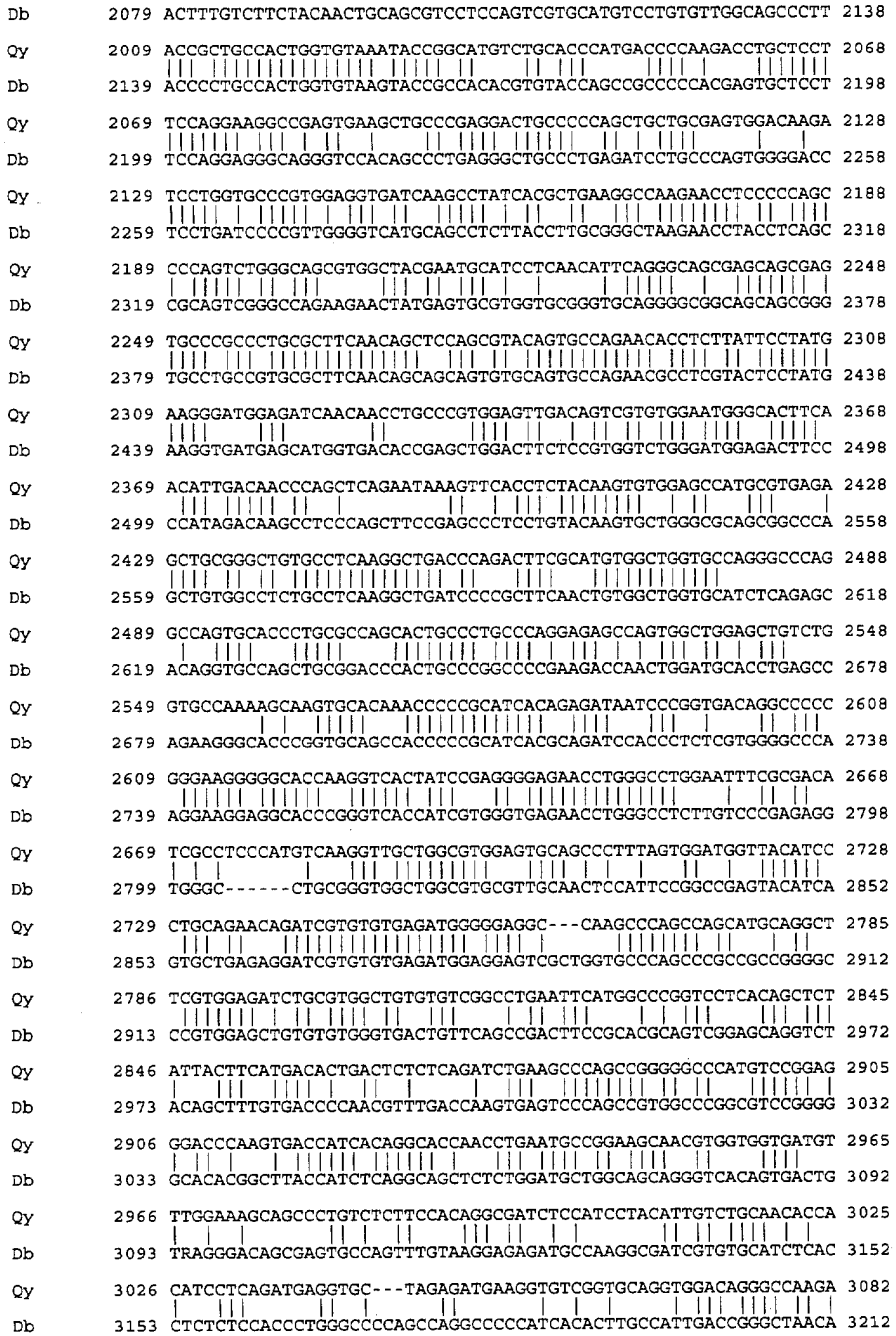
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VERSION AX686475.1 GI:29372168
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REFERENCE 1
AUTHORS Edinger,S., Macdougall,J.R., Millet,I., Ellerman,K., Stone,D.J.,
Gerlach,V., Grosse,W.M., Alsobrook,J.P., Lepley,D.M., Rieger,D.,
Burgess,C.E., Casman,S.J., Spytek,K.A., Boldog,F.L., Li,L.,
Padigaru,M., Mishra,V., Patturajan,M., Shenoy,S., Rastelli,L.,
Tchernev,V.T., Vernet,C.A., Zerhusen,B.D., Malyankar,U.M., Guo,Y.,
Miller,C.E. and Gangolli,E.A.
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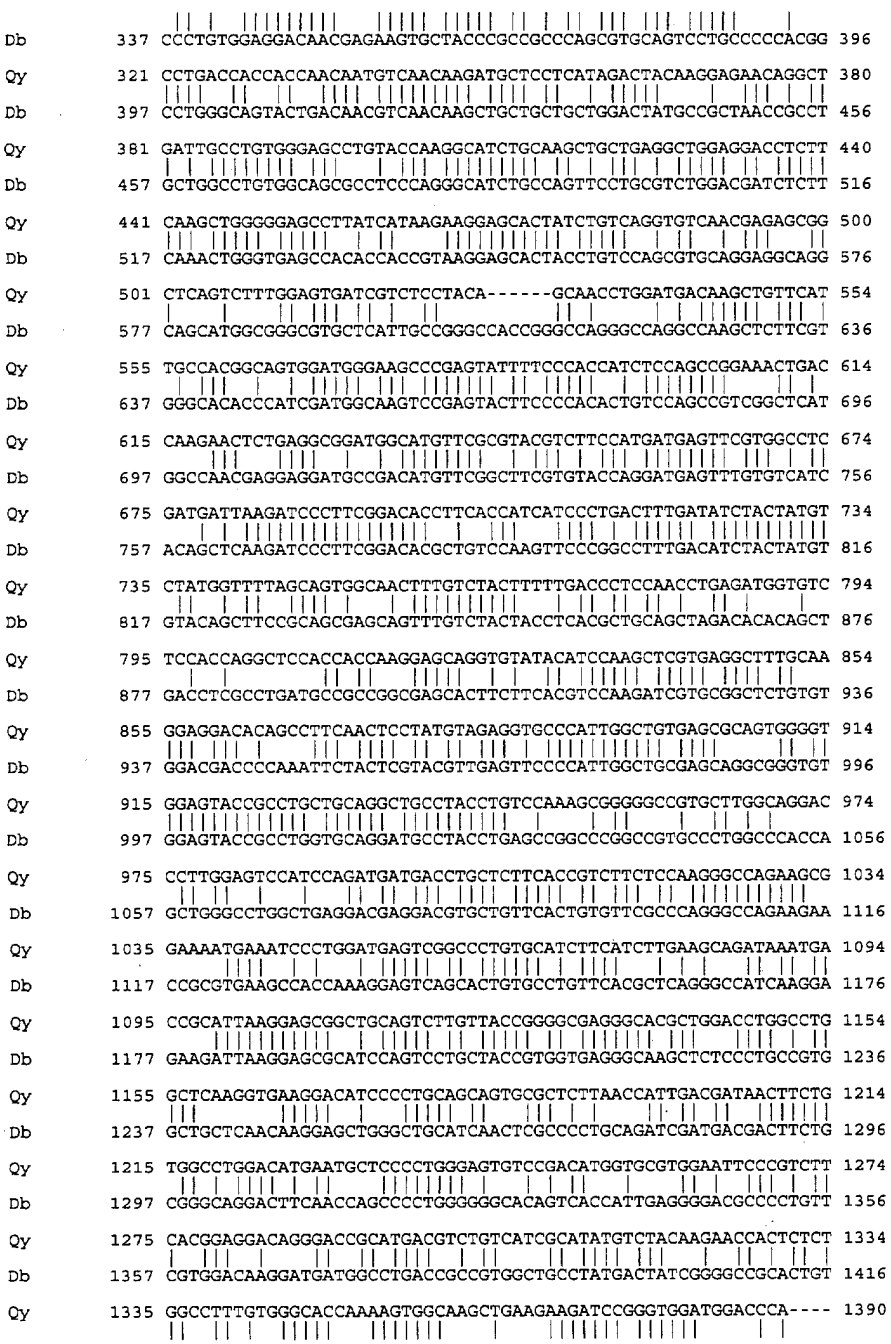

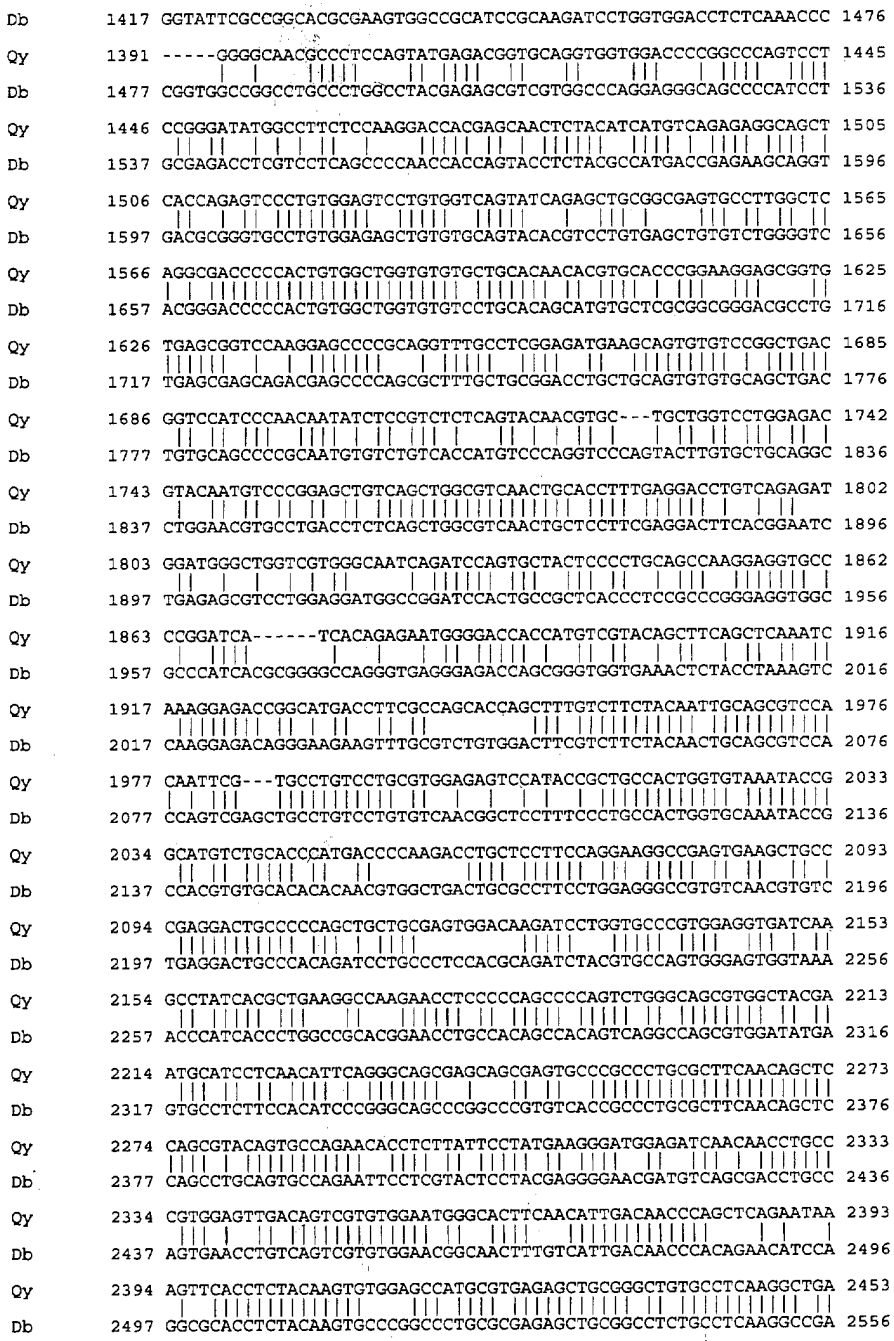

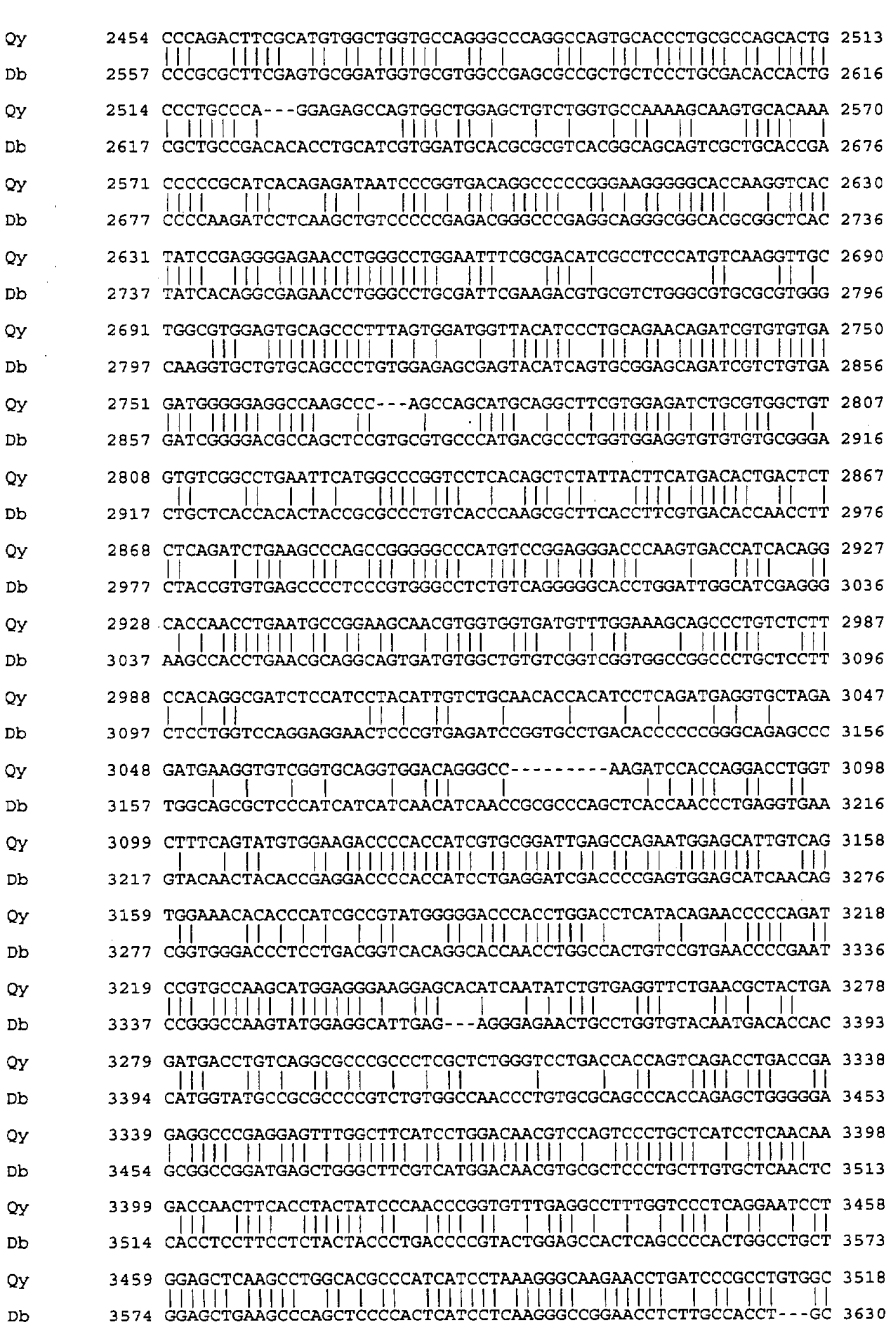
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  AUTHORS   Maestrini,E., Tamagnone,L., Longati,P., Cremona,O., Gulisano,M.,
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  TITLE     A family of transmembrane proteins with homology to the
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 93 (2), 674-678 (1996)
  MEDLINE   96149362
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  AUTHORS   Tamagnone,L., Artigiani,S., Chen,H., He,Z., Ming,G.L., Song,H.L.,
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            Tessier-Lavigne,M. and Comoglio,P.M.
  TITLE     Plexins are a large family of receptors for transmembrane,
            secreted, and GPI-anchored semaphorins in vertebrates
  JOURNAL   Cell 99 (1), 71-80 (1999)
  MEDLINE   99449305
   PUBMED   10520995
REFERENCE   3
  AUTHORS   Toniolo,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-JUN-1995) D. Toniolo, Instituto di Genetica
            Biochimica ed Evoluzionistica, CNR, Via Abbiategrasso 207, 27100
            Pavia, ITALY
  REMARK    Revised by [4]
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  AUTHORS   Tamagnone,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-AUG-1998) L. Tamagnone, University of Torino, IRCC,
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ORIGIN

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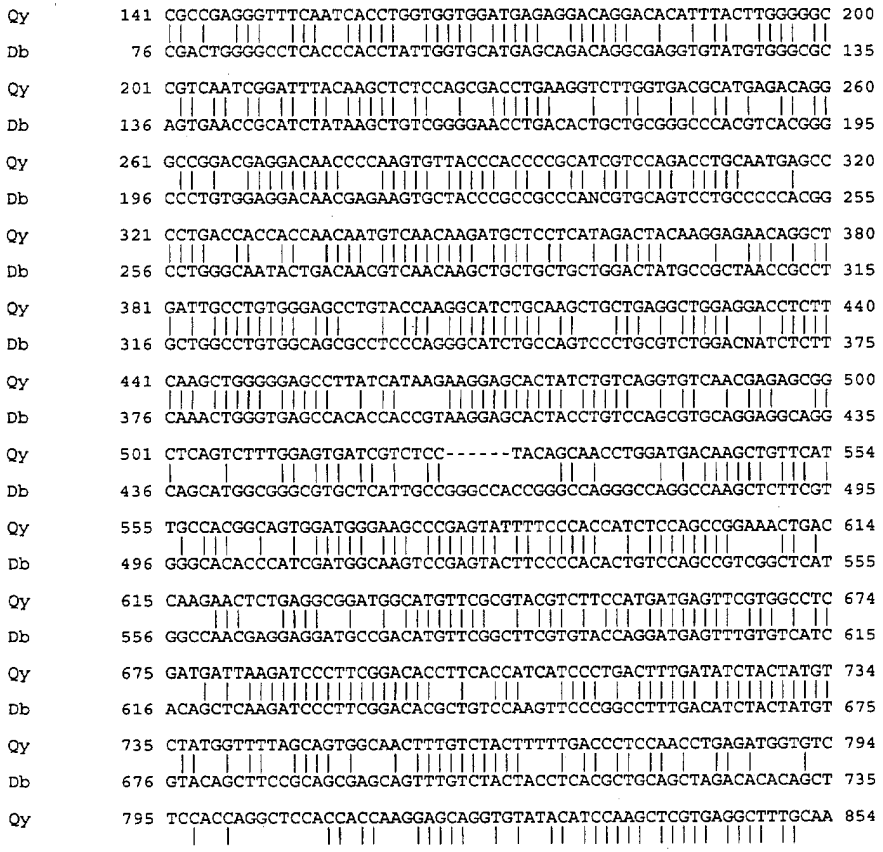

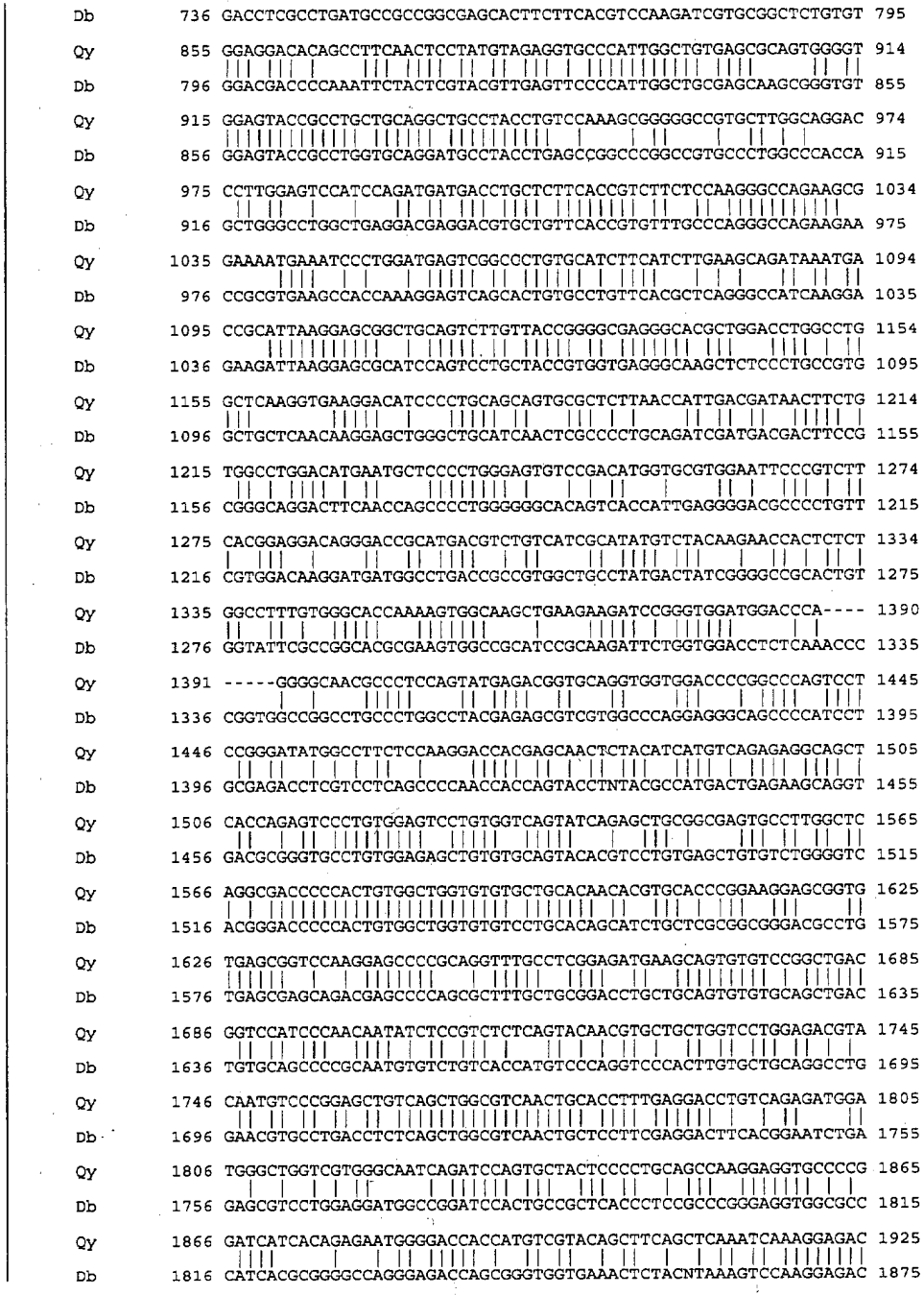

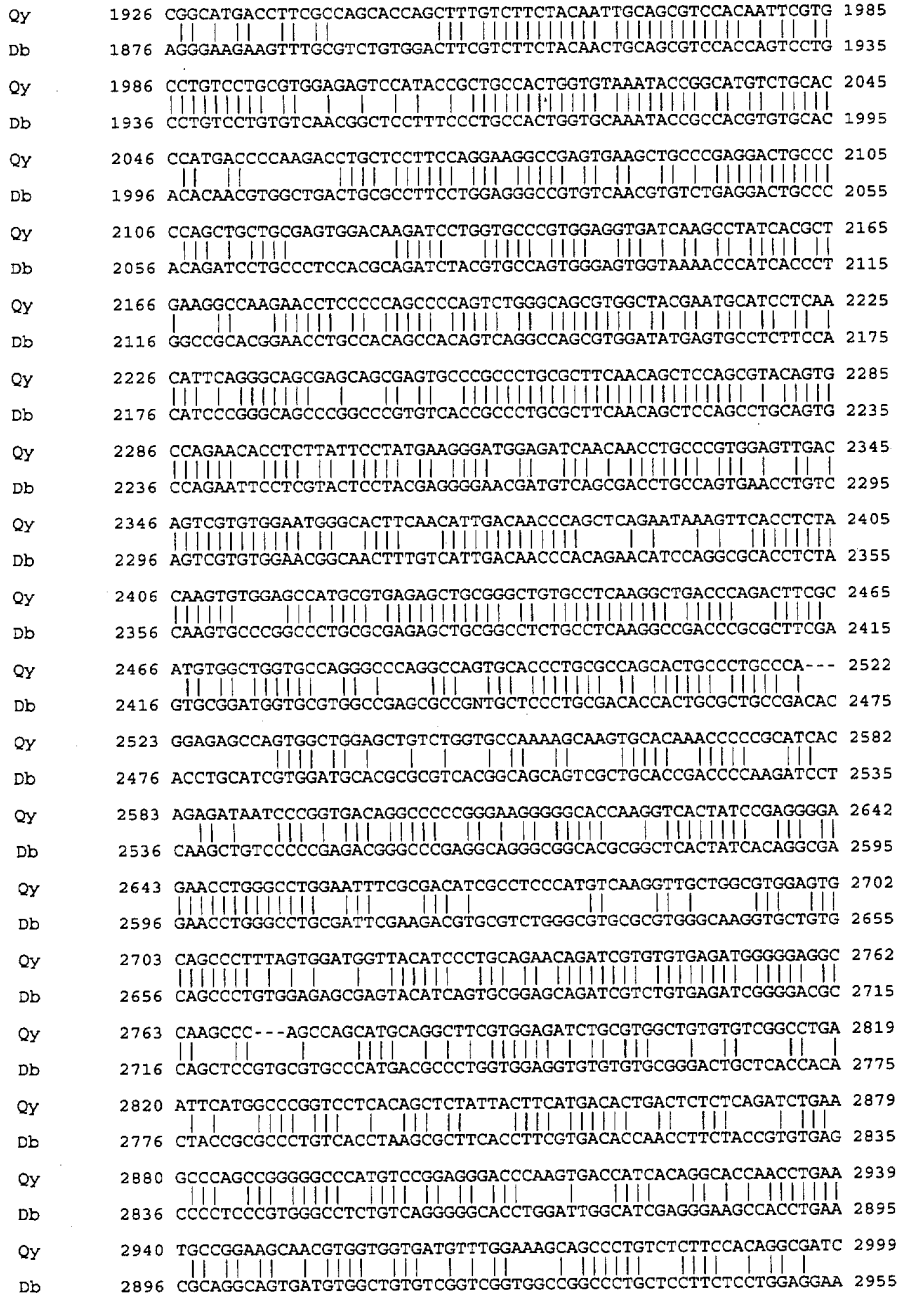
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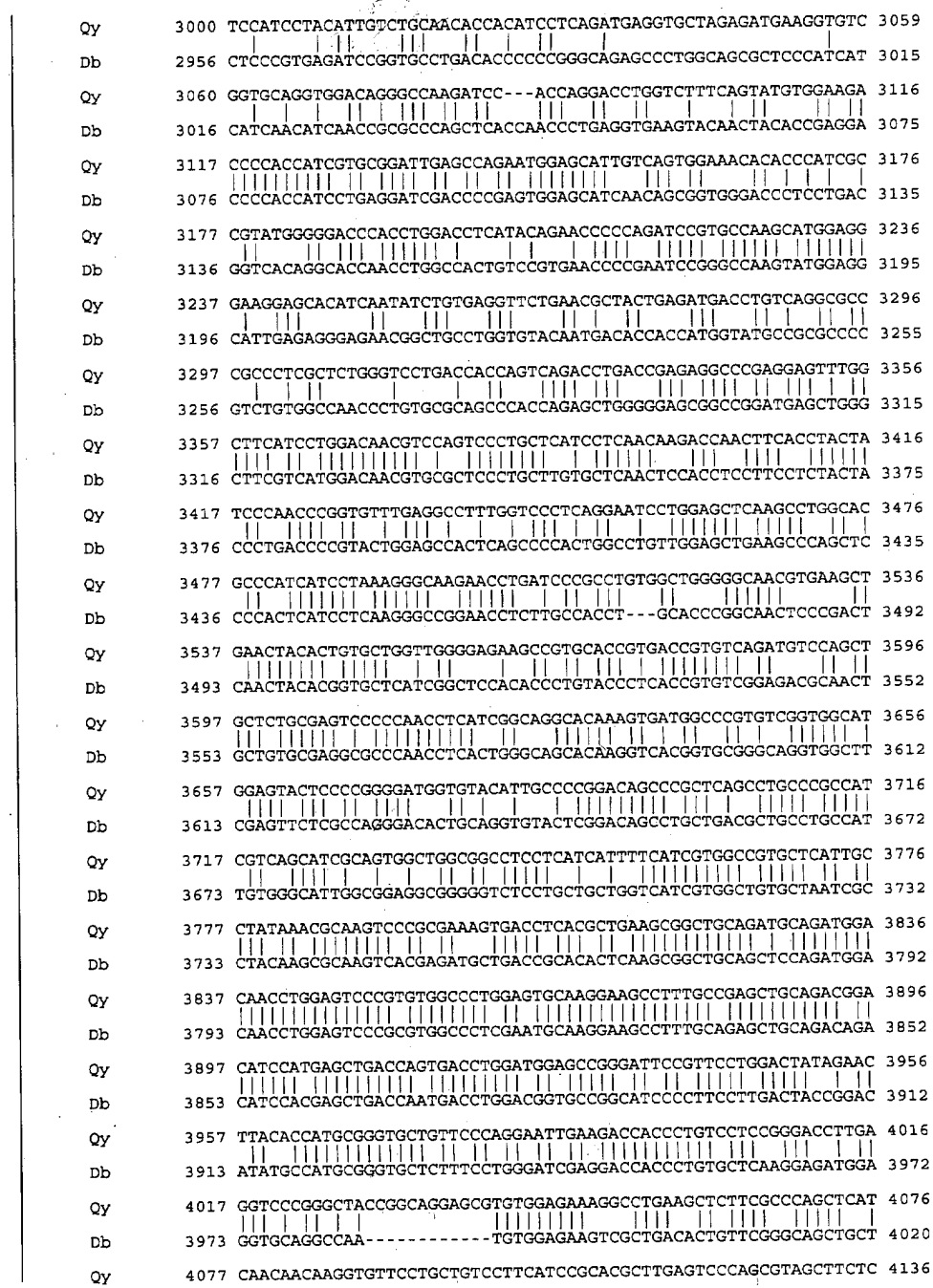
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DEFINITION  Mus musculus mRNA for mKIAA0463 protein.
ACCESSION   AK122289
VERSION     AK122289.1  GI:28972234
KEYWORDS    FLI_CDNA.
SOURCE      Mus musculus (house mouse)
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Okazaki,N., Kikuno,R., Ohara,R., Inamoto,S., Aizawa,H., Yuasa,S.,
            Nakajima,D., Nagase,T., Ohara,O. and Koga,H.
  TITLE     Prediction of the coding sequences of mouse homologues of KIAA
            gene: II. The complete nucleotide sequences of 400 mouse
            KIAA-homologous cDNAs identified by screening of terminal sequences
            of cDNA clones randomly sampled from size-fractionated libraries
  JOURNAL   DNA Res. 10, 35-48 (2003)
REFERENCE   2  (bases 1 to 6893)
  AUTHORS   Okazaki,N., Kikuno,R., Nagase,T., Ohara,O. and Koga,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-FEB-2003) Hisashi Koga, Kazusa DNA Research
            Institute, Laboratory for Genome Informatics; 2-6-7
            Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan
            (E-mail:mouse@kazusa.or.jp, Tel:81-438-52-3919, Fax:81-438-52-3918)
COMMENT     The CREATE program supported by Japan science and technology
            corporation; cDNA full insert sequencing: Kazusa DNA Research
            Institute; cDNA library construction, clone selection and 5'- &
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ORIGIN

Query Match 42.0%; Score 2387.8; DB 10; Length 6893;
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Matches 3245; Conservative 0; Mismatches 1342; Indels 12; Gaps 4;

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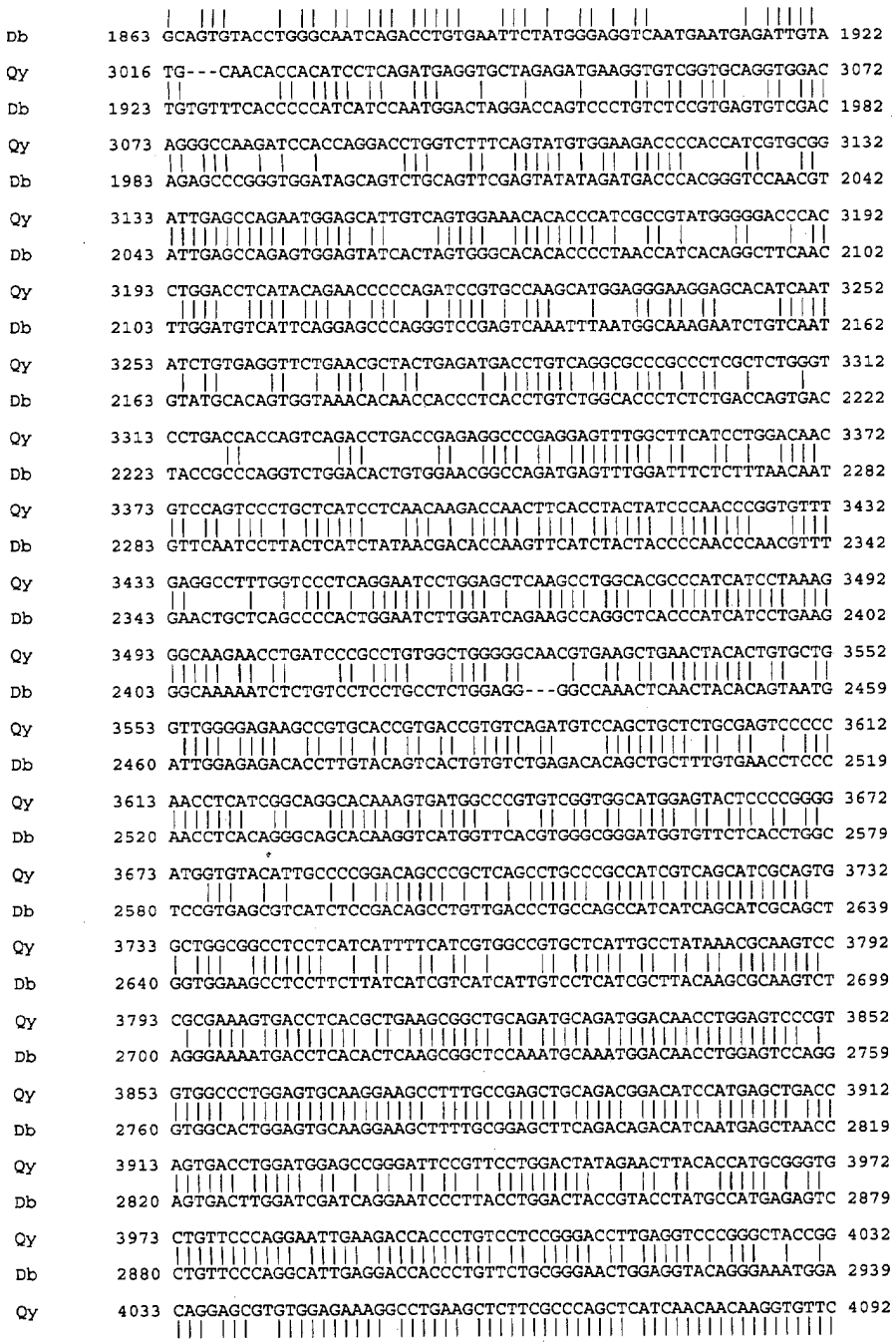
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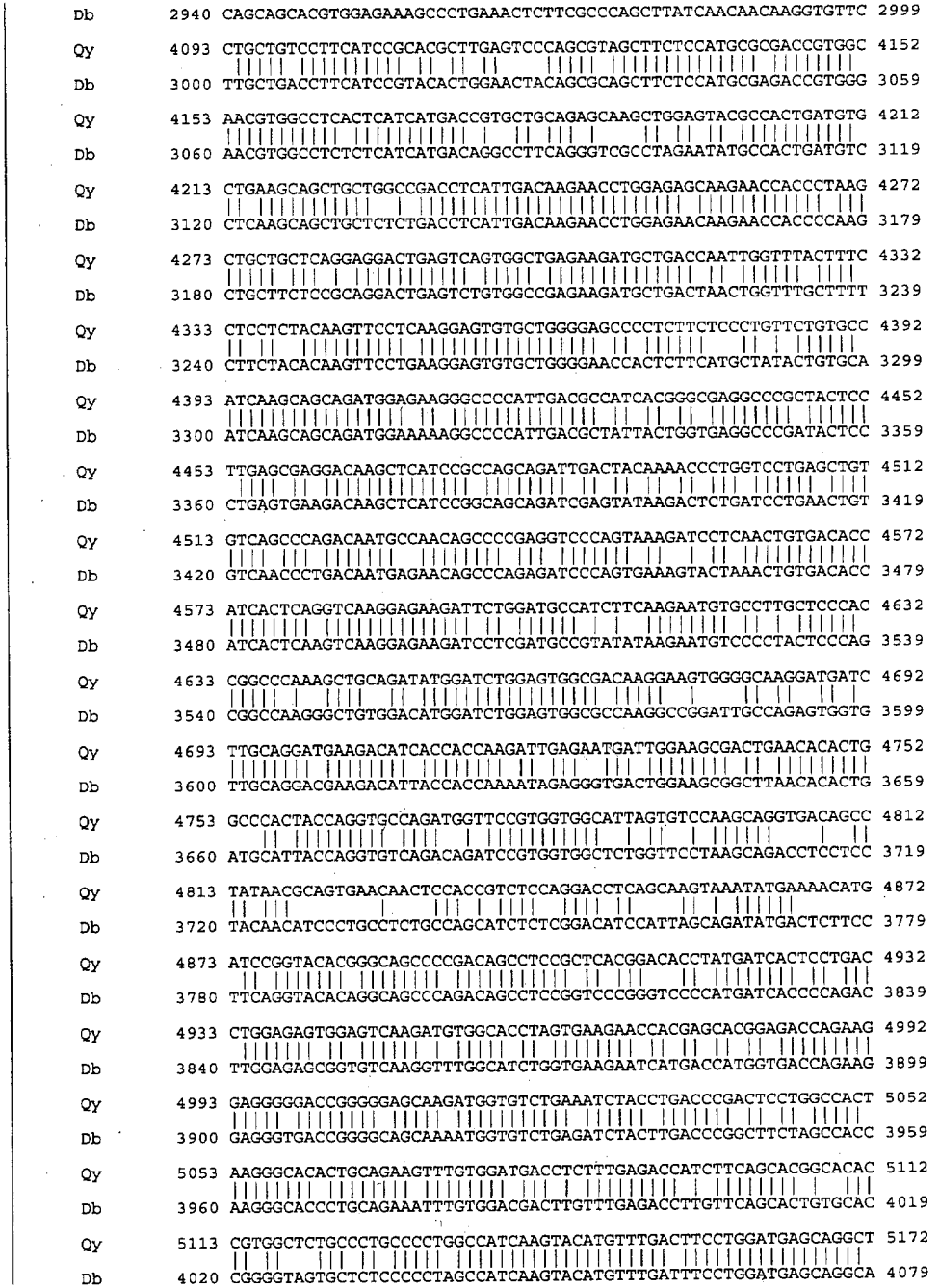
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RESULT 14
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DEFINITION  Xenopus laevis mRNA for plexin, complete cds.
ACCESSION   D38175
VERSION     D38175.1  GI:961514
KEYWORDS    plexin; calcium-dependent cell adhesion molecule; B2; type I
            membrane protein.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
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REFERENCE   1  (sites)
  AUTHORS   Ohta,K., Mizutani,A., Kawakami,A., Murakami,Y., Kasuya,Y.,
            Takagi,S., Tanaka,H. and Fujisawa,H.
  TITLE     Plexin: a novel neuronal cell surface molecule that mediates cell
            adhesion via a homophilic binding mechanism in the presence of
            calcium ions
  JOURNAL   Neuron 14 (6), 1189-1199 (1995)
  MEDLINE   95329274
   PUBMED   7605632
REFERENCE   2  (bases 1 to 6163)
  AUTHORS   Ohta,K.
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 6163)
  AUTHORS   Ohta,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-SEP-1994) Kunimasa Ohta, Kumamoto University Graduate
            School of Medical Sciences, Dept. of Neuroscience and Immunology;
            4-24-1 Kuhonji, Kumamoto, Kumamoto 862, Japan
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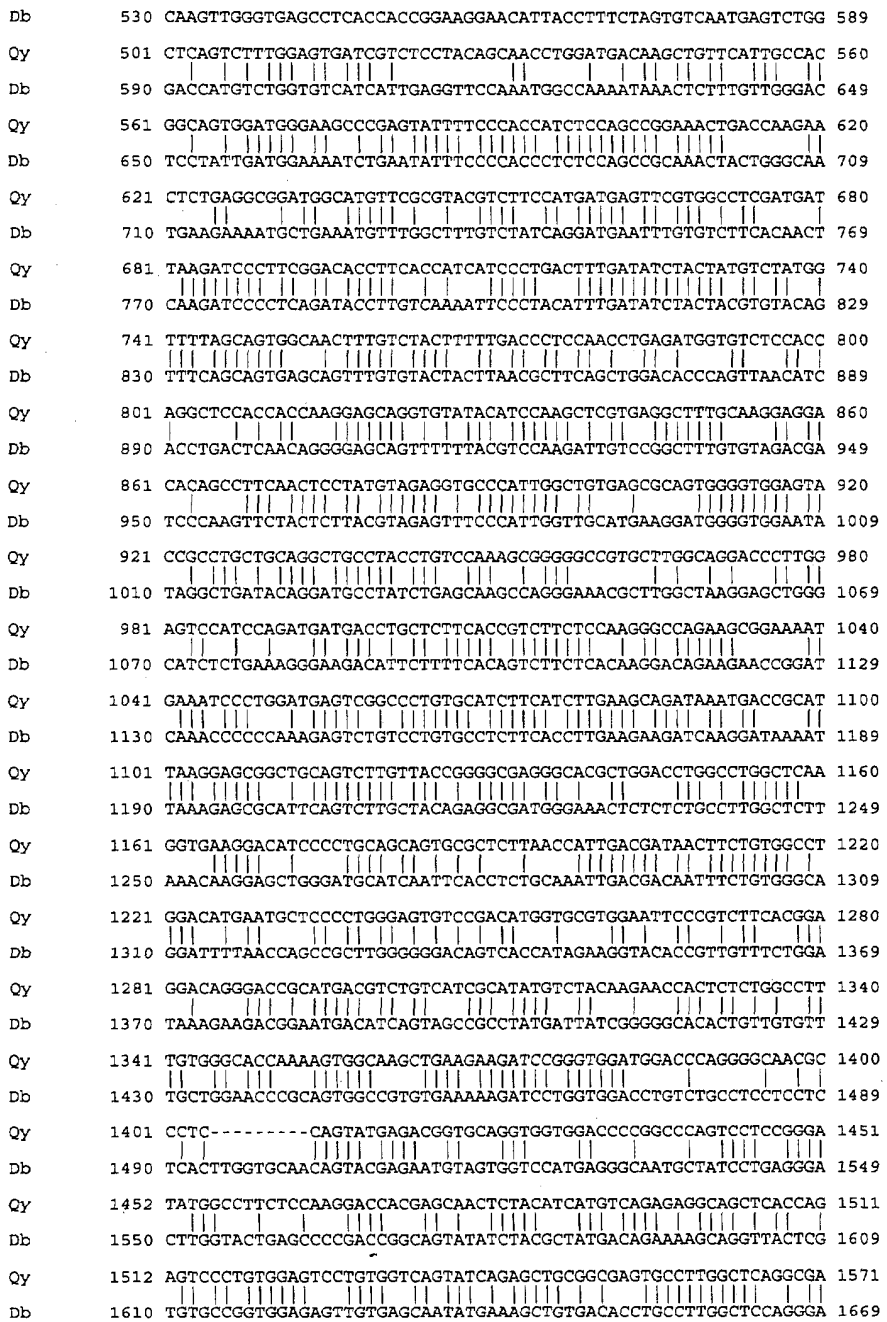
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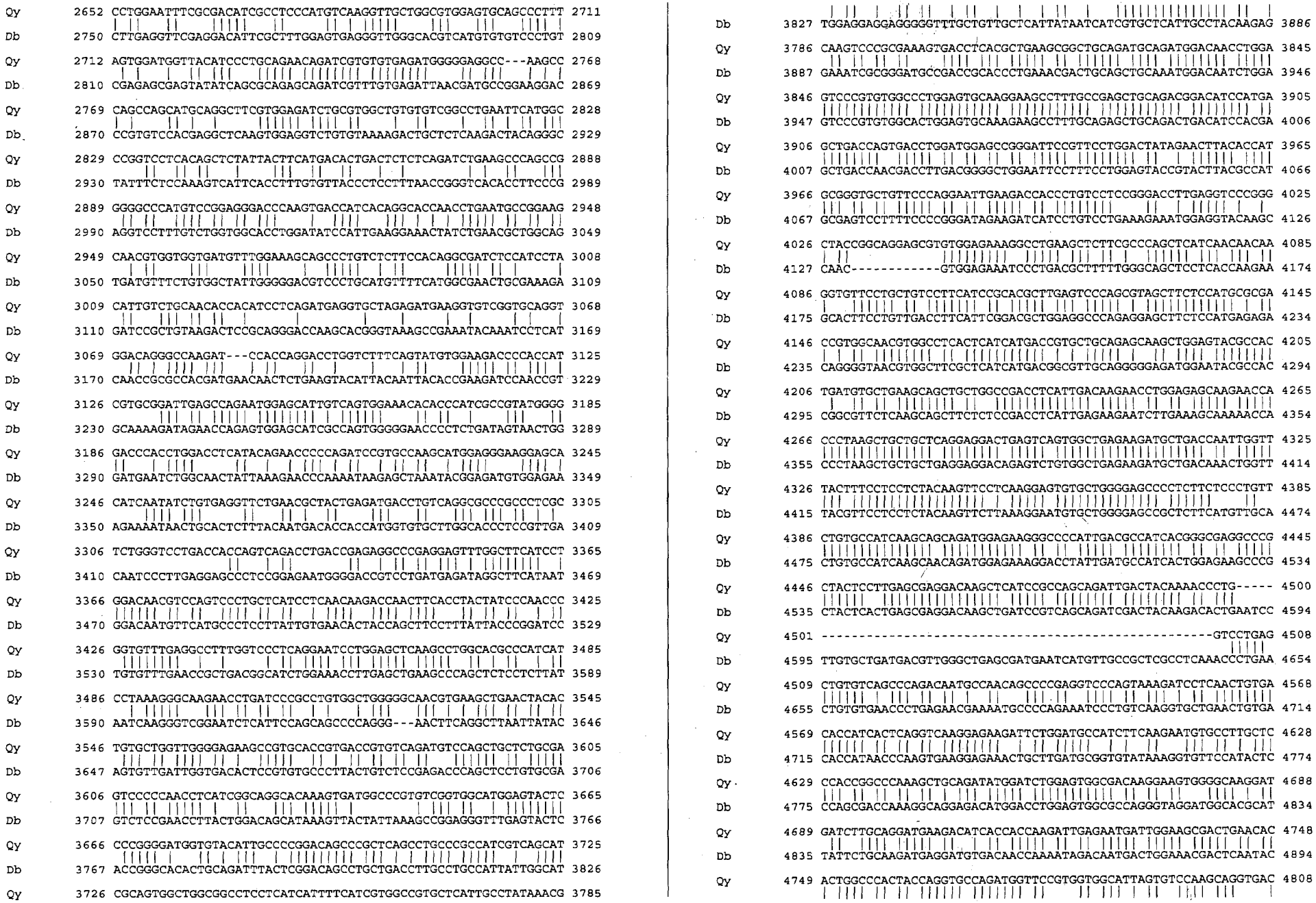
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RESULT 15
D86950

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ACCESSION   D86950
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KEYWORDS    plexin 3.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (sites)
  AUTHORS   Kameyama,T., Murakami,Y., Suto,F., Kawakami,A., Takagi,S.,
            Hirata,T. and Fujisawa,H.
  TITLE     Identification of plexin family molecules in mice
  JOURNAL   Biochem. Biophys. Res. Commun. 226 (2), 396-402 (1996)
  MEDLINE   96400270
   PUBMED   8806646
REFERENCE   2  (sites)
  AUTHORS   Shimizu,M., Murakami,Y., Suto,F. and Fujisawa,H.
  TITLE     Determination of cell adhesion sites of neuropilin-1
  JOURNAL   J. Cell Biol. 148 (6), 1283-1293 (2000)
  MEDLINE   20191894
   PUBMED   10725340
REFERENCE   3  (bases 1 to 5982)
  AUTHORS   Fujisawa,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-AUG-1996) Hajime Fujisawa, Nagoya University Graduate
            School of Science, Division of Biological Science; Furo-cho,
            Chikua-ku, Nagoya, Aichi 464-01, Japan
            (E-mail:fujisawa@bio.nagoya-u.ac.jp, Tel:052-789-2978,
            Fax:052-789-2979)
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ORIGIN
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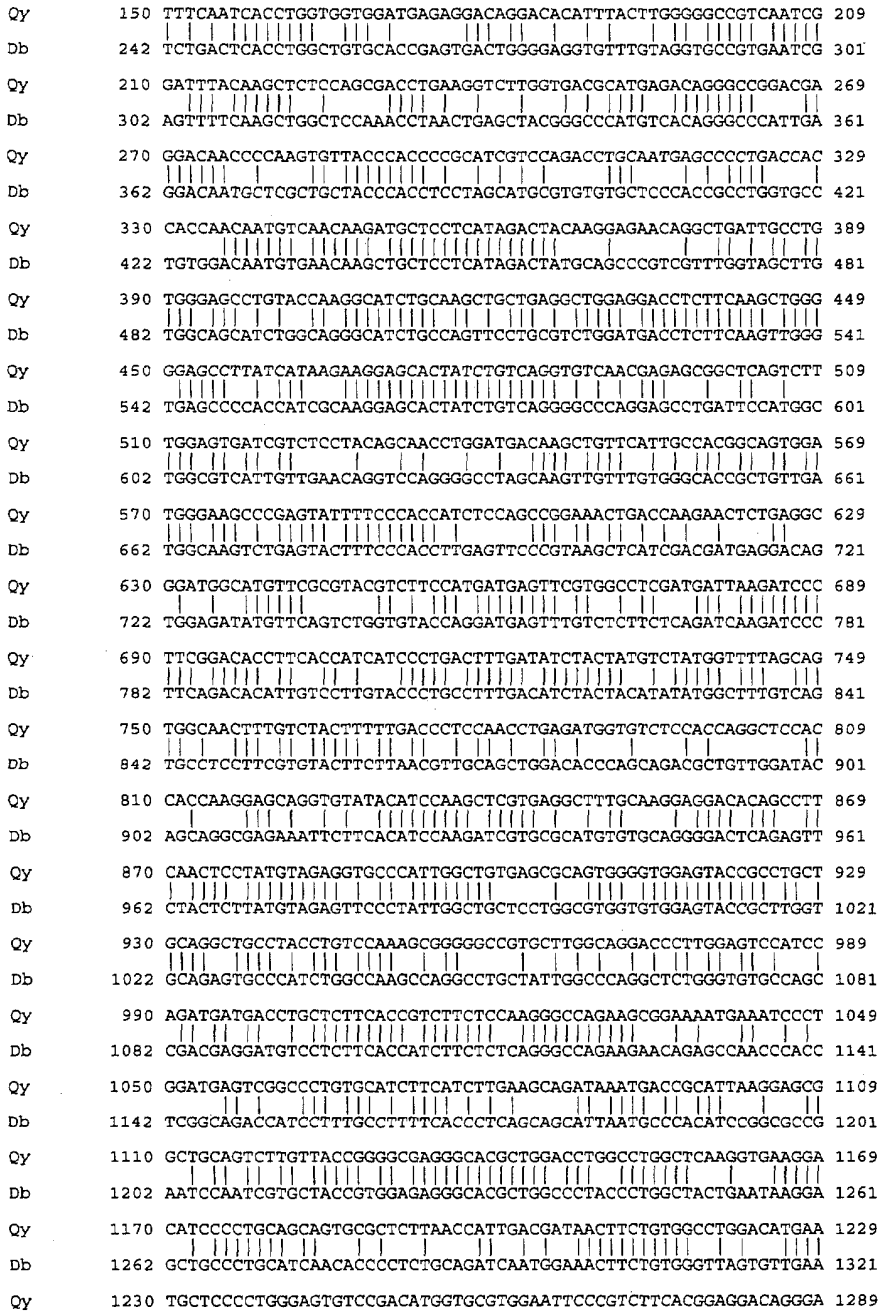

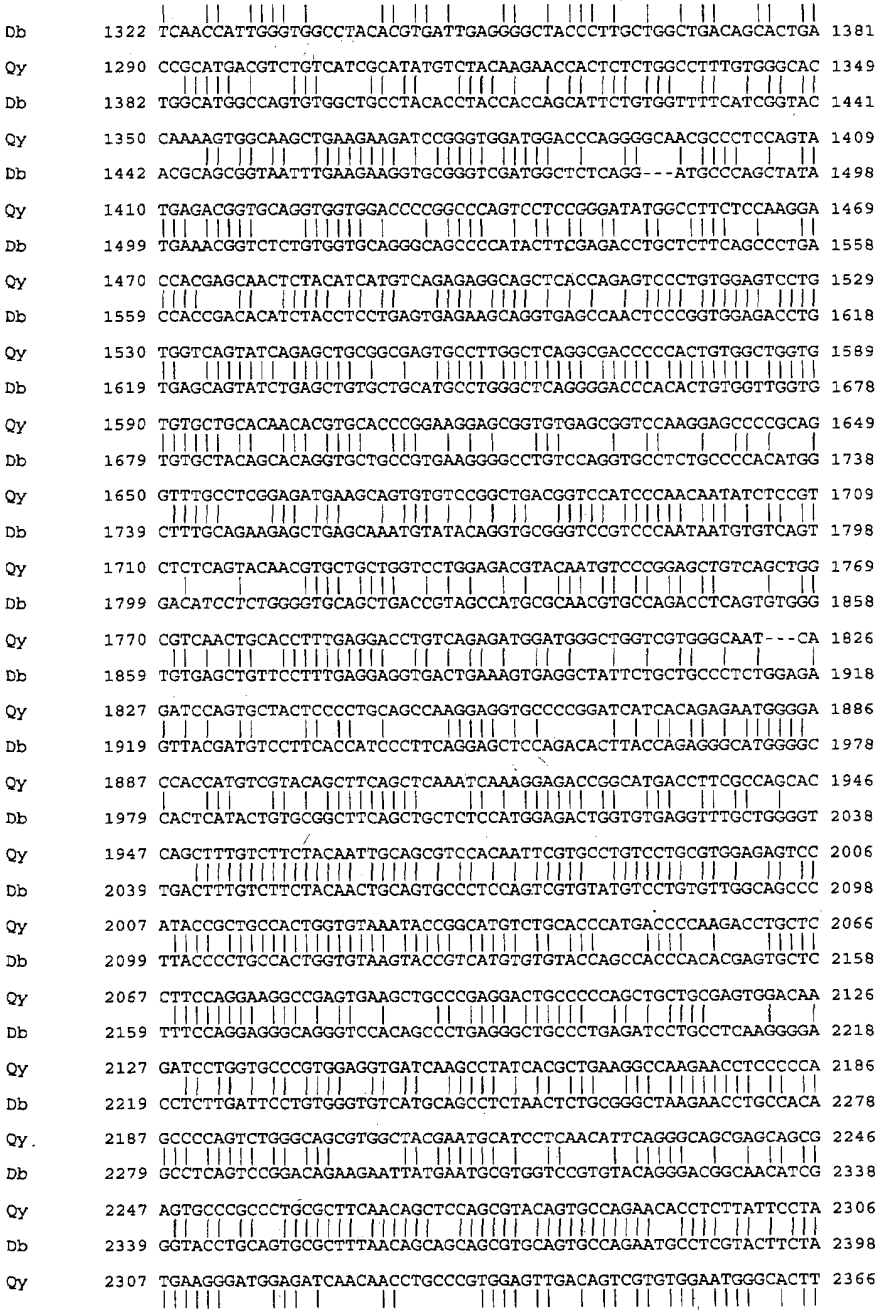

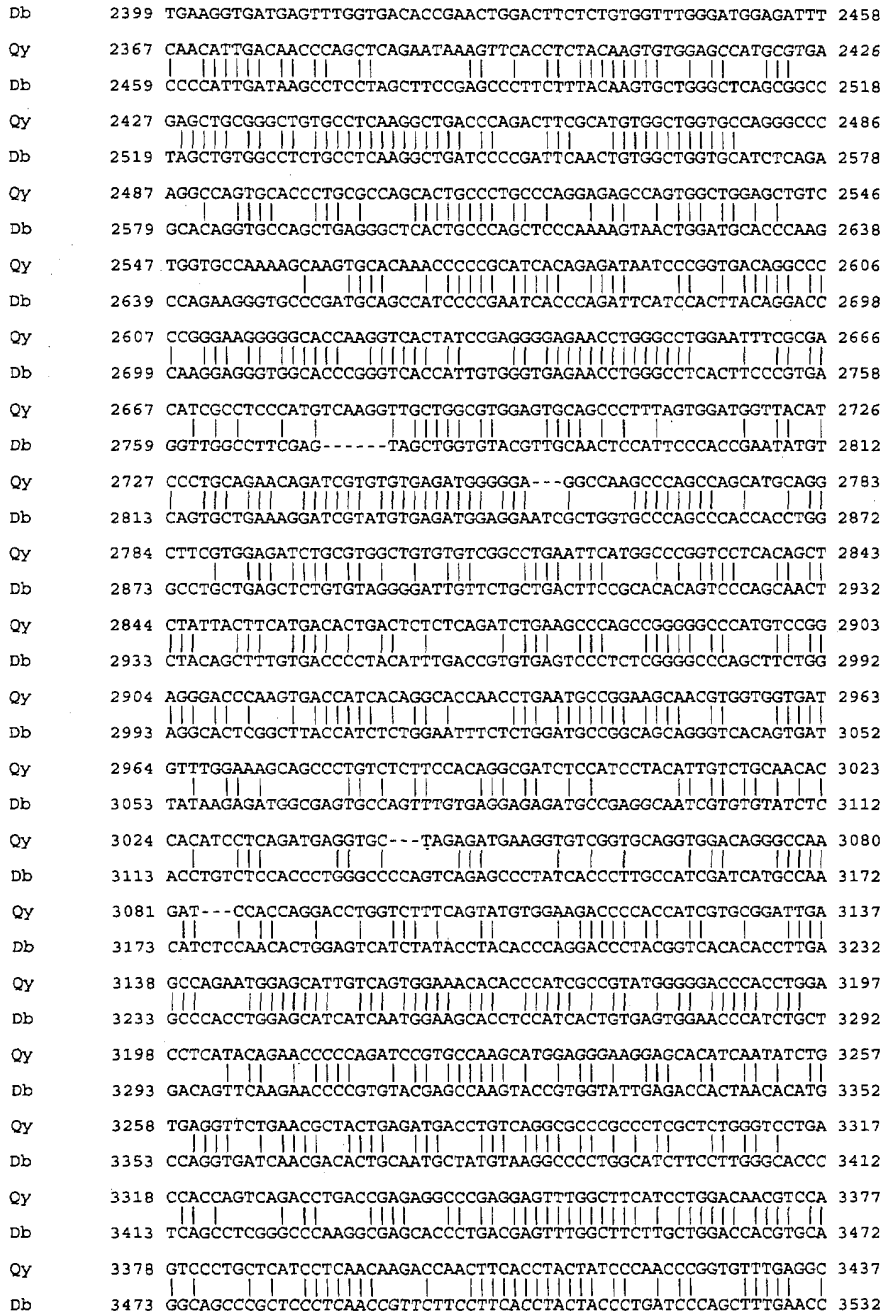

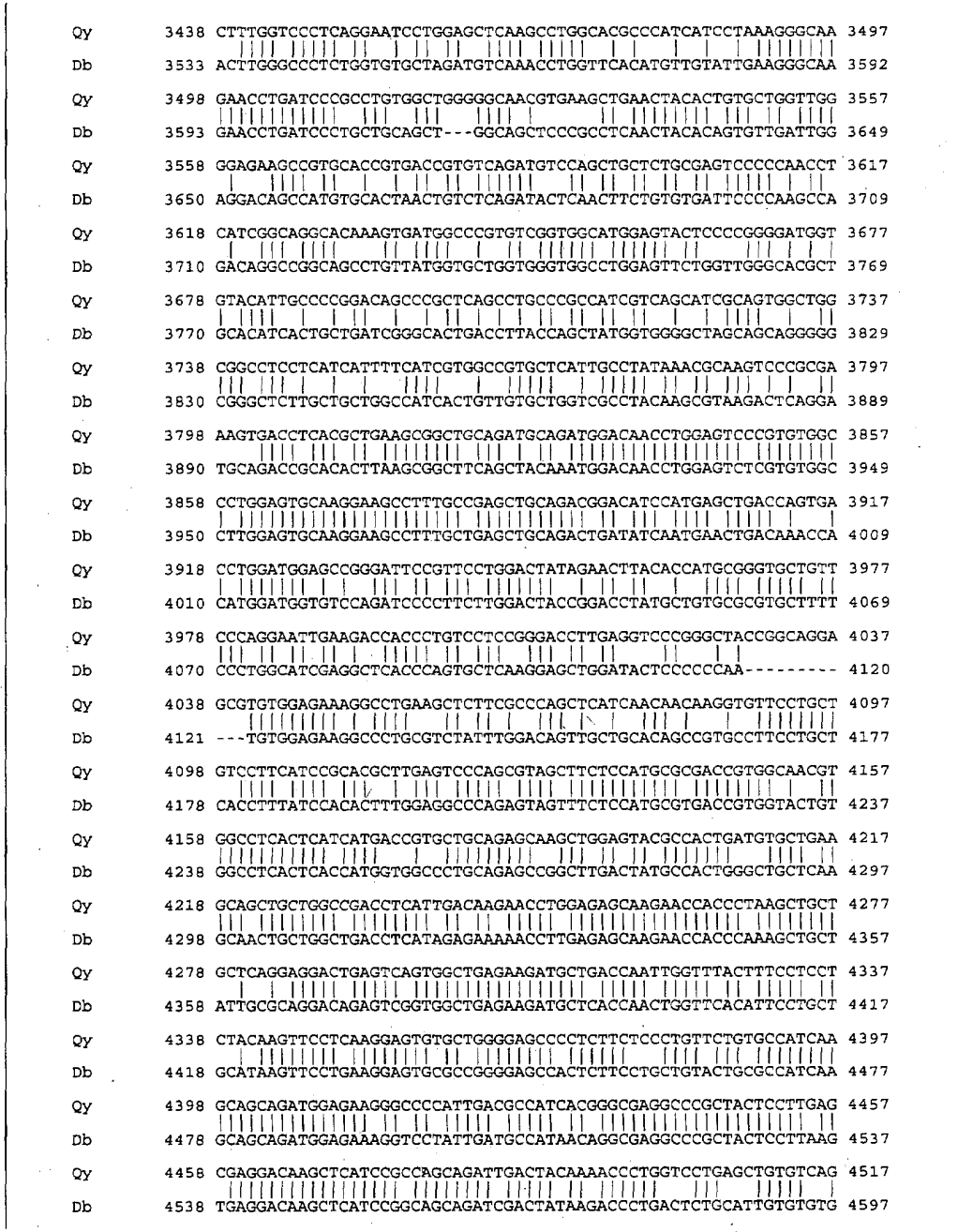

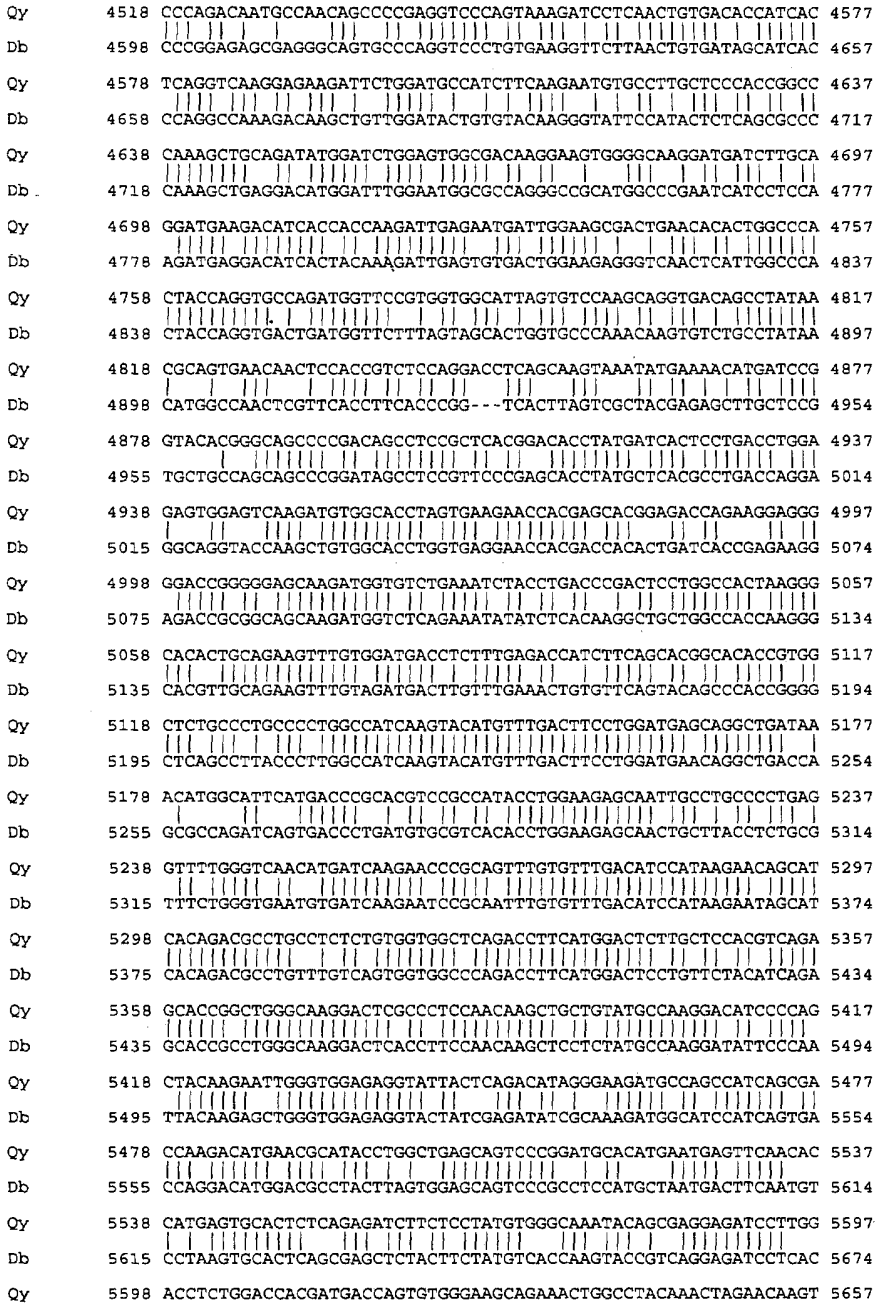

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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(without alignments)
18069.130 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2939.6	51.7	6387	6	ABN59899	Abn59899 Novel hum
5	2778.4	48.8	6730	6	ABI99504	Abi99504 Mouse isc
6	2533.8	44.5	5895	6	ABT06294	Abt06294 Human NOV
7	2455.8	43.2	6826	8	ADA09914	Ada09914 Human rec
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35	793.8	13.9	2597	10	ADE51858	Ade51858 Human cDN
36	793.8	13.9	2597	10	ADE37716	Ade37716 Human cDN
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ALIGNMENTS

RESULT 1
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ID ABS63437 standard; cDNA; 5691 BP.
XX
AC ABS63437;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human cDNA, homologous to plexin, designated NOV4.
XX
KW Human; gene; ss; NOV; NOVX; NOVX-associated disorder; cardiomyopathy;
KW atherosclerosis; diabetes; cell signalling; metabolic pathway;
KW cellular receptor; downstream effector; cancer; gene therapy;
KW hypertension; congenital heart defect; aortic stenosis; obesity;
KW infectious disease; anorexia; Alzheimer's disease; Parkinson's disease;
KW neurodegenerative disorder; haemophilia; dyslipidemia; vaccine;
KW haematopoietic disease; scleroderma; fertility; immunogen;
KW idiopathic thrombocytopenic purpura; graft versus host disease;
KW Crohn's disease; multiple sclerosis; cirrhosis; autoimmune disease;
KW systemic lupus erythematosus; asthma; arthritis; psoriasis; allergy;
KW stroke; anxiety; Lesch-Nyhan syndrome; schizophrenia; cerebellar ataxia;
KW pain; alcoholism; transgenic.
XX
OS Homo sapiens.
XX
PN WO200226826-A2.
XX
PD 04-APR-2002.
XX
PF 27-SEP-2001; 2001WO-US042336.
XX
PR 27-SEP-2000; 2000US-0235631P.
PR 27-SEP-2000; 2000US-0235633P.
PR 27-SEP-2000; 2000US-0235808P.
PR 27-SEP-2000; 2000US-0236064P.
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PR 27-SEP-2000; 2000US-0236066P.
PR 28-SEP-2000; 2000US-0236135P.
PR 03-OCT-2000; 2000US-0237434P.
PR 05-OCT-2000; 2000US-0238321P.
PR 06-OCT-2000; 2000US-0238396P.
PR 06-OCT-2000; 2000US-0238399P.
PR 16-MAR-2001; 2001US-0276667P.
PR 31-MAY-2001; 2001US-0294823P.
PR 12-JUL-2001; 2001US-0304868P.
PR 26-SEP-2001; 2001US-00235631.

XX
PA (CURA-) CURAGEN CORP.
XX
PI Gerlach VL, Macdougall JR, Smithson G, Millet I, Stone D;
PI Gunther E, Ellerman K, Grosse WM, Alsobrook JP, Lepley DM;
PI Burgess CE, Padigaru M, Kekuda R, Spytek KA, Leach MD, Shimkets RA;
XX
DR WPI; 2002-499860/53.
DR P-PSDB; ABG78364.
XX
PT Novel isolated NOVX polypeptides and polynucleotides homologous to
PT attractin, plexin, papin-like family of proteins, useful for treating
PT atherosclerosis, diabetes, cancer, Alzheimer's disease, hemophilia and
PT stroke.
XX
PS Claim 8; Page 58-59; 308pp; English.
XX
CC The invention discloses the isolated human polypetides, and
CC polynucleotides encoding them, that have been designated NOVX. The
CC polypeptides, polynucleotides and antibodies are useful in treating or
CC preventing a NOVX-associated disorder which is cardiomyopathy,
CC atherosclerosis and diabetes in a human, where the disorder is related to
CC cell signal processing and metabolic pathway modulation. They can also be
CC used in determining the presence of, or predisposition to, a disease
CC associated with altered levels of the polypeptides and polynucleotides of
CC any one of the 13 sequences (NOV1-NOV8), for raising antibodies, for
CC identifying an agent that binds to, or that modulates the expression or
CC activity of the polypeptide, for identifying an agent which is cellular
CC receptor or downstream effector, for treating or preventing a NOVX-
CC associated disorder and as a pharmaceutical composition comprising the
CC polypeptide, polynucleotide or the antibody. The polypeptides and
CC polynucleotides are useful in diagnostic applications (e.g. as a marker
CC for cancerous cells or tissue types) where their amounts are assessed, or
CC for the manufacture of a medicament (e.g. gene therapy) for treating or
CC preventing disorders or syndromes such as hypertension, congenital heart
CC defects, aortic stenosis, obesity, infectious disease, anorexia, cancer,
CC Alzheimer's disease, Parkinson's disorders, neurodegenerative disorders,
CC haemophilia, dyslipidemias, haematopoietic diseases, scleroderma,
CC fertility, idiopathic thrombocytopenic purpura, graft versus host
CC diseases, Crohn's disease, multiple sclerosis, cirrhosis, autoimmune
CC disease, systemic lupus erythematosus, asthma, arthritis, psoriasis,
CC allergy, stroke, anxiety, Lesch-Nyhan syndrome, schizophrenia, cerebellar
CC ataxia, pain and alcoholism. They may also be used as immunogens to
CC produce antibodies specific for the invention, and as vaccines.
CC Transgenic cells containing a NOVX expressing construct are useful to
CC produce non-human transgenic animals for studying the function and/or
CC activity of the NOVX proteins and for identifying and/or evaluating
CC modulators of NOVX protein activity. Transgenic cells containing a NOVX
CC expressing construct are useful to produce non-human transgenic animals
CC for studying the function and/or activity of the NOVX proteins and for
CC identifying and/or evaluating modulators of NOVX protein activity. The
CC sequences presented in ABS63431-ABS63444 are the human NOV1-NOV8 cDNAs
XX
SQ Sequence 5691 BP; 1318 A; 1658 C; 1574 G; 1141 T; 0 U; 0 Other;

Query Match 100.0%; Score 5691; DB 6; Length 5691;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5691; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 GGCTCCTCCACTTTGCTCACCCGGCAGCCAGCCCCGCTGTCCCAGAAGCAGCGGTCATTT 120
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Qy        121 GTCACATTCCGAGGAGAGCCCGCCGAGGGTTTCAATCACCTGGTGGTGGATGAGAGGACA 180
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Qy        181 GGACACATTTACTTGGGGGCCGTCAATCGGATTTACAAGCTCTCCAGCGACCTGAAGGTC 240
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Qy        361 GACTACAAGGAGAACAGGCTGATTGCCTGTGGGAGCCTGTACCAAGGCATCTGCAAGCTG 420
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Qy        661 GAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACACCTTCACCATCATCCCTGACTTT 720
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Qy        961 GTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGACCTGCTCTTCACCGTCTTCTCC 1020
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Qy       1021 AAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTCGGCCCTGTGCATCTTCATCTTG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1081 AAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTCTTGTTACCGGGGCGAGGGCACG 1140
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Qy       1141 CTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTGCAGCAGTGCGCTCTTAACCATT 1200
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Qy       1201 GACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCTGGGAGTGTCCGACATGGTGCGT 1260
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Db       1201 GACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCTGGGAGTGTCCGACATGGTGCGT 1260

Qy       1261 GGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGACGTCTGTCATCGCATATGTCTAC 1320
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Db       1261 GGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGACGTCTGTCATCGCATATGTCTAC 1320
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Qy      1321 AAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGGCAAGCTGAAGAAGATCCGGGTG 1380
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Db      1381 GATGGACCCAGGGGCAACGCCCTCCAGTATGAGACGGTGCAGGTGGTGGACCCCGGCCCA 1440

Qy      1441 GTCCTCCGGGATATGGCCTTCTCCAAGGACCACGAGCAACTCTACATCATGTCAGAGAGG 1500
Db      1441 GTCCTCCGGGATATGGCCTTCTCCAAGGACCACGAGCAACTCTACATCATGTCAGAGAGG 1500

Qy      1501 CAGCTCACCAGAGTCCCTGTGGAGTCCTGTGGTCAGTATCAGAGCTGCGGCGAGTGCCTT 1560
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Qy      1561 GGCTCAGGCGACCCCCACTGTGGCTGGTGTGTGCTGCACAACACGTGCACCCGGAAGGAG 1620
Db      1561 GGCTCAGGCGACCCCCACTGTGGCTGGTGTGTGCTGCACAACACGTGCACCCGGAAGGAG 1620

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Qy      1681 CTGACGGTCCATCCCAACAATATCTCCGTCTCTCAGTACAACGTGCTGCTGGTCCTGGAG 1740
Db      1681 CTGACGGTCCATCCCAACAATATCTCCGTCTCTCAGTACAACGTGCTGCTGGTCCTGGAG 1740

Qy      1741 ACGTACAATGTCCCCGGAGCTGTCAGCTGGCGTCAACTGCACCTTTGAGGACCTGTCAGAG 1800
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Qy      1861 CCCCGGATCATCACAGAGAATGGGGACCACCATGTCGTACAGCTTCAGCTCAAATCAAAG 1920
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Qy      1921 GAGACCGGCATGACCTTCGCCAGCACCAGCTTTGTCTTCTACAATTGCAGCGTCCACAAT 1980
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Qy      2161 ACGCTGAAGGCCAAGAACCTCCCCCAGCCCCAGTCTGGGCAGCGTGGCTACGAATGCATC 2220
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Qy      2221 CTCAACATTCAGGGCAGCGAGCAGCGAGTGCCCGCCCTGCGCTTCAACAGCTCCAGCGTA 2280
Db      2221 CTCAACATTCAGGGCAGCGAGCAGCGAGTGCCCGCCCTGCGCTTCAACAGCTCCAGCGTA 2280

Qy      2281 CAGTGCCAGAACACCTCTTATTCCTATGAAGGGATGGAGATCAACAACCTGCCCGTGGAG 2340
Db      2281 CAGTGCCAGAACACCTCTTATTCCTATGAAGGGATGGAGATCAACAACCTGCCCGTGGAG 2340

Qy      2341 TTGACAGTCGTGTGGAATGGGCACTTCAACATTGACAACCCAGCTCAGAATAAAGTTCAC 2400
Db      2341 TTGACAGTCGTGTGGAATGGGCACTTCAACATTGACAACCCAGCTCAGAATAAAGTTCAC 2400

Qy      2401 CTCTACAAGTGTGGAGCCATGCGTGAGAGCTGCGGGCTGTGCCTCAAGGCTGACCCAGAC 2460
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Qy      2581 ACAGAGATAATCCCGGTGACAGGCCCCCGGGAAGGGGGCACCAAGGTCACTATCCGAGGG 2640
Db      2581 ACAGAGATAATCCCGGTGACAGGCCCCCGGGAAGGGGGCACCAAGGTCACTATCCGAGGG 2640

Qy      2641 GAGAACCTGGGCCTGGAATTTCGCGACATCGCCTCCCATGTCAAGGTTGCTGGCGTGGAG 2700
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Db      2761 GCCAAGCCCAGCCAGCATGCAGGCTTCGTGGAGATCTGCGTGGCTGTGTGTCGGCCTGAA 2820

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Db      3181 TGGGGGACCCACCTGGACCTCATACAGAACCCCCAGATCCGTGCCAAGCATGGAGGGAAG 3240

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Qy      3421 AACCCGGTGTTTGAGGCCTTTGGTCCCTCAGGAATCCTGGAGCTCAAGCCTGGCACGCCC 3480
Db      3421 AACCCGGTGTTTGAGGCCTTTGGTCCCTCAGGAATCCTGGAGCTCAAGCCTGGCACGCCC 3480

Qy      3481 ATCATCCTAAAGGGCAAGAACCTGATCCCGCCTGTGGCTGGGGGCAACGTGAAGCTGAAC 3540
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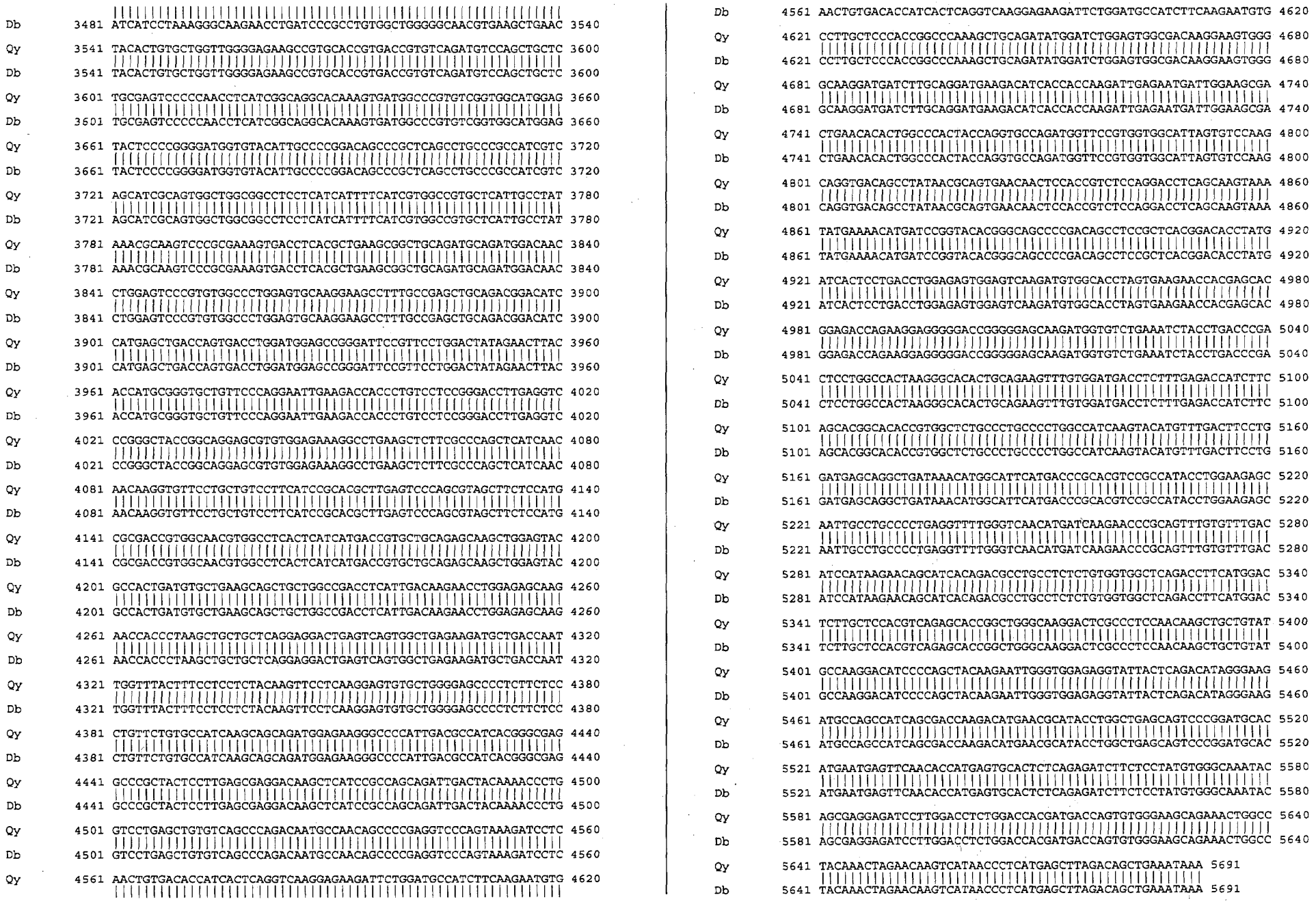
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RESULT 2
ABA00062
ID   ABA00062 standard; cDNA; 6367 BP.
XX
AC   ABA00062;
XX
DT   25-OCT-2002  (first entry)
XX
DE   CADHP-9 coding sequence, Incyte ID No: 7156379CB1.
XX
KW   Gene; human; cell adhesion protein; CADHP; AIDS; Alzheimer's disease;
KW   acquired immunodeficiency syndrome; thymic dysplasia; epilepsy;
KW   renal tubular acidosis; congenital glaucoma; cancer; atherosclerosis;
KW   Parkinson's disease; ss.
XX
OS   Homo sapiens.
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PD   01-AUG-2002.
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PF   18-DEC-2001; 2001WO-US049206.
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XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Duggan BM,  Xu Y,  Lee EA,  Lee S,  Lu DAM,  Warren BA,  Yue H;
PI   Gietzen KJ,  Honchell CD,  Burford N,  Baughn MR,  Tang TY,  Hillman JL;
PI   Gandhi AR,  Kallick DA,  Bandman O,  Graul RC,  Walia NK,  Lu Y;
PI   Ramkumar J,  Yao MG,  Lal PG;
XX
DR   WPI; 2002-590826/63.
DR   P-PSDB; AAG79420.
XX
PT   New human cell adhesion proteins (CADHP) useful for treating, diagnosing
PT   and preventing diseases or conditions associated with the aberrant CADPH
PT   expression e.g. cancer, acquired immunodeficiency syndrome, Alzheimer's
PT   disease and epilepsy.
XX
PS   Claim 5; Page 146-48; 149pp; English.
XX
CC   The sequences given in ABA00054-63 encode novel human cell adhesion
CC   proteins (CADHP). The CADHP polypeptides and polynucleotides are useful
CC   in treating, diagnosing and preventing diseases or conditions associated
CC   with the decreased expression or overexpression of CADHP, e.g. immune
CC   system (acquired immunodeficiency syndrome, thymic dysplasia),
CC   neurological (Alzheimer's disease, Parkinson's disease, epilepsy),
CC   developmental (renal tubular acidosis, congenital glaucoma) and cell
CC   proliferative (cancer, atherosclerosis) disorders. They are also useful
CC   in assessing the effects of exogenous compounds on the expression of
CC   nucleic acid and amino acid sequences of CADHP. The CADHP or its
CC   fragments are useful in screening compounds for effectiveness as agonist
CC   or antagonist of the polypeptides, or in altering the expression of the
CC   target polynucleotide and compounds that specifically bind to or modulate
CC   the activity of the polypeptide. The protein encoded by this cDNA
CC   sequence shows homology to mouse plexin-2
XX
SQ   Sequence 6367 BP; 1423 A; 1885 C; 1799 G; 1259 T; 0 U; 1 Other;

  Query Match             99.8%;  Score 5680.6;  DB 6;  Length 6367;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 5683;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

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Db       1466 GAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGCCTACCTGTCCAAAGCGGGGGCC 1525

Qy        961 GTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGACCTGCTCTTCACCGTCTTCTCC 1020
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Db       1526 GTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGACCTGCTCTTCACCGTCTTCTCC 1585

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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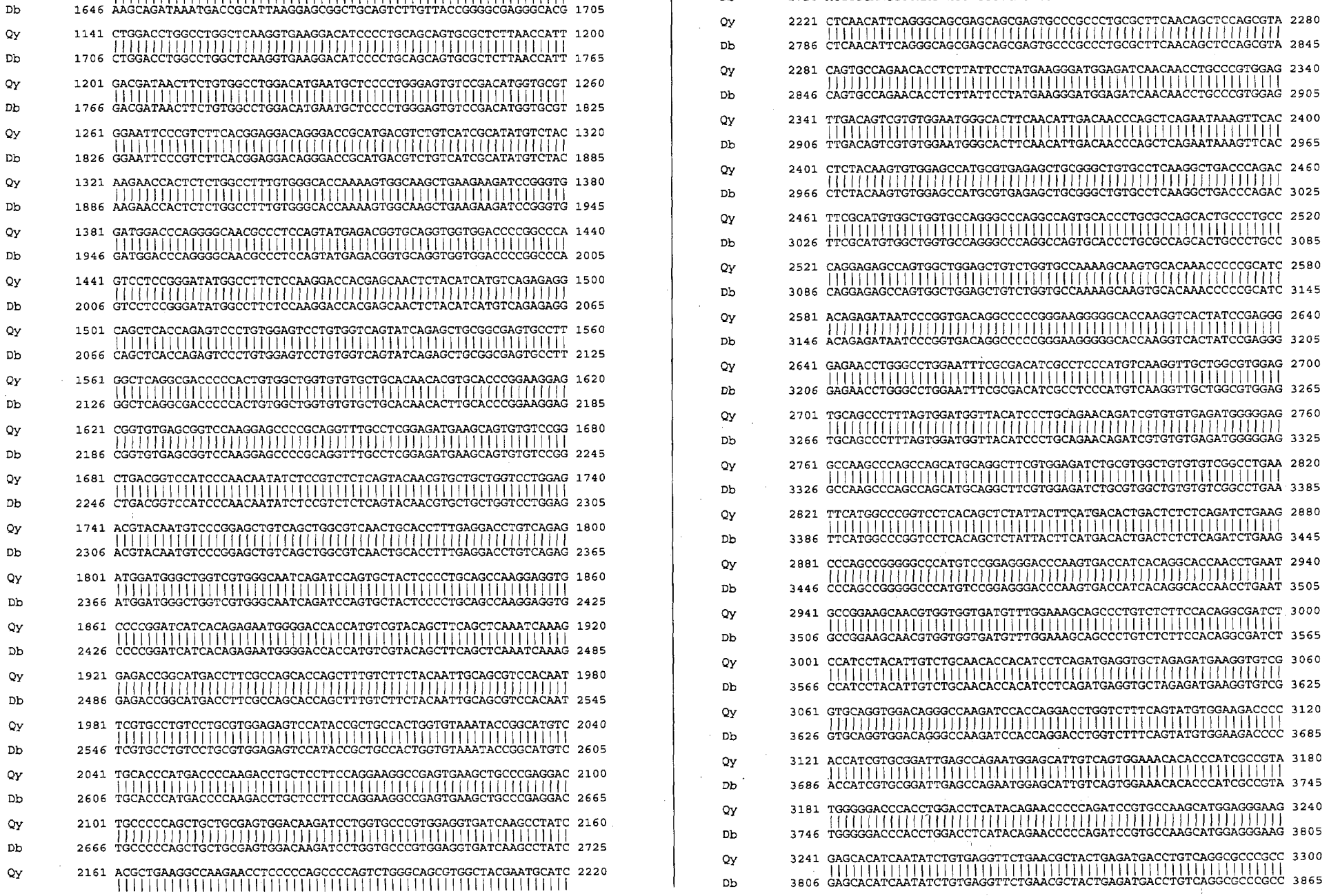
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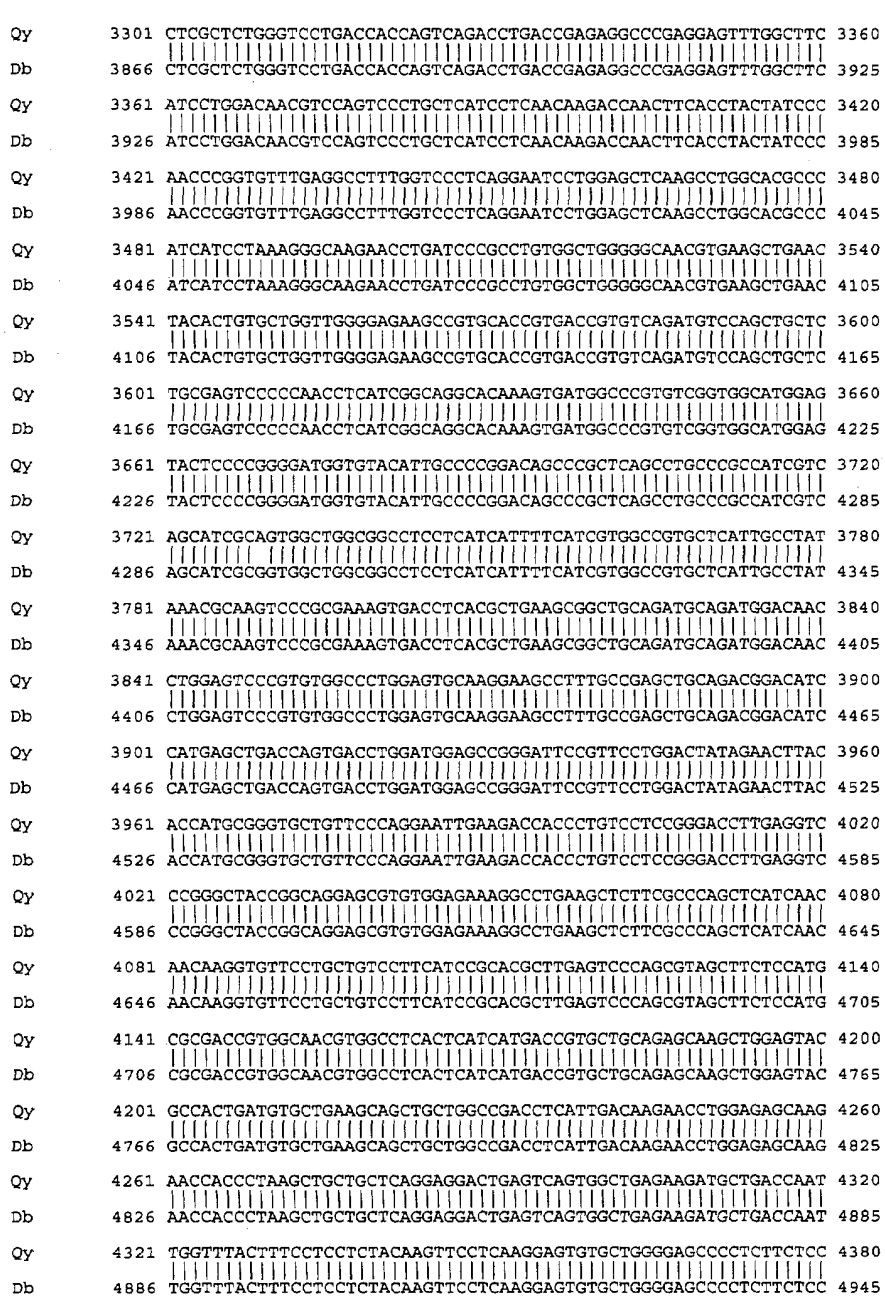
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RESULT 3
ABX34698
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XX
AC   ABX34698;
XX
DT   13-FEB-2003  (first entry)
XX
DE   Human mddt cDNA SEQ ID 259.
XX
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KW   anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;
KW   haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic;
KW   gene therapy; protein replacement therapy; cell proliferative disorder;
KW   cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;
KW   anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
KW   Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;
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PF   27-MAR-2002; 2002WO-US009944.
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PA   (INCY-) INCYTE GENOMICS INC.
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PI   Dufour GE,  Hillman JL,  Yu JY,  Tuason O,  Yap PE,  Amshey SR;
PI   Daugherty SC,  Dam TC,  Liu TF,  Nguyen DA,  Kleefeld Y,  Gerstin EH;
PI   Peralta CH,  David MH,  Lewis SA,  Chen AJ,  Panzer SR,  Harris B;
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DR   WPI; 2003-058431/05.
DR   P-PSDB; ABU11708.
XX
PT   New purified disease detection and treatment molecule proteins and
PT   polynucleotides, useful for diagnosing, treating or preventing cancers
PT   (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
PT   or hepatitis.
XX
PS   Claim 1; SEQ ID NO 259; 339pp + Sequence Listing; English.
XX
CC   This invention describes a novel disease detection and treatment molecule
CC   polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,
CC   osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,
CC   antianaemic, antipsoriatic and hepatotropic activity. The polynucleotides
CC   and the polypeptides of the invention can be used for gene therapy,
CC   protein replacement therapy and are useful for treating a variety of
CC   diseases or conditions. These polypeptides or polynucleotides are
CC   particularly useful for diagnosing, treating or preventing cell
CC   proliferative disorders (e.g. cancers including adenocarcinoma,
CC   leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's
CC   disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's
CC   syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or
CC   hepatitis. ABX34440-ABX34835 encode the MDDT polypeptides represented in
CC   ABU11450-ABU11845, described in the disclosure of the invention. NOTE:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 7136 BP; 1616 A; 2099 C; 1993 G; 1428 T; 0 U; 0 Other;

  Query Match           51.7%;  Score 2941.2;  DB 7;  Length 7136;
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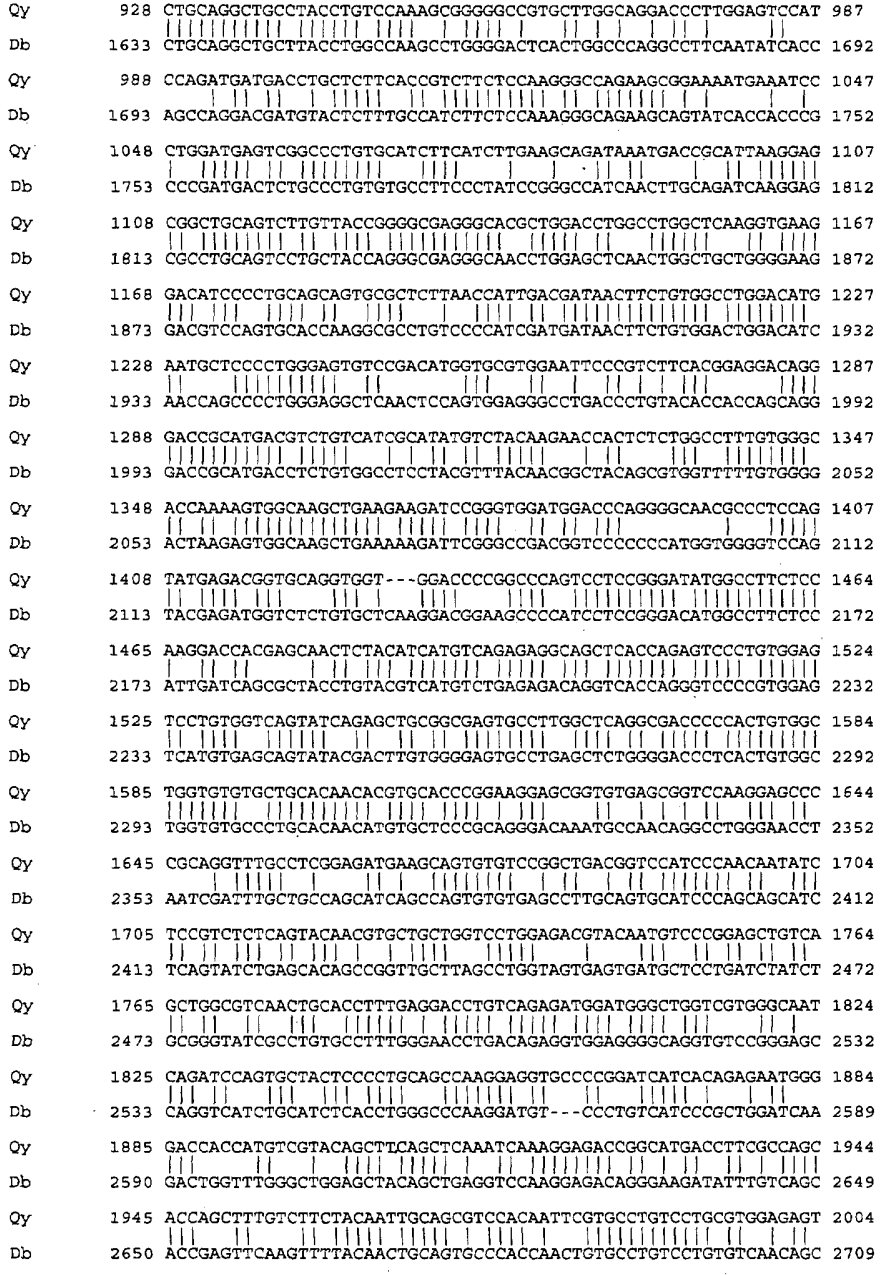
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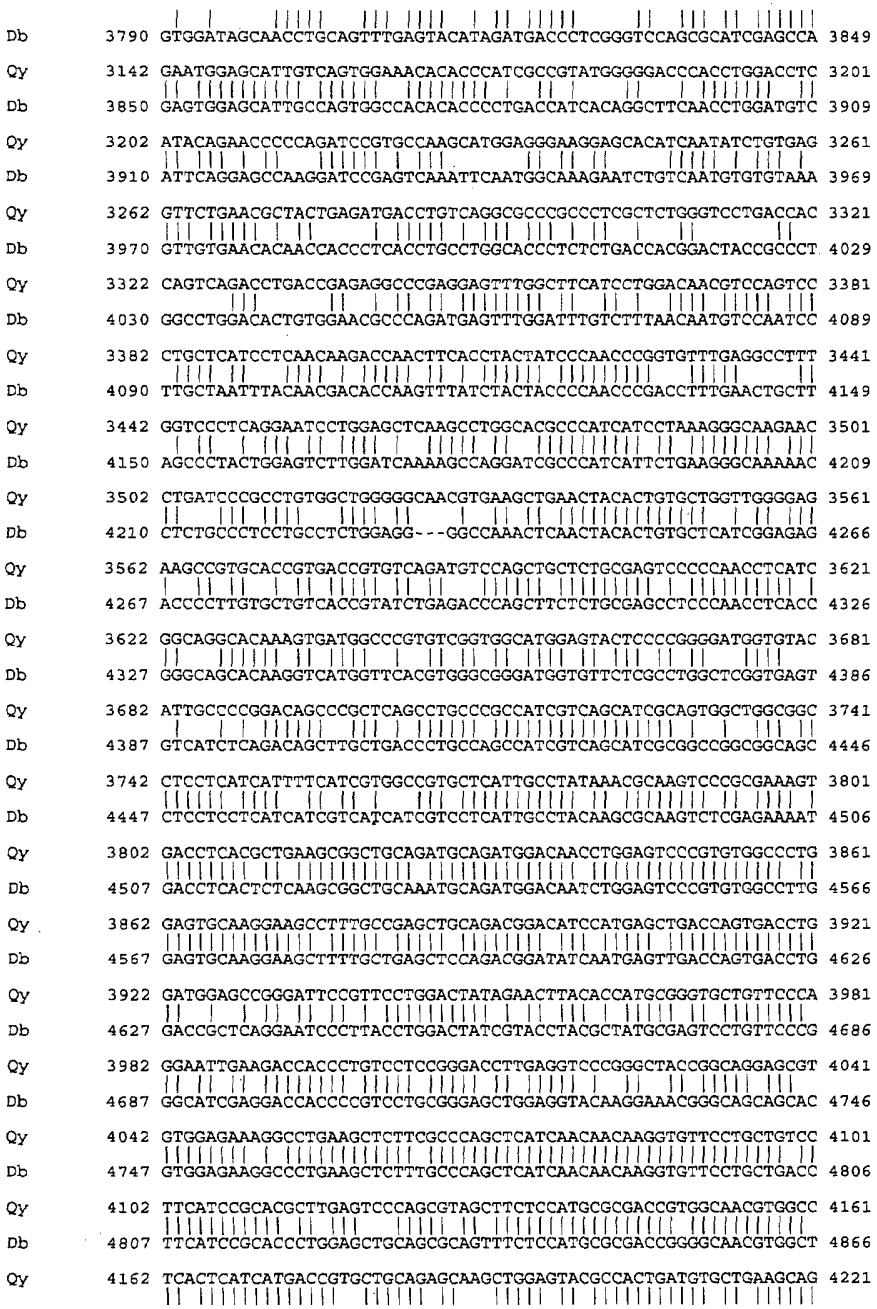
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RESULT 4
ABN59899
ID ABN59899 standard; cDNA; 6387 BP.
XX
AC ABN59899;
XX
DT 28-JUN-2002 (first entry)
XX
DE Novel human coding sequence SEQ ID NO: 310.
XX
KW Human; antianaemic; vulnerary; antiinflammatory; immunomodulator;
KW antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;
KW neuroprotective; antiparkinsonian; protein therapy; EST;
KW expressed sequence tag; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200222660-A2.
XX
PD 21-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US026015.
XX
PR 11-SEP-2000; 2000US-00659671.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XX
DR WPI; 2002-292408/33.
DR P-PSDB; ABB97486.
XX
PT An isolated polynucleotide for treating diseases associated with its
PT encoded polypeptide such as cancer and multiple sclerosis.
XX
PS Claim 1; SEQ ID NO 310; 509pp; English.
XX
CC The present invention provides the protein and coding sequences of 444
CC novel human proteins. These were isolated from expressed sequences tags
CC (ESTs). They can be used to stimulate cell growth, to regulate
CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
CC e.g. in burn treatment, to regulate the immune system e.g. to treat
CC multiple sclerosis, to regulate activin or inhibin e.g. to treat
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke
CC and cancer, to screen for drugs, to treat inflammatory conditions e.g.
CC rheumatoid arthritis, and to treat nervous system disorders e.g.
CC Parkinson's disease. The present sequence is a coding sequence of the
CC invention
XX
SQ Sequence 6387 BP; 1416 A; 1911 C; 1762 G; 1298 T; 0 U; 0 Other;

Query Match 51.7%; Score 2939.6; DB 6; Length 6387;
Best Local Similarity 71.3%; Pred. No. 0;
Matches 3952; Conservative 0; Mismatches 1579; Indels 15; Gaps 5;

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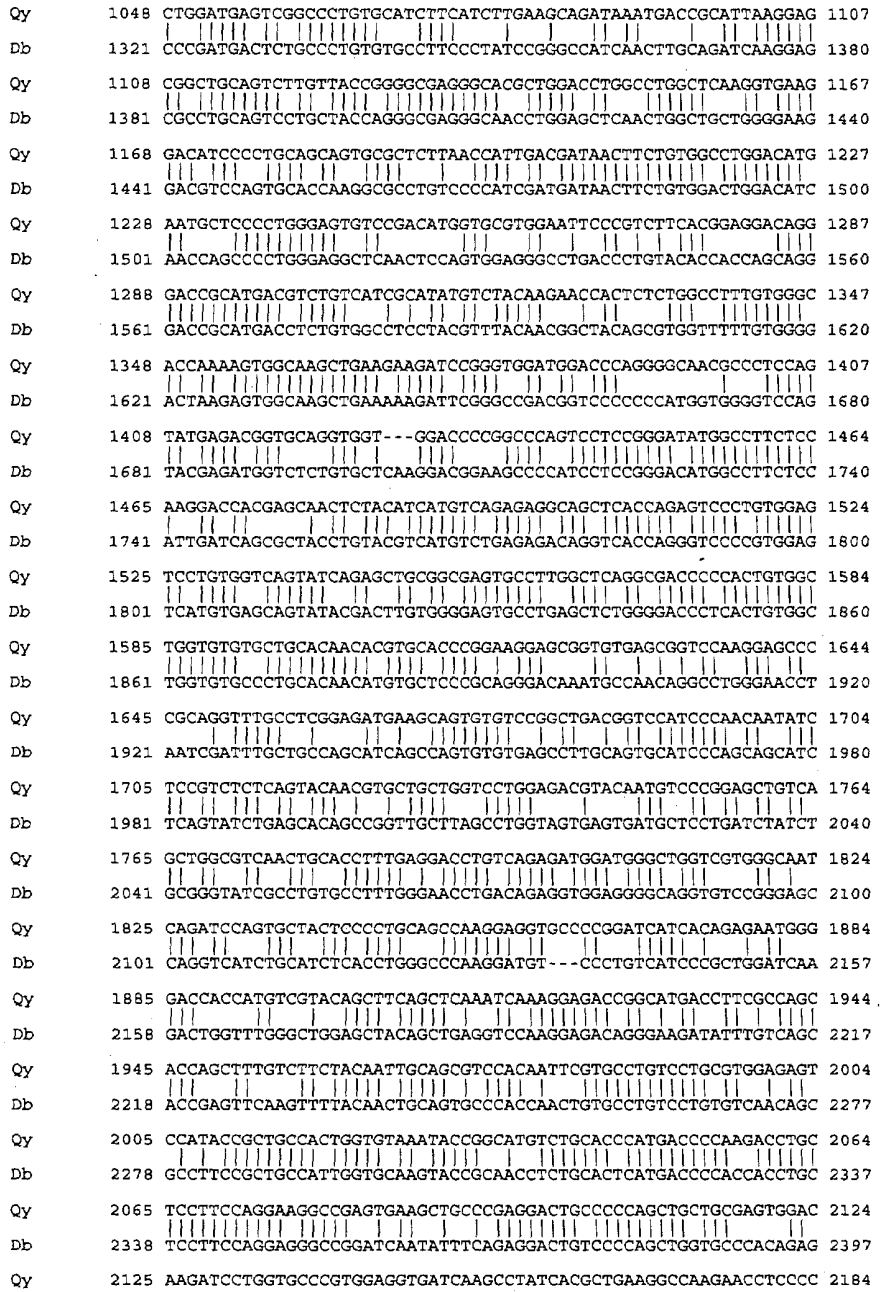
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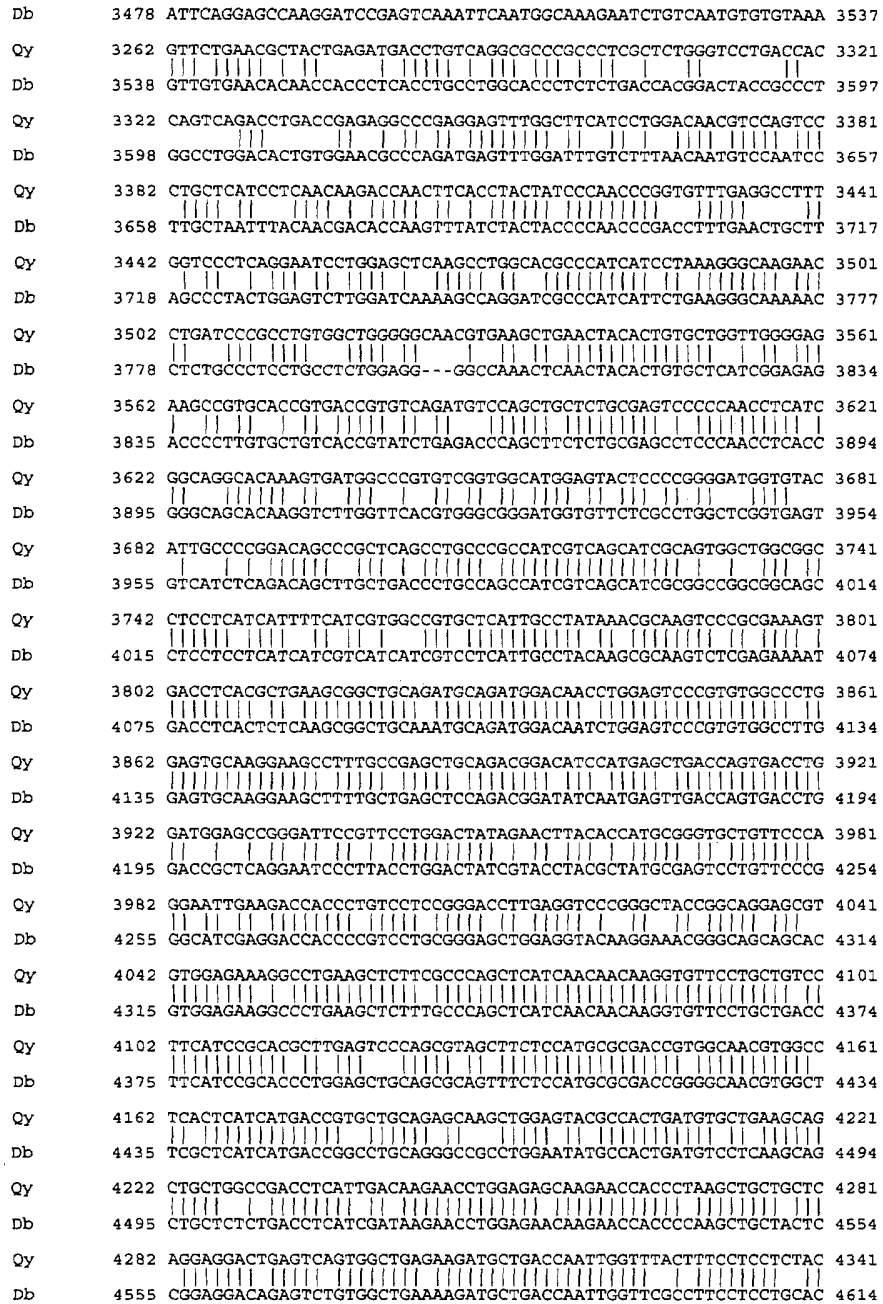

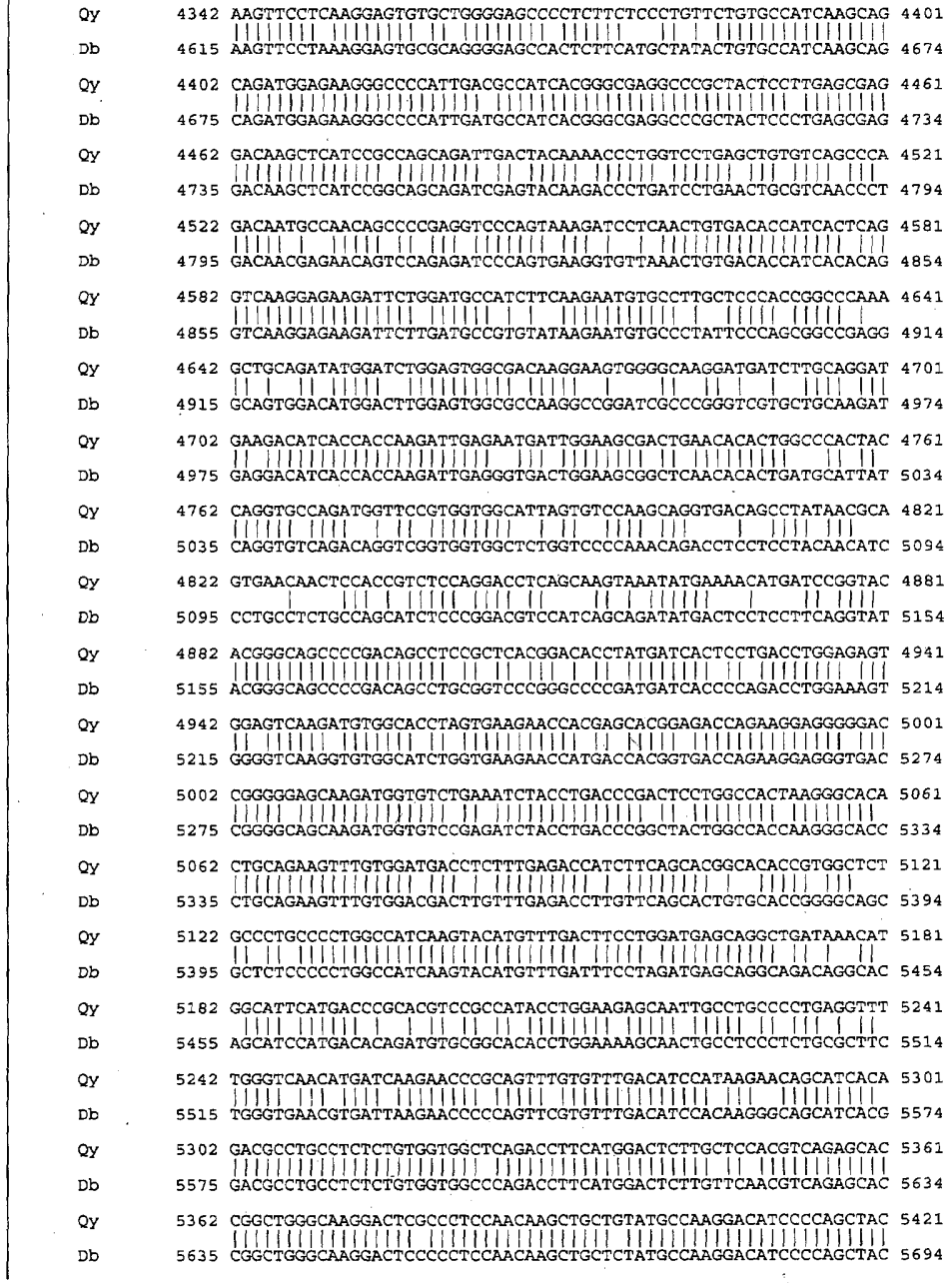

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RESULT 5
ABI99504
ID ABI99504 standard; cDNA; 6730 BP.
XX
AC ABI99504;
XX
DT 07-MAR-2002 (first entry)
XX
DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:479.
XX
KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
KW vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.
XX
OS Mus musculus.
XX
PN WO200188188-A2.
XX
PD 22-NOV-2001.
XX
PF 18-MAY-2001; 2001WO-JP004192.
XX
PR 18-MAY-2000; 2000JP-00145977.
XX
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XX
PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
XX
DR WPI; 2002-034733/04.
DR P-PSDB; ABB57196.
XX
PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
PT expression levels of particular genes defined in the specification or by
PT determining the expression profile of a gene group comprising these
PT genes.
XX
PS Claim 2; Page 1319-1331; 2690pp; English.
XX
CC The present invention describes a method for examining ischaemic
CC conditions, comprising measuring the expression levels of particular
CC genes (I) in a test sample or determining the expression profile of a
CC gene group in the sample comprising genes selected from (I). The method
CC is useful for examining the ischaemic condition (e.g. compressive
CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
CC expression levels of particular genes (ABI99202 to ABI99912, encoding the
CC protein sequences in ABB57020 to ABB57374) or by determining the
CC expression profile of a gene group comprising these genes. The expression
CC levels or expression profiles produced by these genes are used as an
CC indicator when screening for ischaemic condition-improving drugs or
CC therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR
CC primers for a mouse ischaemic condition related sequence, which are used
CC in the exemplification of the present invention
XX

SQ Sequence 6730 BP; 1656 A; 1850 C; 1740 G; 1482 T; 0 U; 2 Other;

Query Match 48.8%; Score 2778.4; DB 6; Length 6730;
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Matches 3858; Conservative 0; Mismatches 1691; Indels 15; Gaps 5;

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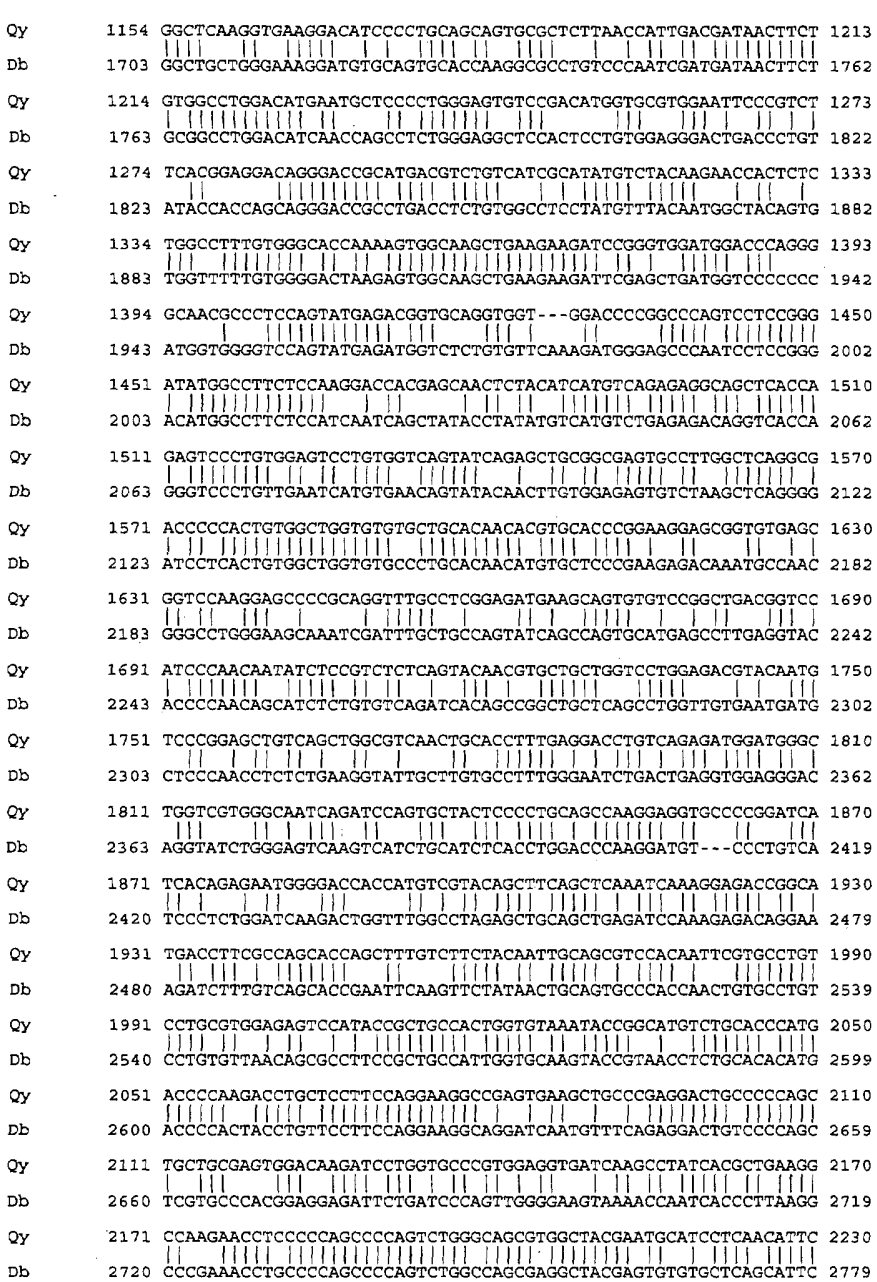
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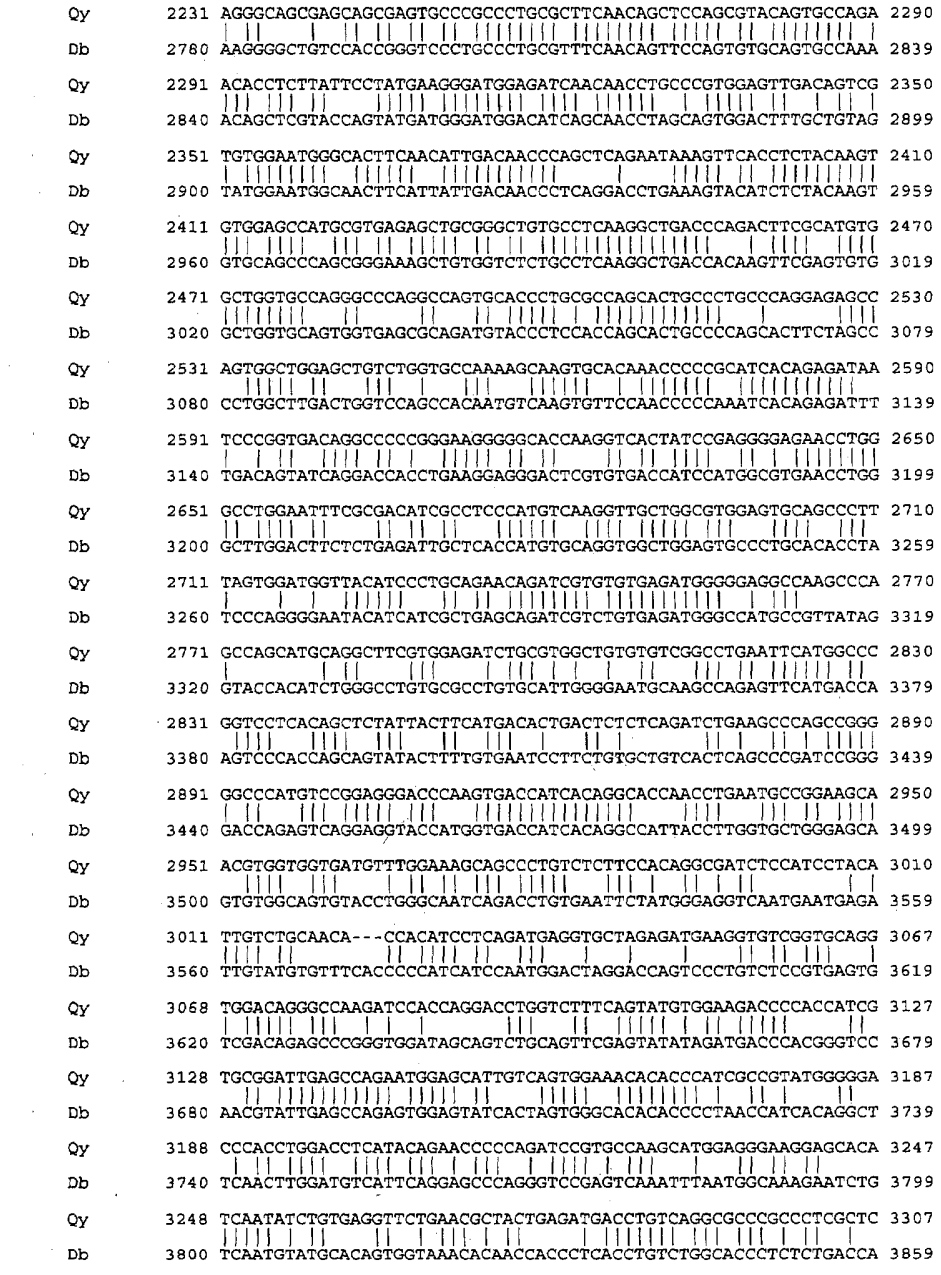
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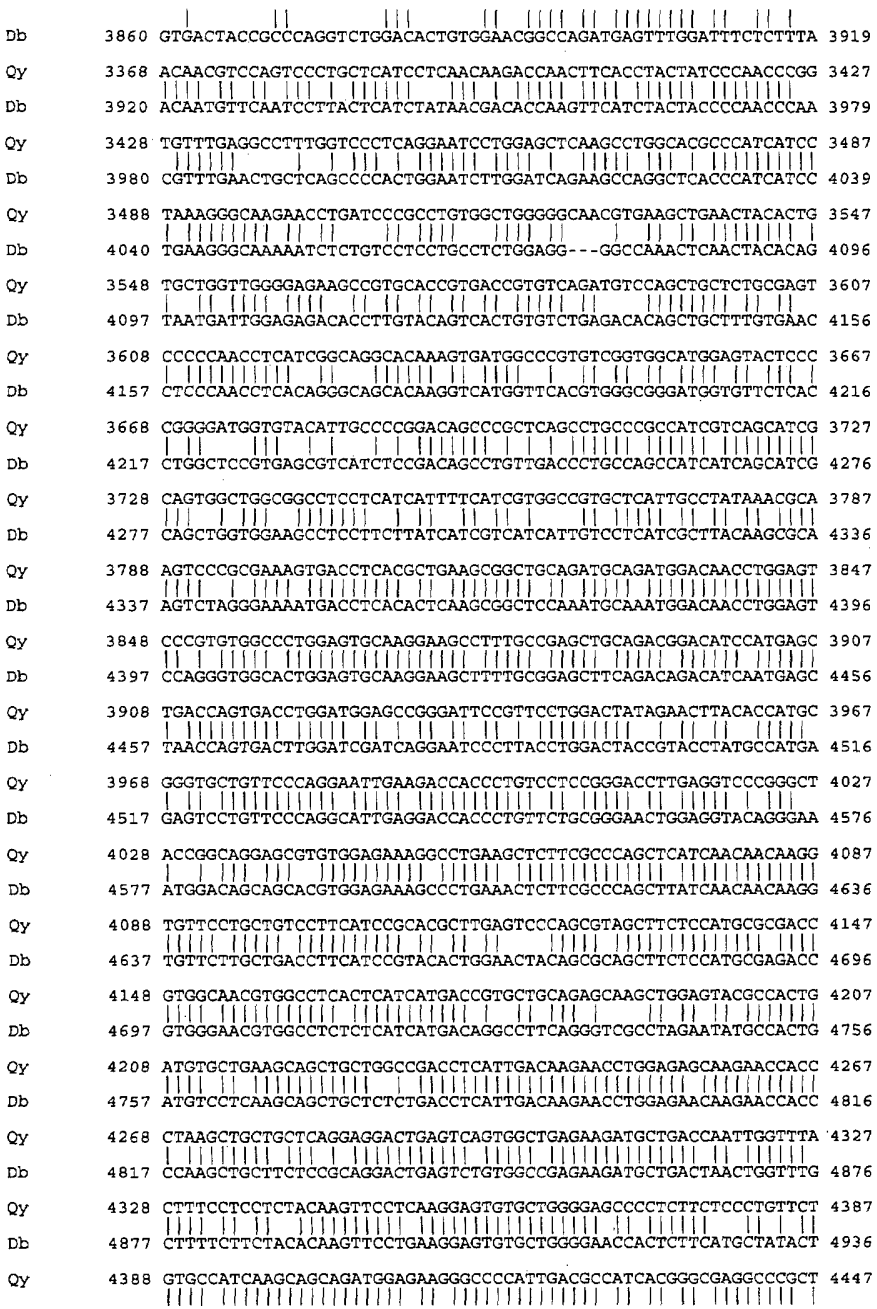
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RESULT 6
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ID ABT06294 standard; cDNA; 5895 BP.
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AC ABT06294;
XX
DT 24-OCT-2002 (first entry)
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DE Human NOV12 coding sequence.
XX
KW Human; NOVX; autoimmune disease; cancer; infection; inflammatory disease;
KW storage disorder; muscle disorder; neurodegenerative disorder; nootropic;
KW developmental defect; neuroprotective; antiparkinsonian; hypotensive;
KW hypertensive; haemostatic; cardiant; antianginal; dermatological;
KW immunosuppressive; antiinflammatory; virucide; antibacterial; anti-HIV;
KW antiparasitic; antiallergic; antiasthmatic; antirheumatic; antiarthritic;
KW vulnerary; anorectic; antidiabetic; immunomodulator; antipsoriatic;
KW nephrotropic; kerolytic; antiulcer; cerebroprotective; anticonvulsant;
KW antiinfertility; antimanic; antidepressant; metabolic; cytostatic;
KW tranquilizer; analgesic; gene; ss.
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PN WO200257450-A2.
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PD 25-JUL-2002.
XX
PF 29-NOV-2001; 2001WO-US048922.
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PR 30-NOV-2000; 2000US-0250926P.
PR 25-JAN-2001; 2001US-0264180P.
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PR 05-OCT-2001; 2001US-0327456P.
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XX
DR WPI; 2002-590741/63.
DR P-PSDB; AAO18749.
XX
PT Novel isolated polypeptide, designated NOVX, useful for treating or
PT preventing in NOVX-associated disorders e.g. cardiomyopathy,
PT atherosclerosis, diabetes, cancer, allergy, asthma, Crohn's disease.
XX
PS Claim 9; Page 130-131; 353pp; English.
XX
CC The present invention provides the protein and coding sequences of
CC several novel human proteins, designated NOVX. These can be used in the
CC treatment of, amongst others, cancers, autoimmune diseases, infections,
CC inflammatory diseases, storage disorders, muscle disorders,
CC neurodegenerative diseases and developmental defects. The present
CC sequence is a coding sequence of the invention
XX
SQ Sequence 5895 BP; 1172 A; 1928 C; 1759 G; 1036 T; 0 U; 0 Other;

  Query Match 44.5%; Score 2533.8; DB 6; Length 5895;
  Best Local Similarity 68.0%; Pred. No. 0;
  Matches 3812; Conservative 0; Mismatches 1712; Indels 81; Gaps 17;

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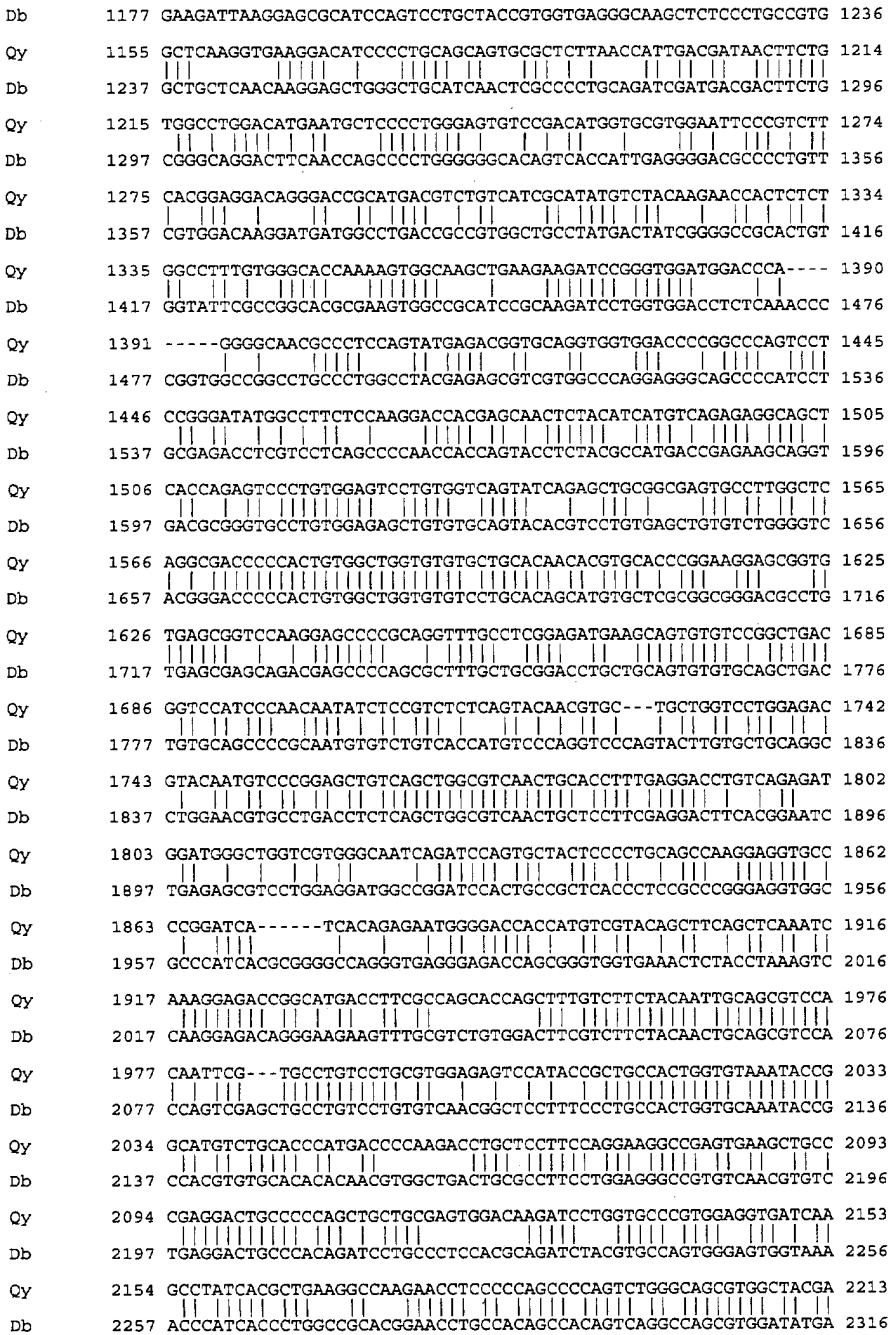
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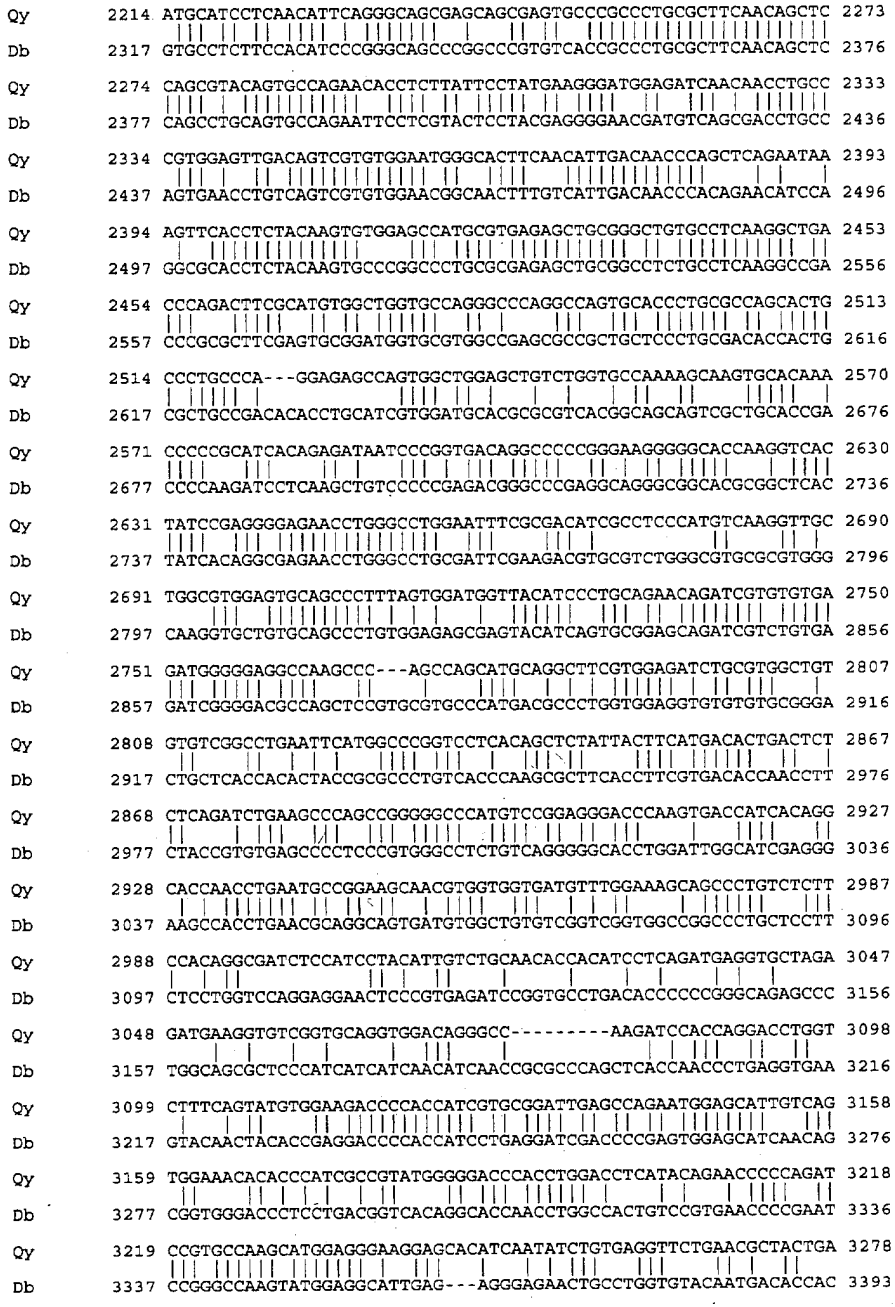
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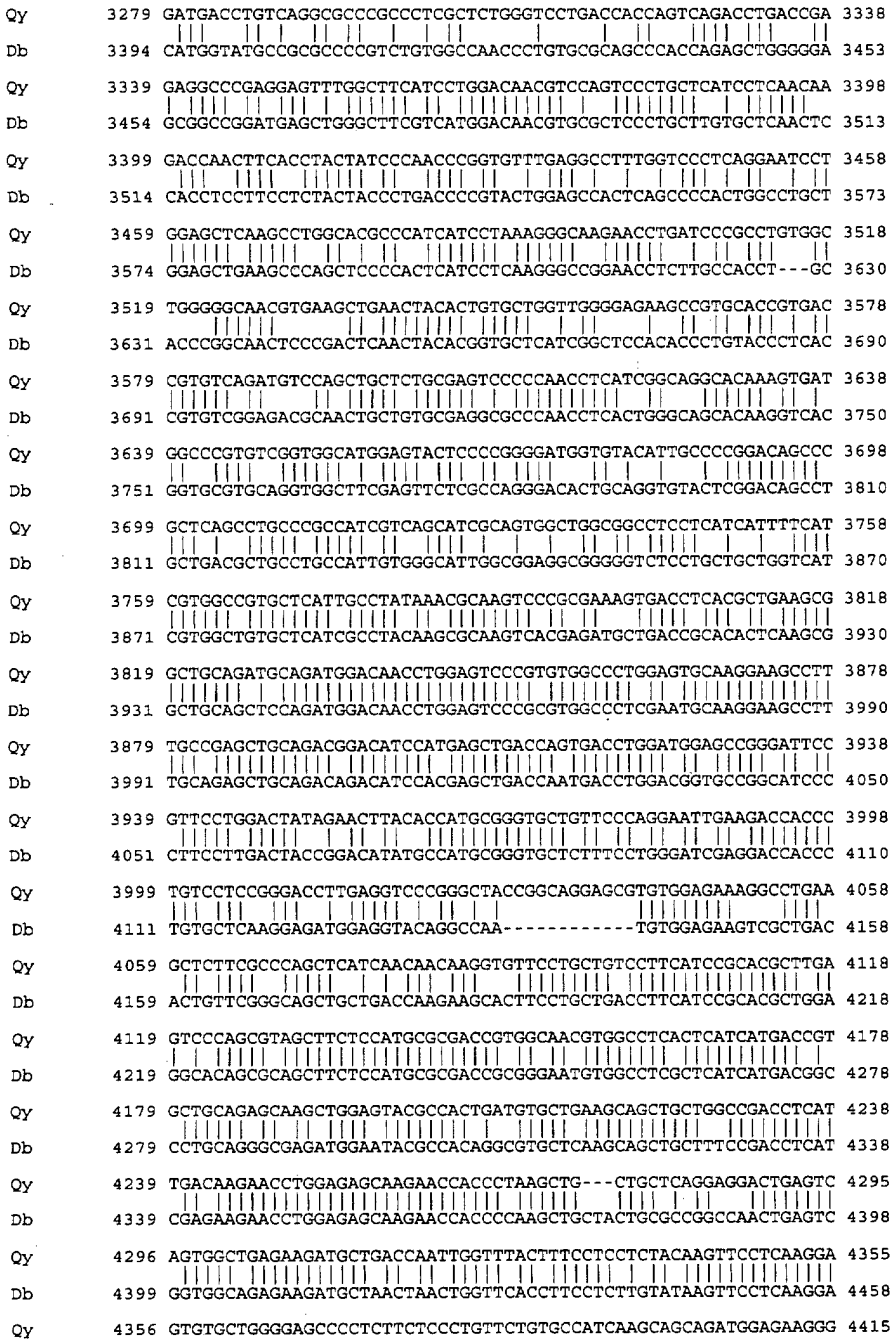
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RESULT 7
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ID   ADA09914 standard; cDNA; 6826 BP.
XX
AC   ADA09914;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human receptor and membrane-associated protein REMAP-18 cDNA, SEQ ID:56.
XX
KW   Human; receptor and membrane-associated protein; REMAP;
KW   cell proliferative disorder; cancer; autoimmune disorder;
KW   inflammatory disorder; infection; neurological disorder;
KW   metabolic disorder; developmental disorder; endocrine disorder;
KW   cytostatic; immunosuppressive; antiinflammatory; neuroprotective;
KW   nootropic; cerebroprotective; gene therapy; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /product= "REMAP-18"
XX
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XX
PD   28-AUG-2003.
XX
PF   18-FEB-2003; 2003WO-US004902.
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PR   29-APR-2002; 2002US-0376669P.
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XX
PA   (INCY-) INCYTE GENOMICS INC.
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PI   Gorvad AE,  Becha SD,  Kable AE,  Swarnakar A,  Jin P,  Hawkins PR;
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PI   Jiang X,  Jackson AA,  Khare R,  Bulloch SA;
XX
DR   WPI; 2003-697610/66.
DR   P-PSDB; ADA09876.
XX
PT   New human receptor and membrane associated proteins and nucleic acids,
PT   useful for diagnosing, treating or preventing e.g. viral, bacterial,
PT   fungal, parasitic, protozoan or helminthic infections, cancers,
PT   neurological disorders.
XX
PS   Claim 5; Page 279-281; 298pp; English.
XX
CC   The invention relates to 38 human receptors and membrane-associated
CC   proteins (REMAP), REMAP-1 to REMAP-38, and the cDNAs encoding them
CC   (ADA09859-ADA09934). The invention also encompasses expression
CC   constructs, host cells and transgenic organisms comprising a REMAP
CC   nucleic acid sequence; the recombinant preparation of a REMAP; an
CC   antibody against a REMAP; methods of detection of REMAP proteins or
CC   nucleic acids; a micro-array containing REMAP nucleic acids; methods of
CC   screening compounds for their ability to modulate REMAP activity or
CC   expression; and pharmaceutical compositions comprising a REMAP protein, a
CC   REMAP agonist or REMAP antagonist. The REMAP proteins, nucleic acids or
CC   compositions comprising them are useful in diagnosing, treating or
CC   preventing a variety of disorders, including cell proliferative disorders
CC   (e.g., arteriosclerosis, cirrhosis, hepatitis, psoriasis, or primary
CC   thrombocytopenia) or cancers (e.g., adenocarcinoma, leukaemia, or cancers
CC   of the bone, brain, breast or uterus); autoimmune/inflammatory disorders
CC   (e.g., AIDS, allergies, anaemia, asthma, bronchitis, gout, multiple
CC   sclerosis, osteoarthritis, rheumatoid arthritis, or systemic lupus
CC   erythematosus); viral, bacterial, fungal, parasitic, protozoan or
CC   helminthic infections; neurological disorders (e.g., epilepsy, stroke,
CC   Alzheimer's disease, dementia, or Parkinson's disease); metabolic
CC   disorders (e.g., hereditary fructose intolerance, obesity, hypoglycaemia
CC   or diabetes); developmental disorders (e.g., achondroplastic dwarfism,
CC   hypothyroidism or hydrocephalus); or endocrine disorders (e.g., disorders
CC   of the hypothalamus or pituitary gland). The present sequence represents
CC   a REMAP cDNA of the invention.
XX
SQ   Sequence 6826 BP; 1232 A; 2259 C; 2022 G; 1313 T; 0 U; 0 Other;
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  Matches 3730;  Conservative    0;  Mismatches 1777;  Indels  108;  Gaps   10;

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Qy       212 TTTACAAGCTCTCCAGCGACCTGAAGGTCTTGGTGACGCATGAGACAGGGCCGGACGAGG 271

Db       333 TCTTTAAGCTGGCCCCCAACCTGACTGAGCTGCGGGCCCATGTCACGGGGCCCGTCGAGG 392

Qy       272 ACAACCCCAAGTGTTACCCACCCCGCATCGTCCAGACCTGCAATGAGCCCCTGACCACCA 331

Db       393 ACAACGCTCGCTGCTACCCGCCCCCCAGCATGCGCGTGTGTGCCCACCGCCTGGCCCCCG 452

Qy       332 CCAACAATGTCAACAAGATGCTCCTCATAGACTACAAGGAGAACAGGCTGATTGCCTGTG 391

Db       453 TGGACAACATCAACAAGCTGCTGCTCATAGACTATGCGGCCCGCCGCCTGGTGGCCTGCG 512

Qy       392 GGAGCCTGTACCAAGGCATCTGCAAGCTGCTGAGGCTGGAGGACCTCTTCAAGCTGGGGG 451

Db       513 GCAGCATCTGGCAGGGCATCTGCCAGTTCCTGCGTCTGGACGACCTCTTCAAGCTGGGTG 572

Qy       452 AGCCTTATCATAAGAAGGAGCACTATCTGTCAGGTGTCAACGAGAGCGGCTCAGTCTTTG 511

Db       573 AGCCGCACCACCGCAAGGAGCACTACCTGTCGGGGGCCCAGGAGCCCGACTCCATGGCTG 632

Qy       512 GAGTGATCGTCTCCTACAGCAACCTGGATGACAAGCTGTTCATTGCCACGGCAGTGGATG 571

Db       633 GTGTCATTGTGGAGCAGGGCCAGGGGCCCAGCAAGCTGTTTGTGGGCACTGCTGTCGACG 692

Qy       572 GGAAGCCCGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGG 631

Db       693 GCAAGTCGGAGTACTTCCCCACCTTGAGCTCCCGCAAGCTCATCAGTGATGAAGACAGCG 752

Qy       632 ATGGCATGTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTT 691

Db       753 CGGACATGTTCAGTCTCGTGTACCAGGATGAGTTTGTGTCCTCCCAGATCAAGATCCCCT 812

Qy       692 CGGACACCTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTG 751

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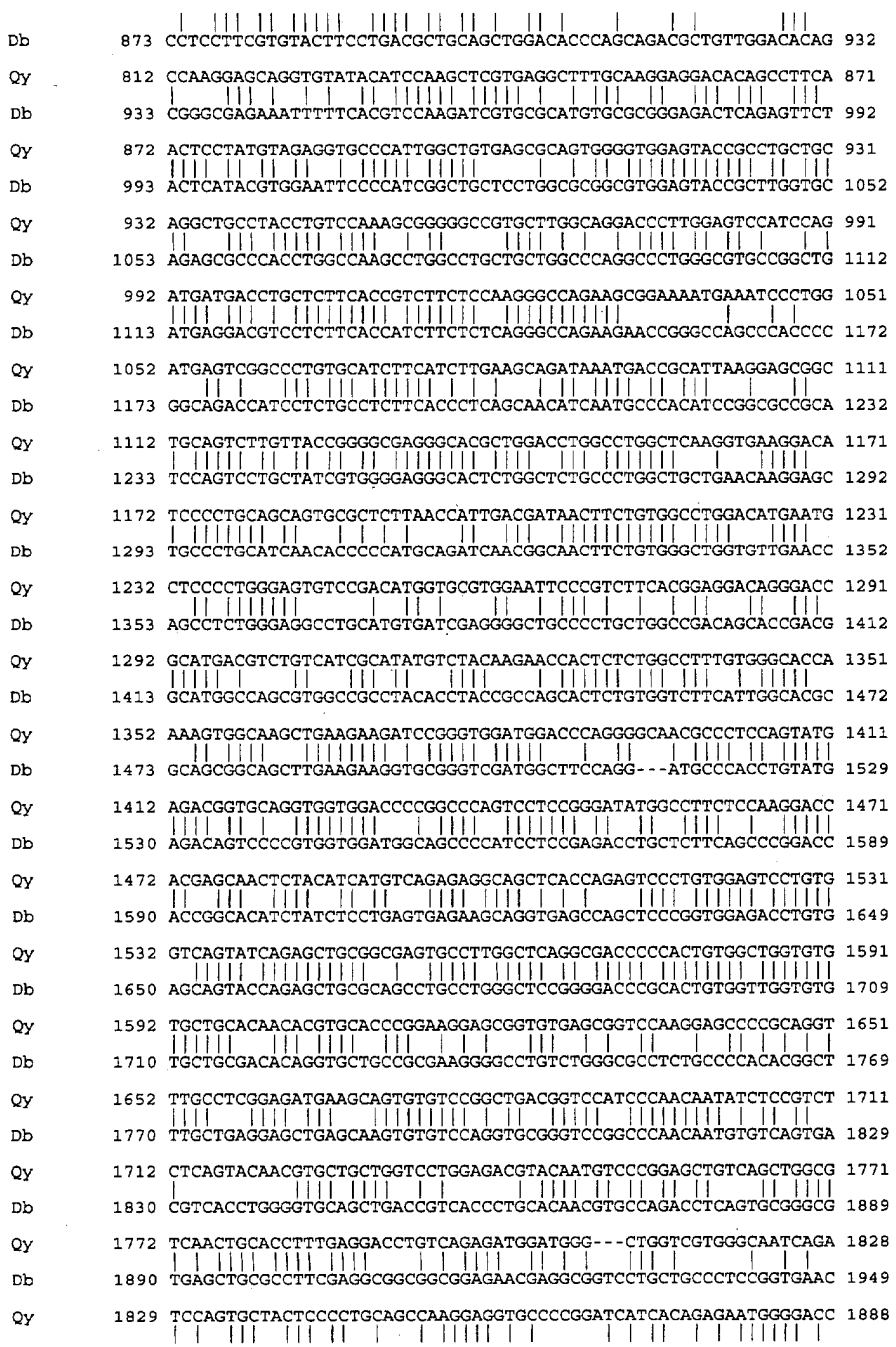
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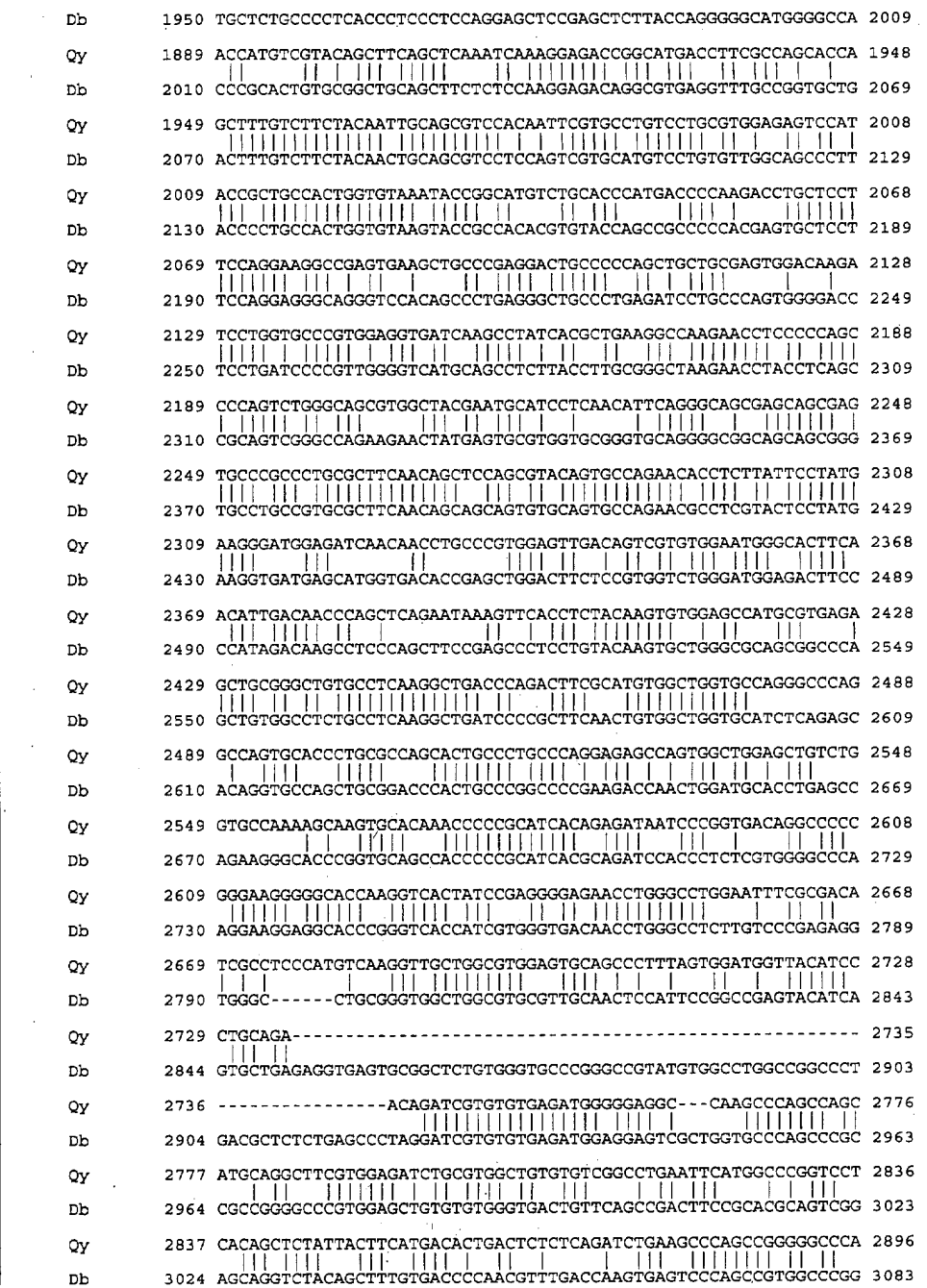
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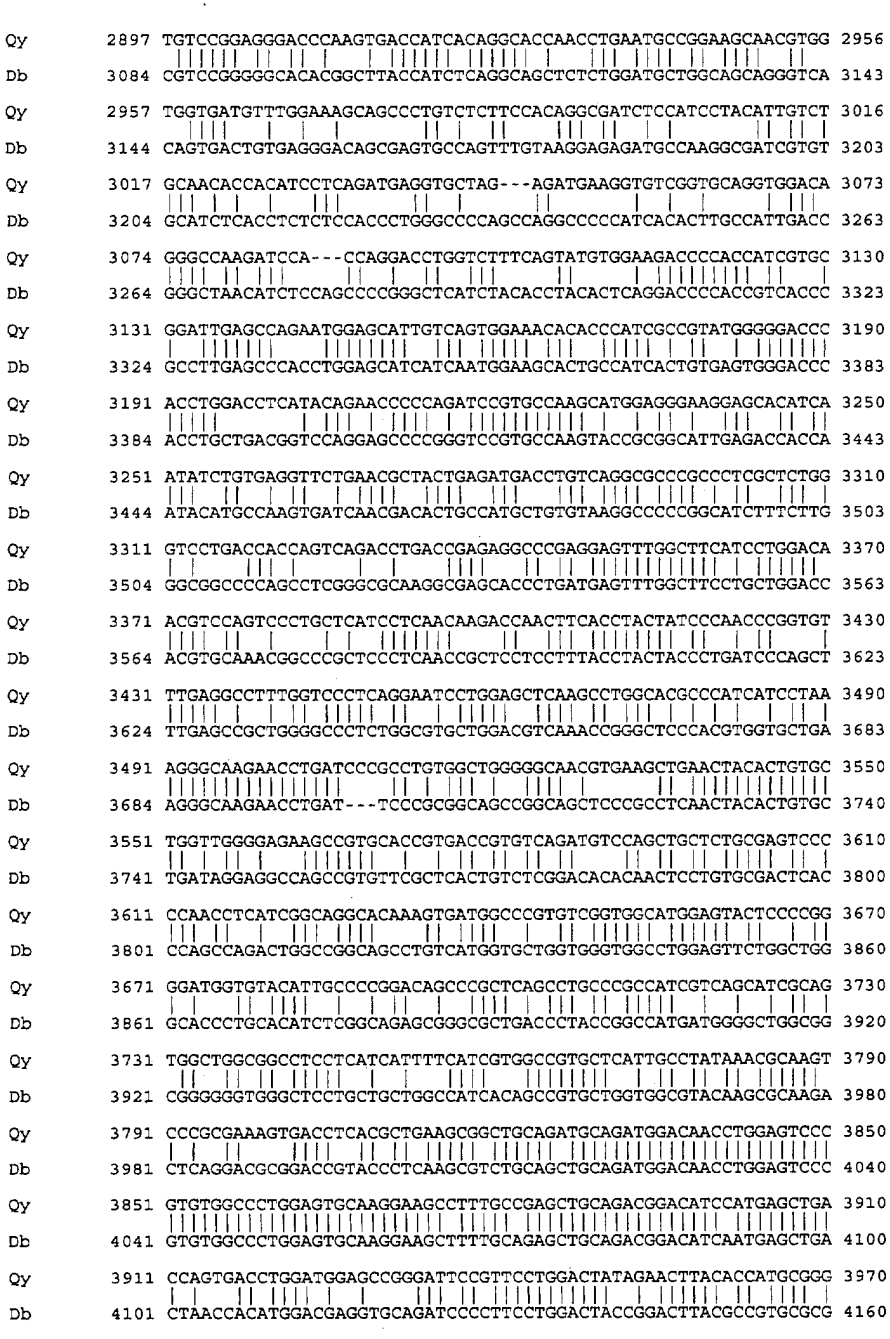
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Qy 3911 CCAGTGACCTGGATGGAGCCGGGATTCCGTTCCTGGACTATAGAACTTACACCATGCGGG 3970
Db 4101 CTAACCACATGGACGAGGTGCAGATCCCCTTCCTGGACTACCGGACTTACGCCGTGCGCG 4160
Qy 3971 TGCTGTTCCCAGGAATTGAAGACCACCCTGTCCTCCGGGACCTTGAGGTCCCGGGCTACC 4030
Db 4161 TGCTCTTCCCGGGCATCGAGGCCCACCCGGTGCTCAAGGAGCTGGATACGCCACCCAAC- 4219
Qy 4031 GGCAGGAGCGTGTGGAGAAAGGCCTGAAGCTCTTCGCCCAGCTCATCAACAACAAGGTGT 4090
Db 4220 ----------GTGGAGAAGGCCCTGCGCCTCTTCGGGCAGCTGCTGCACAGCCGCGCGT 4268
Qy 4091 TCCTGCTGTCCTTCATCCGCACGCTTGAGTCCCAGCGTAGCTTCTCCATGCGCGACCGTG 4150
Db 4269 TCGTGCTTACCTTCATCCACACGCTGGAGGCCCAGAGCAGCTTCTCCATGCGCGACCGCG 4328
Qy 4151 GCAACGTGGCCTCACTCATCATGACCGTGCTGCAGAGCAAGCTGGAGTACGCCACTGATG 4210
Db 4329 GCACCGTGGCCTCGCTCACCATGGTGGCCCTGCAGAGCCGGCTCGACTATGCCACGGGGC 4388
Qy 4211 TGCTGAAGCAGCTGCTGGCCGACCTCATTGACAAGAACCTGGAGAGCAAGAACCACCCTA 4270
Db 4389 TGCTCAAGCAACTGCTGGCCGACCTCATCGAGAAGAACCTCGAGAGCAAGAACCACCCCA 4448
Qy 4271 AGCTGCTGCTCAGGAGGACTGAGTCAGTGGCTGAGAAGATGCTGACCAATTGGTTTACTT 4330
Db 4449 AGCTGCTGCTACGCAGGACAGAGTCAGTGGCTGAGAAGATGCTTACCAACTGGTTCACGT 4508
Qy 4331 TCCTCCTCTACAAGTTCCTCAAGGAGTGTGCTGGGGAGCCCCTCTTCTCCCTGTTCTGTG 4390
Db 4509 TCCTGCTGCATAAGTTTCTGAAGGAGTGTGCTGGGGAGCCTCTCTTCCTGCTTTACTGTG 4568
Qy 4391 CCATCAAGCAGCAGATGGAGAAGGGCCCCATTGACGCCATCACGGGCGAGGCCCGCTACT 4450
Db 4569 CCATCAAGCAGCAGATGGAGAAGGGCCCCATTGATGCCATCACGGGCGAGGCACGATACT 4628
Qy 4451 CCTTGAGCGAGGACAAGCTCATCCGCCAGCAGATTGACTACAAAACCCTGGTCCTGAGCT 4510
Db 4629 CCCTGAGCGAGGACAAGCTCATCCGTCAGCAGATCGACTACAAGACACTGACCCTTCACT 4688
Qy 4511 GTGTCAGCCCAGACAATGCCAACAGCCCCGAGGTCCCAGTAAAGATCCTCAACTGTGACA 4570
Db 4689 GCGTGTGTCCGGAGAACGAGGGCAGCGCCCAGGTCCCAGTGAAGGTTCTCAACTGTGACA 4748
Qy 4571 CCATCACTCAGGTCAAGGAGAAGATTCTGGATGCCATCTTCAAGAATGTGCCTTGCTCCC 4630
Db 4749 GCATCACCCAGGCCAAAGATAAGCTGCTGGACACTGTGTACAAGGGCATTCCGTACTCCC 4808
Qy 4631 ACCGGCCCAAAGCTGCAGATATGGATCTGGAGTGGCGACAAGGAAGTGGGGCAAGGATGA 4690
Db 4809 AGCGTCCCAAAGCTGAGGACATGGACCTGGAGTGGCGCCAGGGCCGCATGACTCGCATCA 4868
Qy 4691 TCTTGCAGGATGAAGACATCACCACCAAGATTGAGAATGATTGGAAGCGACTGAACACAC 4750
Db 4869 TCCTCCAGGATGAGGATGTCACCACCAAGATCGAGTGTGACTGGAAGAGGCTCAACTCAC 4928
Qy 4751 TGGCCCACTACCAGGTGCCAGATGGTTCCGTGGTGGCATTAGTGTCCAAGCAGGTGACAG 4810
Db 4929 TGGCCCACTACCAGGTGACAGACGGTTCCTTGGTGGCATTGGTGCCCAAACAAGTGTCTG 4988
Qy 4811 CCTATAACGCAGTGAACAACTCCACCGTCTCCAGGACCTCAGCAAGTAAATATGAAAACA 4870
Db 4989 CCTATAACATGGCCAACTCCTTCACCTTCACCCG---CTCCCTCAGCCGCTACGAGAGCT 5045
Qy 4871 TGATCCGGTACACGGGCAGCCCCGACAGCCTCCGCTCACGGACACCTATGATCACTCCTG 4930
Db 5046 TGCTCCGCACGGCCAGCAGCCCTGATAGCCTCCGCTCACGGGCACCCATGATTACGCCTG 5105
Qy 4931 ACCTGGAGAGTGGAGTCAAGATGTGGCACCTAGTGAAGAACCACGAGCACGGAGACCAGA 4990
Db 5106 ACCAGGAGACAGGCACCAAATTGTGGCACCTGGTGAAAAACCACGACCATGCCGACCATC 5165
Qy 4991 AGGAGGGGGACCGGGGGAGCAAGATGGTGTCTGAAATCTACCTGACCCGACTCCTGGCCA 5050
Db 5166 GCGAGGGGGACCGTGGCAGCAAGATGGTCTCCGAGATCTACCTGACACGGCTGCTGGCCA 5225
Qy 5051 CTAAGGGCACACTGCAGAAGTTTGTGGATGACCTCTTTGAGACCATCTTCAGCACGGCAC 5110

```
Db       5226 CCAAGGGCACACTGCAGAAGTTCGTGGATGACCTCTTTGAGACAGTGTTCAGCACAGCCC 5285

Qy       5111 ACCGTGGCTCTGCCCTGCCCCTGGCCATCAAGTACATGTTTGACTTCCTGGATGAGCAGG 5170

Db       5286 ACCGGGGCTCGGCCCTGCCCCTGGCCATCAAGTACATGTTCGACTTCCTGGATGAGCAGG 5345

Qy       5171 CTGATAAACATGGCATTCATGACCCGCACGTCCGCCATACCTGGAAGAGCAATTGCCTGC 5230

Db       5346 CGGACCAGCGCCAGATCAGCGACCCCGATGTGCGCCACACCTGGAAGAGCAACTGCCTGC 5405

Qy       5231 CCCTGAGGTTTTGGGTCAACATGATCAAGAACCCGCAGTTTGTGTTTGACATCCATAAGA 5290

Db       5406 CGCTGCGCTTCTGGGTGAATGTGATCAAGAACCCGCAGTTCGTGTTCGACATCCACAAGA 5465

Qy       5291 ACAGCATCACAGACGCCTGCCTCTCTGTGGTGGCTCAGACCTTCATGGACTCTTGCTCCA 5350

Db       5466 ACAGCATCACGGATGCCTGCCTGTCGGTGGTAGCCCAGACCTTCATGGACTCCTGCTCTA 5525

Qy       5351 CGTCAGAGCACCGGCTGGGCAAGGACTCGCCCTCCAACAAGCTGCTGTATGCCAAGGACA 5410

Db       5526 CATCCGAGCACCGCCTGGGGAAGGACTCGCCCTCCAACAAACTGCTCTACGCCAAGGACA 5585

Qy       5411 TCCCCAGCTACAAGAATTGGGTGGAGAGGTATTACTCAGACATAGGGAAGATGCCAGCCA 5470

Db       5586 TCCCCAACTACAAGAGCTGGGTGGAGAGGTATTATCGAGACATTGCAAAGATGGCATCCA 5645

Qy       5471 TCAGCGACCAAGACATGAACGCATACCTGGCTGAGCAGTCCCGGATGCACATGAATGAGT 5530

Db       5646 TCAGCGACCAGGACATGGATGCCTACCTGGTGGAGCAGTCCCGCCTCCACGCCAGCGACT 5705

Qy       5531 TCAACACCATGAGTGCACTCTCAGAGATCTTCTCCTATGTGGGCAAATACAGCGAGGAGA 5590

Db       5706 TCAGCGTCCTGAGTGCGCTCAACGAGCTGTATTTCTATGTCACCAAGTACCGCCAGGAGA 5765

Qy       5591 TCCTTGGACCTCTGGACCACGATGACCAGTGTGGGAAGCAGAAACTGGCCTACAAACTAG 5650

Db       5766 TTCTCACGGCTCTGGACCGAGATGCCTCTTGTCGGAAGCATAAGTTGCGGCAGAAACTGG 5825

Qy       5651 AACAAGTCATAACCCTCATGAGCTTAGACAGCTGA 5685

Db       5826 AACAGATCATCAGCCTCGTGTCCAGCGACAGCTAA 5860


RESULT 8
ABV76746
ID   ABV76746 standard; cDNA; 3914 BP.
XX
AC   ABV76746;
XX
DT   28-MAR-2003  (first entry)
XX
DE   Human plexin 2 protein 56.11-encoding cDNA.
XX
KW   Human; plexin 2 protein 56.11; recombinant production; gene therapy;
KW   palsy; dementia; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1391. .2926
FT                   /*tag= a
FT                   /product= "Human plexin 2 protein 56.11"
XX
PN   CN1359955-A.
XX
PD   24-JUL-2002.
XX
PF   20-DEC-2000; 2000CN-00135177.
XX
PR   20-DEC-2000; 2000CN-00135177.
XX
PA   (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-733643/80.
DR   P-PSDB; ABP58529.
XX
PT   Polypeptide-human plexin 2 protein 56.11 and polynucleotide for coding
PT   it.
XX
PS   Claim 6; Page 24-26 (Disclosure); 35pp; Chinese.
XX
CC   The invention relates to human plexin 2 protein 56.11 (ABP58529) and
CC   nucleic acids encoding it (ABV76746). The protein has a molecular weight
CC   of 56.11 kD. The invention also relates to a method for the recombinant
CC   production of the protein, an antagonist of the protein, and the use of
CC   the protein, gene and antagonist in therapeutic applications. Plexin 2
CC   protein 56.11 can be used in the treatment of a variety of diseases such
CC   as palsy and dementia. The present sequence represents cDNA encoding
CC   human plexin 2 protein 56.11
XX
SQ   Sequence 3914 BP; 924 A; 1181 C; 1016 G; 793 T; 0 U; 0 Other;

  Query Match           17.1%;  Score 974;  DB 6;  Length 3914;
  Best Local Similarity  67.4%;  Pred. No. 2.2e-224;
  Matches 1527;  Conservative    0;  Mismatches  510;  Indels  227;  Gaps    2;

Qy       3023 CCACATCCTCAGATGAGGTGCTAGAGATGAAGGTGTCGGTGCAGGTGGACAGGGCCAAGA 3082

Db       1416 CCCCATCATCCAATGGCCTTGGCCCGGTCCCTGTTTCTGTGAGAGTCGACCGAGCCCATG 1475

Qy       3083 TCCACCAGGACCTGGTCTTTCAGTATGTGGAAGACCCCACCATCGTGCGGATTGAGCCAG 3142

Db       1476 TGGATAGCAACCTGCAGTTTGAGTACATAGATGACCCTCGGGTCCAGCGCATCGAGCCAG 1535

Qy       3143 AATGGAGCATTGTCAGTGGAAACACACCCATCGCCGTATGGGGGACCCACCTGGACCTCA 3202

Db       1536 AGTGGAGCATTGCCAGTGGCCACACACCCCTGACCATCACAGGCTTCAACCTGGATGTCA 1595

Qy       3203 TACAGAACCCCCAGATCCGTGCCAAGCATGGAGGGAAGGAGCACATCAATATCTGTGAGG 3262

Db       1596 TTCAGGAGCCAAGGATCCGAGTCAAATTCAATGGCAAAGAATCTGTCAATGTGTGTAAAG 1655

Qy       3263 TTCTGAACGCTACTGAGATGACCTGTCAGGCGCCCGCCCTCGCTCTGGGTCCTGACCACC 3322

Db       1656 TTGTGAACACAACCACCCTCACCTGCCTGGCACCCTCTCTGACCACGGACTACCGCCCTG 1715

Qy       3323 AGTCAGACCTGACCGAGAGGCCCGAGGAGTTTGGCTTCATCCTGGACAACGTCCAGTCCC 3382

Db       1716 GCCTGGACACTGTGGAACGCCCAGATGAGTTTGGATTTGTCTTTAACAATGTCCAATCCT 1775

Qy       3383 TGCTCATCCTCAACAAGACCAACTTCACCTACTATCCCAACCCGGTGTTTGAGGCCTTTG 3442

Db       1776 TGCTAATTTACAACGACACCAAGTTTATCTACTACCCCAACCCGACCTTTGAACTGCTTA 1835

Qy       3443 GTCCCTCAGGAATCCTGGAGCTCAAGCCTGGCACGCCCATCATCCTAAAGGGCAAGAACC 3502

Db       1836 GCCCTACTGGAGTCTTGGATCAAAAGCCAGGATCGCCCATCATTCTGAAGGGCAAAAACC 1895

Qy       3503 TGATCCCGCCTGTGGCTGGGGGCAACGTGAAGCTGAACTACACTGTGCTGGTTGGGGAGA 3562

Db       1896 TCTGCCCTCCTGCCTCTGGAGG---GGCCAAACTCAACTACACTGTGCTCATCGGAGAGA 1952

Qy       3563 AGCCGTGCACCGTGACCGTGTCAGATGTCCAGCTGCTCTGCGAGTCCCCCAACCTCATCG 3622

Db       1953 CCCCTTGTGCTGTCACCGTATCTGAGACCCAGCTTCTCTGCGAGCCTCCCAACCTCACCG 2012

Qy       3623 GCAGGCACAAAGTGATGGCCCGTGTCGGTGGCATGGAGTACTCCCCGGGGATGGTGTACA 3682

Db       2013 GGCAGCACAAGGTCATGGTTCACGTGGGCGGGATGGTGTTCTCGCCTGGCTCGGTGAGTG 2072

Qy       3683 TTGCCCCGGACAGCCCGCTCAGCCTGCCCGCCATCGTCAGCATCGCAGTGGCTGGCGGCC 3742

Db       2073 TCATCTCAGACAGCTTGCTGACCCTGCCAGCCATCGTCAGCATCGCGGCCGGCGGCAGCC 2132
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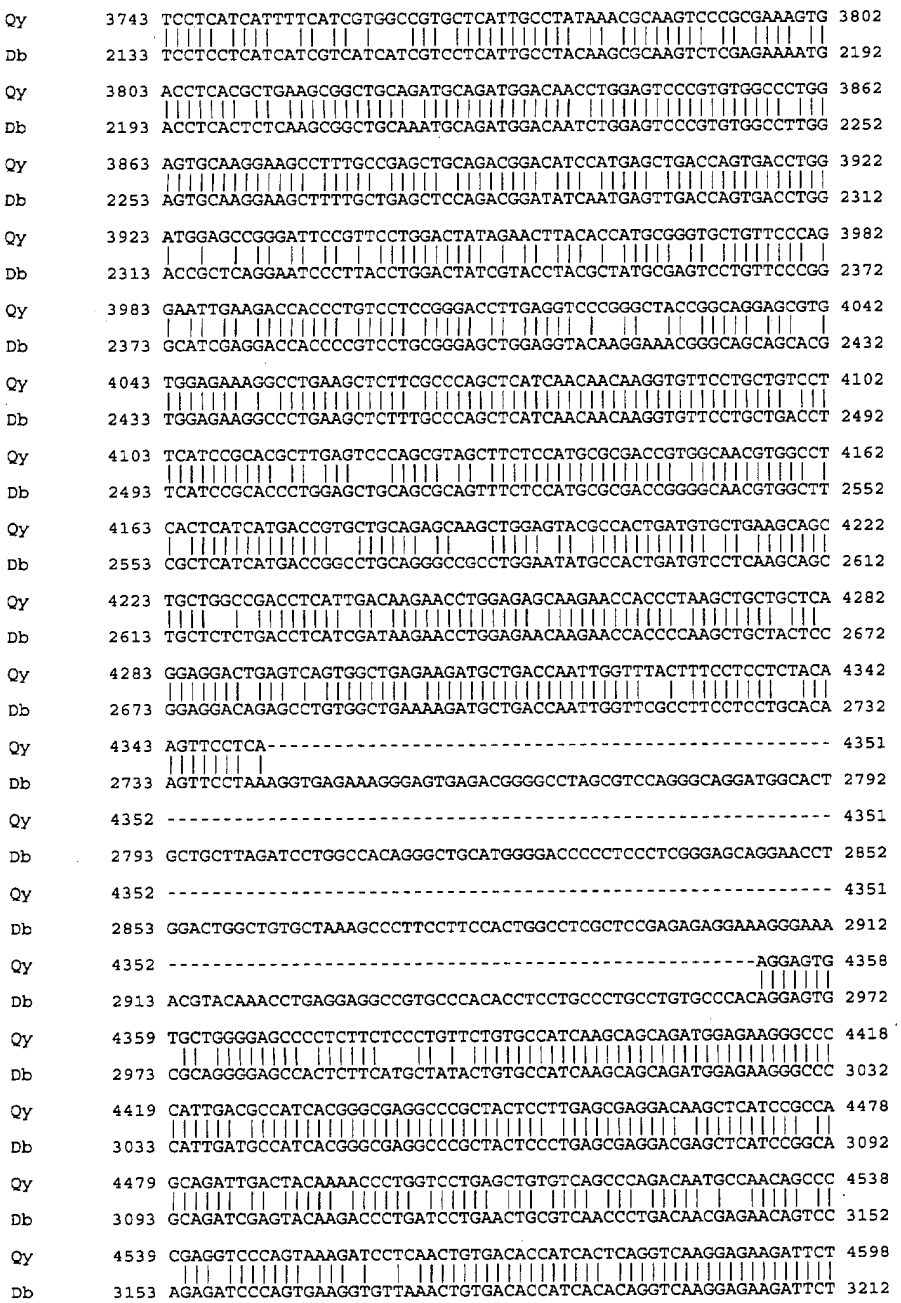

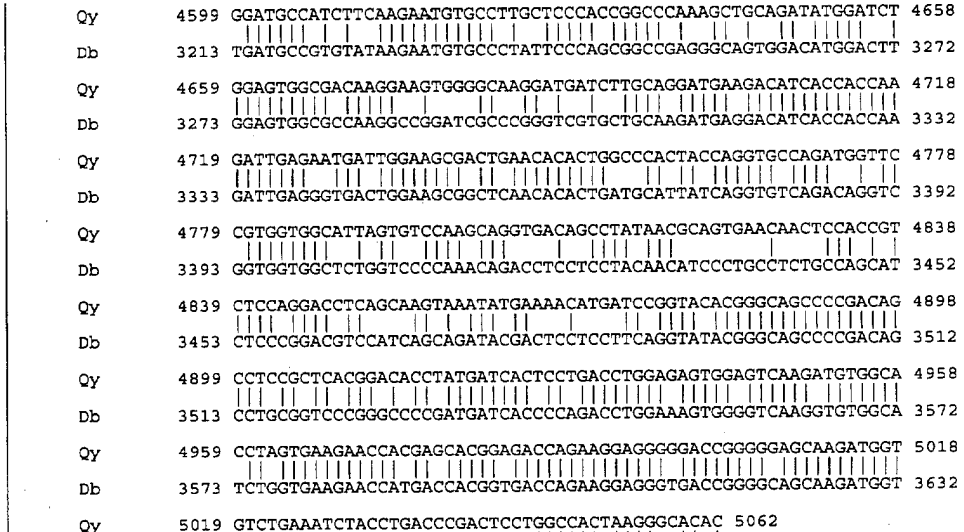

RESULT 9
ABK70006
ID ABK70006 standard; DNA; 2597 BP.
XX
AC ABK70006;
XX
DT 15-JUL-2002 (first entry)
XX
DE cDNA encoding human Pro peptide #46.
XX
KW Human; ss; gene; PRO; secreted protein; transmembrane protein;
KW genetic disorder; tumour; cancer.
XX
OS Homo sapiens.
XX
PN WO200224888-A2.
XX
PD 28-MAR-2002.
XX
PF 29-AUG-2001; 2001WO-US027099.
XX
PR 01-SEP-2000; 2000US-0229896P.
PR 05-SEP-2000; 2000US-0230621P.
PR 22-SEP-2000; 2000US-0235147P.
PR 10-NOV-2000; 2000WO-US030873.
PR 12-JAN-2001; 2001US-0261878P.
PR 16-JAN-2001; 2001US-0261910P.
PR 16-JAN-2001; 2001US-0261939P.
PR 16-JAN-2001; 2001US-0262150P.
PR 25-JAN-2001; 2001US-0264395P.
PR 02-FEB-2001; 2001US-0266421P.
PR 09-FEB-2001; 2001US-0267623P.
PR 28-FEB-2001; 2001WO-US006520.
PR 09-MAR-2001; 2001US-0274399P.
PR 03-APR-2001; 2001US-0280982P.
PR 04-APR-2001; 2001US-0282129P.
PR 04-APR-2001; 2001US-0282199P.
PR 09-MAY-2001; 2001US-0290589P.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.

PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX
DR WPI; 2002-362426/39.
DR P-PSDB; ABG34075.
XX
PT New PRO polypeptides and polynucleotides encoding the polypeptides,
PT useful in gene therapy, chromosome identification, tissue typing, or for
PT genetic analysis of individuals with genetic disorders.
XX
PS Claim 2; Fig 91; 218pp; English.
XX
CC This invention relates to the cDNA and protein sequences of novel
CC secreted and transmembrane polypeptides PRO polypeptides. The invention
CC also comprises a method for producing the proteins of the invention by
CC recombinant means and antibodies specific for the protein of the
CC invention. The antibody may be used for detecting the PRO proteins of the
CC invention and may be used to modify their activity. polynucleotides may
CC be used as hybridisation probes for a cDNA library to isolate the full-
CC length PRO cDNA or to isolate other cDNAs, to construct hybridisation
CC probes for mapping the gene which encodes that PRO and for genetic
CC analysis of individuals with genetic disorders, in assays to identify
CC other proteins or molecules involved in binding reaction, to generate
CC transgenic animals or knock-out animals which in turn are useful in the
CC development and screening of therapeutically useful reagents, for
CC chromosome identification, and tissue typing. The PRO polypeptides are
CC useful in gene therapy, and as molecular weight markers for protein
CC electrophoresis purposes. The sequences may also be used to detect
CC overexpression on PRO polypeptides in cancerous tumours and for screening
CC for differentially expressed genes using microarray technology. The
CC present sequence represents a cDNA encoding a human PRO protein of the
CC invention
XX
SQ Sequence 2597 BP; 688 A; 570 C; 642 G; 697 T; 0 U; 0 Other;

Query Match 13.9%; Score 793.8; DB 6; Length 2597;
Best Local Similarity 99.7%; Pred. No. 6.1e-181;
Matches 795; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy        579 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 60

Qy        639 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 120

Qy        699 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 180

Qy        759 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 240

Qy        819 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 300

Qy        879 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 938
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 360

Qy        939 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 420

Qy        999 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 480

Qy       1059 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 540

Qy       1119 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 1178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 600

Qy       1179 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 1238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 660

Qy       1239 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 1298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 720

Qy       1299 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 1358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 780

Qy       1359 CAAGCTGAAGAAGATCC 1375
              ||||||||||||||| | |
Db        781 CAAGCTGAAGAAGGTGC 797
```

RESULT 10
ADA01359
ID ADA01359 standard; cDNA; 2597 BP.
XX
AC ADA01359;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human PRO polynucleotide #46.
XX
KW Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide;
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
KW adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;
KW microvascular endothelial cell; endothelial cell tube formation;
KW sports-related joint problem; articular cartilage defect; osteoarthritis;
KW rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.
XX
OS Homo sapiens.
XX
PN US2003068779-A1.
XX
PD 10-APR-2003.
XX
PF 16-SEP-2002; 2002US-00245107.
XX
PR 09-MAY-2001; 2001US-0290589P.
PR 29-AUG-2001; 2001WO-US027099.
PR 18-JUL-2002; 2002US-00197942.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX
DR WPI; 2003-625484/59.
DR P-PSDB; ADA01360.
XX
PT Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for
PT stimulating proliferation of human microvascular endothelial cells, and
PT PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
PT cells.
XX

```
PS   Claim 2; Fig 91; 307pp; English.
XX
CC   The invention relates to isolated human PRO polypeptides (secreted and
CC   transmembrane polypeptides) and the polynucleotides encoding them. The
CC   invention also relates to an antibody which specifically binds to a PRO
CC   polypeptide, a method for stimulating the release of tumour necrosis
CC   factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC   proliferation or differentiation of chondrocyte cells and a method for
CC   detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
CC   colon, breast, prostate, rectal, cervical and liver tumours). The
CC   polynucleotides are useful in molecular biology, including uses as
CC   hybridisation probes, in chromosome and gene mapping, in generating
CC   antisense RNA and DNA and in gene therapy. The polynucleotides may also
CC   be used in preparing PRO polypeptides by recombinant techniques and in
CC   generating either transgenic animals or knock-out animals which are
CC   useful in the development and screening of therapeutically useful
CC   reagents. The PRO polypeptides or antibodies are used in preparing a
CC   medicament for treating a condition responsive to the polypeptides or
CC   antibodies, such as tumours, for stimulating and inhibiting proliferation
CC   of human microvascular endothelial cells, for inducing endothelial cell
CC   tube formation and for treating sports-related joint problems, articular
CC   cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence
CC   represents a human PRO polynucleotide of the invention.
XX
SQ   Sequence 2597 BP; 688 A; 570 C; 642 G; 697 T; 0 U; 0 Other;

  Query Match             13.9%;  Score 793.8;  DB 8;  Length 2597;
  Best Local Similarity   99.7%;  Pred. No. 6.1e-181;
  Matches  795;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        579 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 60

Qy        639 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 120

Qy        699 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 180

Qy        759 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 240

Qy        819 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 300

Qy        879 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 938
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 360

Qy        939 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 420

Qy        999 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 480

Qy       1059 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 540

Qy       1119 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 1178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 600

Qy       1179 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 1238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 660

Qy       1239 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 1298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 720

Qy       1299 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 1358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 780

Qy       1359 CAAGCTGAAGAAGATCC 1375
              ||||||||||||| | |
Db        781 CAAGCTGAAGAAGGTGC 797


RESULT 11
ADA43788
ID   ADA43788 standard; cDNA; 2597 BP.
XX
AC   ADA43788;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human cDNA encoding secreted/transmembrane polypeptide PRO34003.
XX
KW   ss; gene; human; PRO; secreted protein; transmembrane protein;
KW   endothelial cell tube formation; chondrocyte cell differentiation;
KW   microvascular endothelial cell; tumour; lung tumour; colon tumour;
KW   breast tumour; prostate tumour; rectal tumour; kidney tumour;
KW   liver tumour; cytostatic; vaccine.
XX
OS   Homo sapiens.
XX
PN   US2003064474-A1.
XX
PD   03-APR-2003.
XX
PF   16-SEP-2002; 2002US-00245859.
XX
PR   29-AUG-2001; 2001WO-US027099.
PR   18-JUL-2002; 2002US-00197942.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Eaton DL,  Filvaroff E,  Goddard A,  Grimaldi JC;
PI   Gurney AL,  Smith V,  Stephan JP,  Watanabe CK,  Wood WI,  Zhang Z;
PI   Fong S;
XX
DR   WPI; 2003-605867/57.
DR   P-PSDB; ADA43789.
XX
PT   New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
PT   PRO21383, useful in molecular biology, chromosome and gene mapping, in
PT   generating antisense RNA and DNA, and in gene therapy.
XX
PS   Claim 2; Fig 91; 308pp; English.
XX
CC   The invention relates to an isolated secreted/transmembrane (PRO)
CC   polypeptide, having at least 80% sequence identity to a sequence selected
CC   from any one of the 57 amino acid sequences given in specification, or to
CC   a sequence encoded by a nucleic acid molecule selected from any one of
CC   the nucleic acids deposited under any of the ATCC accession numbers given
CC   in specification, or a sequence having at least 80% identity to PRO
CC   lacking its associated signal peptide, an extracellular domain of PRO
CC   with or without its associated signal peptide. Also included are vectors,
CC   transformed host cells, anti-PRO antibodies, the nucleic acids encoding
CC   PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
CC   administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
CC   PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
CC   an oligonucleotide probe derived from any one of the above nucleotide
CC   sequences. PRO6018 polypeptide is useful for stimulating the
CC   proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
CC   and PRO21383 polypeptides are useful for stimulating the proliferation of
CC   human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
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CC   polypeptides are useful for inhibiting the proliferation of human
CC   microvascular endothelial cells. PRO polypeptides are useful for
CC   detecting the presence of tumour in a mammal, including tumours of lung,
CC   colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
CC   PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
CC   PRO34274 polypeptides are useful for inducing endothelial cell tube
CC   formation. PRO or the antibody are useful in the preparation of a
CC   medicament for treating a condition responsive to PRO polypeptide. The
CC   oligonucleotide probes are useful for isolating genomic and cDNA
CC   nucleotide sequences, for measuring or detecting the expression of an
CC   associated gene, and as antisense probes. PRO nucleic acid is useful as a
CC   hybridisation probe, in chromosome and gene mapping, in the generation of
CC   antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
CC   PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
CC   present sequence encodes a PRO protein.
XX
SQ   Sequence 2597 BP; 688 A; 570 C; 642 G; 697 T; 0 U; 0 Other;

  Query Match           13.9%;  Score 793.8;  DB 8;  Length 2597;
  Best Local Similarity   99.7%;  Pred. No. 6.1e-181;
  Matches  795;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        579 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 60

Qy        639 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 120

Qy        699 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 180

Qy        759 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 240

Qy        819 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 300

Qy        879 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 938
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 360

Qy        939 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 420

Qy        999 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 480

Qy       1059 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 540

Qy       1119 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 1178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 600

Qy       1179 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 1238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 660

Qy       1239 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 1298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 720

Qy       1299 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 1358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 780

Qy       1359 CAAGCTGAAGAAGATCC 1375
              |||||||||||||| | |
Db        781 CAAGCTGAAGAAGGTGC 797


RESULT 12
ADA43556
ID   ADA43556 standard; cDNA; 2597 BP.
XX
AC   ADA43556;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human cDNA encoding secreted/transmembrane polypeptide PRO34003.
XX
KW   ss; gene; human; PRO; secreted protein; transmembrane protein;
KW   endothelial cell tube formation; chondrocyte cell differentiation;
KW   microvascular endothelial cell; tumour; lung tumour; colon tumour;
KW   breast tumour; prostate tumour; rectal tumour; kidney tumour;
KW   liver tumour; cytostatic; vaccine.
XX
OS   Homo sapiens.
XX
PN   US2003073196-A1.
XX
PD   17-APR-2003.
XX
PF   18-SEP-2002; 2002US-00246210.
XX
PR   04-APR-2001; 2001US-0282199P.
PR   29-AUG-2001; 2001WO-US027099.
PR   18-JUL-2002; 2002US-00197942.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Eaton DL,  Filvaroff E,  Goddard A,  Grimaldi JC;
PI   Gurney AL,  Smith V,  Stephan JP,  Watanabe CK,  Wood WI,  Zhang Z;
PI   Fong S;
XX
DR   WPI; 2003-743814/70.
DR   P-PSDB; ADA43557.
XX
PT   New secreted and transmembrane PRO polypeptides, e.g. PRO20080 or
PT   PRO21383 useful for stimulating the proliferation or differentiation of
PT   chondrocyte cells and detecting the presence of a tumor in a mammal.
XX
PS   Claim 2; Fig 91; 307pp; English.
XX
CC   The invention relates to an isolated secreted/transmembrane (PRO)
CC   polypeptide, having at least 80% sequence identity to a sequence selected
CC   from any one of the 57 amino acid sequences given in specification, or to
CC   a sequence encoded by a nucleic acid molecule selected from any one of
CC   the nucleic acids deposited under any of the ATCC accession numbers given
CC   in specification, or a sequence having at least 80% identity to PRO
CC   lacking its associated signal peptide, an extracellular domain of PRO
CC   with or without its associated signal peptide. Also included are vectors,
CC   transformed host cells, anti-PRO antibodies, the nucleic acids encoding
CC   PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
CC   administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
CC   PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
CC   an oligonucleotide probe derived from any one of the above nucleotide
CC   sequences. PRO6018 polypeptide is useful for stimulating the
CC   proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
CC   and PRO21383 polypeptides are useful for stimulating the proliferation of
CC   human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
CC   polypeptides are useful for inhibiting the proliferation of human
CC   microvascular endothelial cells. PRO polypeptides are useful for
CC   detecting the presence of tumour in a mammal, including tumours of lung,
CC   colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
CC   PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
CC   PRO34274 polypeptides are useful for inducing endothelial cell tube
CC   formation. PRO or the antibody are useful in the preparation of a
```

```
CC   medicament for treating a condition responsive to PRO polypeptide. The
CC   oligonucleotide probes are useful for isolating genomic and cDNA
CC   nucleotide sequences, for measuring or detecting the expression of an
CC   associated gene, and as antisense probes. PRO nucleic acid is useful as a
CC   hybridisation probe, in chromosome and gene mapping, in the generation of
CC   antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
CC   PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
CC   present sequence encodes a PRO protein.
XX
SQ   Sequence 2597 BP; 688 A; 570 C; 642 G; 697 T; 0 U; 0 Other;

  Query Match           13.9%;  Score 793.8;  DB 8;  Length 2597;
  Best Local Similarity  99.7%;  Pred. No. 6.1e-181;
  Matches  795;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        579 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 60

Qy        639 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 120

Qy        699 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 180

Qy        759 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 240

Qy        819 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 300

Qy        879 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 938
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 360

Qy        939 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 420

Qy        999 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 480

Qy       1059 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 540

Qy       1119 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 1178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 600

Qy       1179 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 1238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 660

Qy       1239 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 1298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 720

Qy       1299 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 1358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 780

Qy       1359 CAAGCTGAAGAAGATCC 1375
              ||||||||||||| | |
Db        781 CAAGCTGAAGAAGGTGC 797

RESULT 13
ADA01231
ID   ADA01231 standard; cDNA; 2597 BP.
XX
AC   ADA01231;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Human PRO polynucleotide #46.
XX
KW   Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide;
KW   tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
KW   cancer; lung; colon; breast; prostate; rectum; kidney; liver;
KW   microvascular endothelial cell; endothelial cell tube formation.
XX
OS   Homo sapiens.
XX
PN   US2003068782-A1.
XX
PD   10-APR-2003.
XX
PF   16-SEP-2002; 2002US-00245851.
XX
PR   27-APR-1999;   99US-0131271P.
PR   29-OCT-1999;   99US-0162506P.
PR   02-DEC-1999;   99WO-US028551.
PR   29-AUG-2001; 2001WO-US027099.
PR   18-JUL-2002; 2002US-00197942.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Eaton DL,  Filvaroff E,  Goddard A,  Grimaldi JC;
PI   Gurney AL,  Smith V,  Stephan JP,  Watanabe CK,  Wood WI,  Zhang Z;
PI   Fong S;
XX
DR   WPI; 2003-625487/59.
DR   P-PSDB; ADA01232.
XX
PT   Novel isolated PRO polypeptides e.g. PRO281 and PRO1560, useful in the
PT   preparation of a medicament for treating a condition responsive to PRO
PT   polypeptide, and as therapeutic agents e.g. vaccines.
XX
PS   Claim 2; Fig 91; 308pp; English.
XX
CC   The invention relates to isolated human PRO polypeptides (secreted and
CC   transmembrane polypeptides) and the polynucleotides encoding them. The
CC   invention also relates to an antibody which specifically binds to a PRO
CC   polypeptide, a method for stimulating the release of tumour necrosis
CC   factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC   proliferation or differentiation of chondrocyte cells and a method for
CC   detecting the presence of a tumour in a mammal (e.g. lung, colon, breast,
CC   prostate, rectal, kidney and liver tumours). The polynucleotides are
CC   useful in molecular biology, including uses as hybridisation probes, in
CC   chromosome and gene mapping, in generating antisense RNA and DNA and in
CC   gene therapy. The polynucleotides may also be used in preparing PRO
CC   polypeptides by recombinant techniques and in generating either
CC   transgenic animals or knock-out animals which are useful in the
CC   development and screening of therapeutically useful reagents. The PRO
CC   polypeptides or antibodies are used in preparing a medicament for
CC   treating a condition responsive to the polypeptides or antibodies, such
CC   as tumours, for stimulating and inhibiting proliferation of human
CC   microvascular endothelial cells and for inducing endothelial cell tube
CC   formation. This sequence represents a human PRO polynucleotide of the
CC   invention.
XX
SQ   Sequence 2597 BP; 688 A; 570 C; 642 G; 697 T; 0 U; 0 Other;

  Query Match           13.9%;  Score 793.8;  DB 8;  Length 2597;
  Best Local Similarity  99.7%;  Pred. No. 6.1e-181;
  Matches  795;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        579 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 60
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Qy        639 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 120

Qy        699 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 180

Qy        759 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 240

Qy        819 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 300

Qy        879 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 938
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 360

Qy        939 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 420

Qy        999 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 480

Qy       1059 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 540

Qy       1119 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 1178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 600

Qy       1179 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 1238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 660

Qy       1239 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 1298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 720

Qy       1299 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 1358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 780

Qy       1359 CAAGCTGAAGAAGATCC 1375
              ||||||||||||| | |
Db        781 CAAGCTGAAGAAGGTGC 797
```

RESULT 14
ADA01115
ID ADA01115 standard; cDNA; 2597 BP.
XX
AC ADA01115;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human cDNA encoding secreted/transmembrane polypeptide PRO34003.
XX
KW ss; gene; human; PRO; secreted protein; transmembrane protein;
KW endothelial cell tube formation; chondrocyte cell differentiation;
KW microvascular endothelial cell; tumour; lung tumour; colon tumour;
KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
KW liver tumour; cytostatic; vaccine.
XX
OS Homo sapiens.
XX
PN US2003068780-A1.
XX
PD 10-APR-2003.
XX
PF 16-SEP-2002; 2002US-00245143.
XX
PR 02-AUG-2000; 2000US-0222695P.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-AUG-2001; 2001WO-US027099.
PR 18-JUL-2002; 2002US-00197942.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX
DR WPI; 2003-625485/59.
DR P-PSDB; ADA01116.
XX
PT Novel isolated PRO polypeptides e.g. PRO281 and PRO1560, useful in the
PT preparation of a medicament for treating a condition responsive to PRO
PT polypeptide, and as therapeutic agents e.g. vaccines.
XX
PS Claim 2; Fig 91; 307pp; English.
XX
CC The invention relates to an isolated secreted/transmembrane (PRO)
CC polypeptide, having at least 80% sequence identity to a sequence selected
CC from any one of the 57 amino acid sequences given in specification, or to
CC a sequence encoded by a nucleic acid molecule selected from any one of
CC the nucleic acids deposited under any of the ATCC accession numbers given
CC in specification, or a sequence having at least 80% identity to PRO
CC lacking its associated signal peptide, an extracellular domain of PRO
CC with or without its associated signal peptide. Also included are vectors,
CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
CC an oligonucleotide probe derived from any one of the above nucleotide
CC sequences. PRO6018 polypeptide is useful for stimulating the
CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
CC and PRO21383 polypeptides are useful for stimulating the proliferation of
CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
CC polypeptides are useful for inhibiting the proliferation of human
CC microvascular endothelial cells. PRO polypeptides are useful for
CC detecting the presence of tumour in a mammal, including tumours of lung,
CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
CC PRO34274 polypeptides are useful for inducing endothelial cell tube
CC formation. PRO or the antibody are useful in the preparation of a
CC medicament for treating a condition responsive to PRO polypeptide. The
CC oligonucleotide probes are useful for isolating genomic and cDNA
CC nucleotide sequences, for measuring or detecting the expression of an
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
CC hybridisation probe, in chromosome and gene mapping, in the generation of
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
CC present sequence encodes a PRO protein.
XX
SQ Sequence 2597 BP; 688 A; 570 C; 642 G; 697 T; 0 U; 0 Other;

Query Match 13.9%; Score 793.8; DB 8; Length 2597;
Best Local Similarity 99.7%; Pred. No. 6.1e-181;
Matches 795; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy        699 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 758
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Db        241 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 300

Qy        879 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 938

Db        301 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 360

Qy        939 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 998

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Db        541 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 600

Qy       1179 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 1238

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RESULT 15
ADA43672
ID ADA43672 standard; cDNA; 2597 BP.
XX
AC ADA43672;
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DT 20-NOV-2003 (first entry)
XX
DE Human cDNA encoding secreted/transmembrane polypeptide PRO34003.
XX
KW ss; gene; human; PRO; secreted protein; transmembrane protein;
KW endothelial cell tube formation; chondrocyte cell differentiation;
KW microvascular endothelial cell; tumour; lung tumour; colon tumour;
KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
KW liver tumour; cytostatic; vaccine.
XX
OS Homo sapiens.
XX
PN US2003073190-A1.
XX
PD 17-APR-2003.
XX
PF 09-SEP-2002; 2002US-00238283.
XX
PR 01-JUL-1998; 98US-0091358P.
PR 02-JUN-1999; 99WO-US012252.
PR 20-JUL-1999; 99US-0144758P.
PR 28-JUL-1999; 99US-0146222P.
PR 25-AUG-1999; 99US-00380137.
PR 30-MAR-2000; 2000WO-US008439.
PR 02-JUN-2000; 2000WO-US015264.
PR 29-AUG-2001; 2001WO-US027099.
PR 18-JUL-2002; 2002US-00197942.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX
DR WPI; 2003-585304/55.
DR P-PSDB; ADA43673.
XX
PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
PT PRO21383, useful in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and in gene therapy.
XX
PS Claim 2; Fig 91; 352pp; English.
XX
CC The invention relates to an isolated secreted/transmembrane (PRO)
CC polypeptide, having at least 80% sequence identity to a sequence selected
CC from any one of the 57 amino acid sequences given in specification, or to
CC a sequence encoded by a nucleic acid molecule selected from any one of
CC the nucleic acids deposited under any of the ATCC accession numbers given
CC in specification, or a sequence having at least 80% identity to PRO
CC lacking its associated signal peptide, an extracellular domain of PRO
CC with or without its associated signal peptide. Also included are vectors,
CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
CC an oligonucleotide probe derived from any one of the above nucleotide
CC sequences. PRO6018 polypeptide is useful for stimulating the
CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
CC and PRO21383 polypeptides are useful for stimulating the proliferation of
CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
CC polypeptides are useful for inhibiting the proliferation of human
CC microvascular endothelial cells. PRO polypeptides are useful for
CC detecting the presence of tumour in a mammal, including tumours of lung,
CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
CC PRO34274 polypeptides are useful for inducing endothelial cell tube
CC formation. PRO or the antibody are useful in the preparation of a
CC medicament for treating a condition responsive to PRO polypeptide. The
CC oligonucleotide probes are useful for isolating genomic and cDNA
CC nucleotide sequences, for measuring or detecting the expression of an
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
CC hybridisation probe, in chromosome and gene mapping, in the generation of
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
CC present sequence encodes a PRO protein.
XX
SQ Sequence 2597 BP; 688 A; 570 C; 642 G; 697 T; 0 U; 0 Other;

  Query Match   13.9%; Score 793.8; DB 8; Length 2597;
  Best Local Similarity   99.7%; Pred. No. 6.1e-181;
  Matches 795; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

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Qy        579 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 638

Db          1 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 60

Qy        639 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 698

Db         61 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 120

Qy        699 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 758
```

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Db        121 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 180

Qy        759 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	579.2	10.2	2477	4	US-09-907-794A-169	Sequence 169, App
2	579.2	10.2	2477	4	US-09-905-125A-169	Sequence 169, App
3	579.2	10.2	2477	4	US-09-902-775A-169	Sequence 169, App
4	284.2	5.0	3458	4	US-09-023-655-603	Sequence 603, App
5	201.2	3.5	4707	3	US-09-181-706-1	Sequence 1, Appli
6	201.2	3.5	4707	3	US-09-458-791-1	Sequence 1, Appli
7	201.2	3.5	4707	3	US-09-459-066-1	Sequence 1, Appli
8	201.2	3.5	4707	4	US-09-459-065-1	Sequence 1, Appli
c 9	86.4	1.5	1024	4	US-09-328-475C-37	Sequence 37, Appl
10	57.8	1.0	288	4	US-09-313-294A-6281	Sequence 6281, Ap
c 11	49.6	0.9	7218	1	US-08-232-463-14	Sequence 14, Appl
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13	49.4	0.9	1867	2	US-08-634-642-3	Sequence 3, Appli
14	49.4	0.9	1867	3	US-08-989-370-3	Sequence 3, Appli
15	49.4	0.9	1867	4	US-09-398-169-3	Sequence 3, Appli
16	49.2	0.9	4626	1	US-08-306-691B-22	Sequence 22, Appl
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18	48.6	0.9	3012	4	US-09-551-974A-94	Sequence 94, Appl
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21	48.6	0.9	3012	4	US-09-874-923-94	Sequence 94, Appl
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40	48.2	0.8	1241	2	US-08-469-334-39	Sequence 39, Appl
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45	48.2	0.8	1358	2	US-08-471-044-45	Sequence 45, Appl

ALIGNMENTS

RESULT 1
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; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
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; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547

; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 169
; LENGTH: 2477
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-794A-169

Query Match 10.2%; Score 579.2; DB 4; Length 2477;
Best Local Similarity 67.1%; Pred. No. 1.4e-131;
Matches 837; Conservative 0; Mismatches 408; Indels 3; Gaps 1;

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Qy        451 GAGCCTTATCATAAGAAGGAGCACTATCTGTCAGGTGTCAACGAGAGCGGCTCAGTCTTT 510
              |||||  |  || |||||||||||||| |||||  |||||||  |||  ||| |  | |
Db        1276 GAGCCATCCCACAAGAAGGAGCACTACCTGTCCAGTGTCAACAAGACGGGCACCATGTAC 1335

Qy        511 GGAGTGATCGTCTCCTACAGCAACCTGGATGACAAGCTGTTCATTGCCACGGCAGTGGAT 570
              ||  |||||  ||   ||           ||||| ||||| ||||| | ||||||  ||||||
Db        1336 GGGGTGATTGTGCGCTCTGAGGGTGAGGATGGCAAGCTCTTCATCGGCACGGCTGTGGAT 1395

Qy        571 GGGAAGCCCGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCG 630
              |||||||  || || || || ||| | |||||||||| ||| ||    || |||||  |
Db        1396 GGGAAGCAGGATTACTTCCCGACCCTGTCCAGCCGGAAGCTGCCCCGAGACCCTGAGTCC 1455

Qy        631 GATGGCATGTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCT 690
                | |||| |||  || |   | ||    || || ||  ||||  | || |||||||||
Db        1456 TCAGCCATGCTCGACTATGAGCTACACAGCGATTTTGTCTCCTCTCTCATCAAGATCCCT 1515

Qy        691 TCGGACACCTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGT 750
              || |||||| |  || |  || |  |||||| |||| |||  |||| || |||   |||
Db        1516 TCAGACACCCTGGCCCTGGTCTCCCACTTTGACATCTTCTACATCTACGGCTTTGCTAGT 1575

Qy        751 GGCAACTTTGTCTACTTTTTGACCCTCCAACCTGAGA---TGGTGTCTCCACCAGGCTCC 807
              ||   |||||||||||||| | ||  |||| || ||||     | |  |    |  | |
Db        1576 GGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCGAGACCCCTGAGGGTGTGGCCATCAAC 1635

Qy        808 ACCACCAAGGAGCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCC 867
              || |   || |  | || || ||      |||| |||| |||||||| ||| |
Db        1636 TCCGCTGGAGACCTCTTCTACACCTCACGCATCGTGCGGCTCTGCAAGGATGACCCCAAG 1695

Qy        868 TTCAACTCCTATGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTG 927
              ||| |||| || ||     ||||| | |||||   ||    |||||||| ||||||||
Db        1696 TTCCACTCATACGTGTCCCTGCCCTTCGGCTGCACCCGGGCCGGGGTGGAATACCGCCTC 1755

Qy        928 CTGCAGGCTGCCTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCAT 987
              |||||||||| |||||| |||| | |||| |   || | |  | ||  |     ||
Db        1756 CTGCAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCCAGGCCTTCAATATCACC 1815

Qy        988 CCAGATGATGACCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCC 1047
                | || ||  | |||||  || |||||||||| || |||||| | |  |  | |
Db        1816 AGCCAGGACGATGTACTCTTTGCCATCTTCTCCAAAGGGCAGAAGCAGTATCACCACCCG 1875

Qy        1048 CTGGATGAGTCGGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAG 1107
               |  |||| || |||||||  ||||    |   || ||    |  || ||||||
Db        1876 CCCGATGACTCTGCCCTGTGTGCCTTCCCTATCCGGGCCATCAACTTGCAGATCAAGGAG 1935

Qy        1108 CGGCTGCAGTCTTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAG 1167
               || |||||||| || |||| |||||||||||  |||| ||  ||||||  || ||||
Db        1936 CGCCTGCAGTCCTGCTACCAGGGCGAGGGCAACCTGGAGCTCAACTGGCTGCTGGGGAAG 1995

Qy        1168 GACATCCCCTGCAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATG 1227
               ||| |||  |||| |  |||| |  |||| || |||||||||||||  ||||||||
Db        1996 GACGTCCAGTGCACGAAGGCGCCTGTCCCCATCGATGATAACTTCTGTGGACTGGACATC 2055

Qy        1228 AATGCTCCCCTGGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGG 1287
               ||   |||||||||  ||       |||  ||  |  || | | |||       ||||
Db        2056 AACCAGCCCCTGGGAGGCTCAACTCCAGTGGAGGGCCTGACCCTGTACACCACCAGCAGG 2115

Qy        1288 GACCGCATGACGTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGC 1347
               |||||||||| |||||   | | || || |||||  | ||     |||  |||||||
Db        2116 GACCGCATGACCTCTGTGGCCTCCTACGTTTACAACGGCTACAGCGTGGTTTTTGTGGGG 2175

Qy        1348 ACCAAAAGTGGCAAGCTGAAGAAGATCCGGGTGGATGGACCCAGGGGC 1395
               || || |||||||||||||| ||| |  | || |||    ||| ||
Db        2176 ACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTCAGATGC 2223
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RESULT 2
US-09-905-125A-169
; Sequence 169, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

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;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/905,125A
;  CURRENT FILING DATE:  2001-07-12
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 169
;   LENGTH: 2477
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-905-125A-169

  Query Match            10.2%;  Score 579.2;  DB 4;  Length 2477;
  Best Local Similarity  67.1%;  Pred. No. 1.4e-131;
  Matches  837;  Conservative    0;  Mismatches  408;  Indels    3;  Gaps    1;

Qy        151 TTCAATCACCTGGTGGTGGATGAGAGGACAGGACACATTTACTTGGGGGCCGTCAATCGG 210
              ||||| ||| ||   ||  |  |  |||| ||   | | ||  |||||||| |||| |||
Db        976 TTCAACCACTTGACCGTCCACCAAGGGACGGGGGCCGTCTATGTGGGGGCCATCAACCGG 1035

Qy        211 ATTTACAAGCTCTCCAGCGACCTGAAGGTCTTGGTGACGCATGAGACAGGGCCGGACGAG 270
              | || |||||  |  ||  ||||||   ||  |||| | ||| ||||||||||  || |||
Db       1036 GTCTATAAGCTGACAGGCAACCTGACCATCCAGGTGGCTCATAAGACAGGGCCAGAAGAG 1095

Qy        271 GACAACCCCAAGTGTTACCCACCCCGCATCGTCCAGACCTGCAATGAGCCCCTGACCACC 330
              ||||||        |||||| |||| |||||| ||| ||||||   ||     || |||  |
Db       1096 GACAACAAGTCTCGTTACCCGCCCCTCATCGTGCAGCCCTGCAGCGAAGTGCTCACCCTC 1155

Qy        331 ACCAACAATGTCAACAAGATGCTCCTCATAGACTACAAGGAGAACAGGCTGATTGCCTGT 390
              |||||||||||||||||| ||||| |||| ||||||    ||||||  | ||| | ||||||
Db       1156 ACCAACAATGTCAACAAGCTGCTCATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGT 1215

Qy        391 GGGAGCCTGTACCAAGGCATCTGCAAGCTGCTGAGGCTGGAGGACCTCTTCAAGCTGGGG 450
              ||||||||  |||||  ||  ||||||||||||||| |||||||  ||||||||||  |||| |
Db       1216 GGGAGCCTCTACCAGGGGGTCTGCAAGCTGCTGCGGCTGGATGACCTCTTCATCCTGGTG 1275

Qy        451 GAGCCTTATCATAAGAAGGAGCACTATCTGTCAGGTGTCAACGAGAGCGGCTCAGTCTTT 510
              |||||  |  || |||||||||||||| |||||  ||||||||  |||  |||  |  |  |
Db       1276 GAGCCATCCCACAAGAAGGAGCACTACCTGTCCAGTGTCAACAAGACGGGCACCATGTAC 1335

Qy        511 GGAGTGATCGTCTCCTACAGCAACCTGGATGACAAGCTGTTCATTGCCACGGCAGTGGAT 570
              ||  |||||  ||   ||          |||||  ||||||  |||||  | ||||||  ||||||
Db       1336 GGGGTGATTGTGCGCTCTGAGGGTGAGGATGGCAAGCTCTTCATCGGCACGGCTGTGGAT 1395

Qy        571 GGGAAGCCCGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCG 630
              |||||||   ||  ||  ||  ||  |||  | ||||||||||  |||  ||    ||  |||||  |
Db       1396 GGGAAGCAGGATTACTTCCCGACCCTGTCCAGCCGGAAGCTGCCCCGAGACCCTGAGTCC 1455

Qy        631 GATGGCATGTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCT 690
                |  ||||  |||   ||  |   | ||     ||  ||  ||   ||||   |  ||  |||||||||
Db       1456 TCAGCCATGCTCGACTATGAGCTACACAGCGATTTTGTCTCCTCTCTCATCAAGATCCCT 1515

Qy        691 TCGGACACCTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGT 750
              ||  ||||||  |   ||  |  ||  |  |||||||  ||||  |||   ||||  ||  |||    |||
Db       1516 TCAGACACCCTGGCCCTGGTCTCCCACTTTGACATCTTCTACATCTACGGCTTTGCTAGT 1575

Qy        751 GGCAACTTTGTCTACTTTTTGACCCTCCAACCTGAGA---TGGTGTCTCCACCAGGCTCC 807
              ||    ||||||||||||||  |  ||   ||||  ||  ||||      |  |   |  |  |
Db       1576 GGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCGAGACCCCTGAGGGTGTGGCCATCAAC 1635

Qy        808 ACCACCAAGGAGCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCC 867
              | |  |  ||  |   |  ||  ||  ||     |||||  ||||  ||||||||  |||  |
Db       1636 TCCGCTGGAGACCTCTTCTACACCTCACGCATCGTGCGGCTCTGCAAGGATGACCCCAAG 1695

Qy        868 TTCAACTCCTATGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTG 927
              |||  ||||  ||  ||      |||||  |  |||||     ||     ||||||||  ||||||||
Db       1696 TTCCACTCATACGTGTCCCTGCCCTTCGGCTGCACCCGGGCCGGGGGTGGAATACCGCCTC 1755

Qy        928 CTGCAGGCTGCCTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCAT 987
              ||||||||||  ||||||  ||||  |  ||||  |  ||  |  |  |  |  ||  ||
Db       1756 CTGCAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCCAGGCCTTCAATATCACC 1815

Qy        988 CCAGATGATGACCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCC 1047
                |  ||  ||  |  |||||  ||  ||||||||||  ||  |||||||  |  |      |  |
Db       1816 AGCCAGGACGATGTACTCTTTGCCATCTTCTCCAAAGGGCAGAAGCAGTATCACCACCCG 1875

Qy       1048 CTGGATGAGTCGGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAG 1107
              |  |||||  ||  ||||||||  ||||  |  |  ||  ||  |  ||  ||||||
Db       1876 CCCGATGACTCTGCCCTGTGTGCCTTCCCTATCCGGGCCATCAACTTGCAGATCAAGGAG 1935

Qy       1108 CGGCTGCAGTCTTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAG 1167
              ||  ||||||||  ||  ||||  ||||||||||  |||||  ||    ||||||    ||  ||||
Db       1936 CGCCTGCAGTCCTGCTACCAGGGCGAGGGCAACCTGGAGCTCAACTGGCTGCTGGGGAAG 1995

Qy       1168 GACATCCCCTGCAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATG 1227
              |||  |||  ||||  |  ||||   |  ||||  ||  ||||||||||||||  ||||||||
Db       1996 GACGTCCAGTGCACGAAGGCGCCTGTCCCCATCGATGATAACTTCTGTGGACTGGACATC 2055

Qy       1228 AATGCTCCCCTGGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGG 1287
              ||      ||||||||||  ||          |||  ||  |  |  |  |||      ||||
Db       2056 AACCAGCCCCTGGGAGGCTCAACTCCAGTGGAGGGCCTGACCCTGTACACCACCAGCAGG 2115

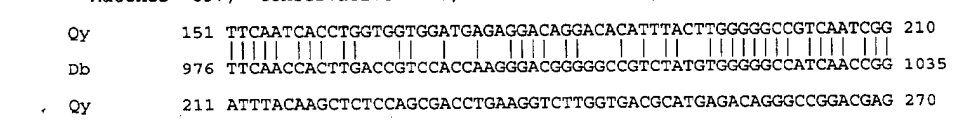
Qy       1288 GACCGCATGACGTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGC 1347
              ||||||||||  |||||   |  ||  ||  |||||   |  ||     |||  ||||||||
Db       2116 GACCGCATGACCTCTGTGGCCTCCTACGTTTACAACGGCTACAGCGTGGTTTTTGTGGGG 2175

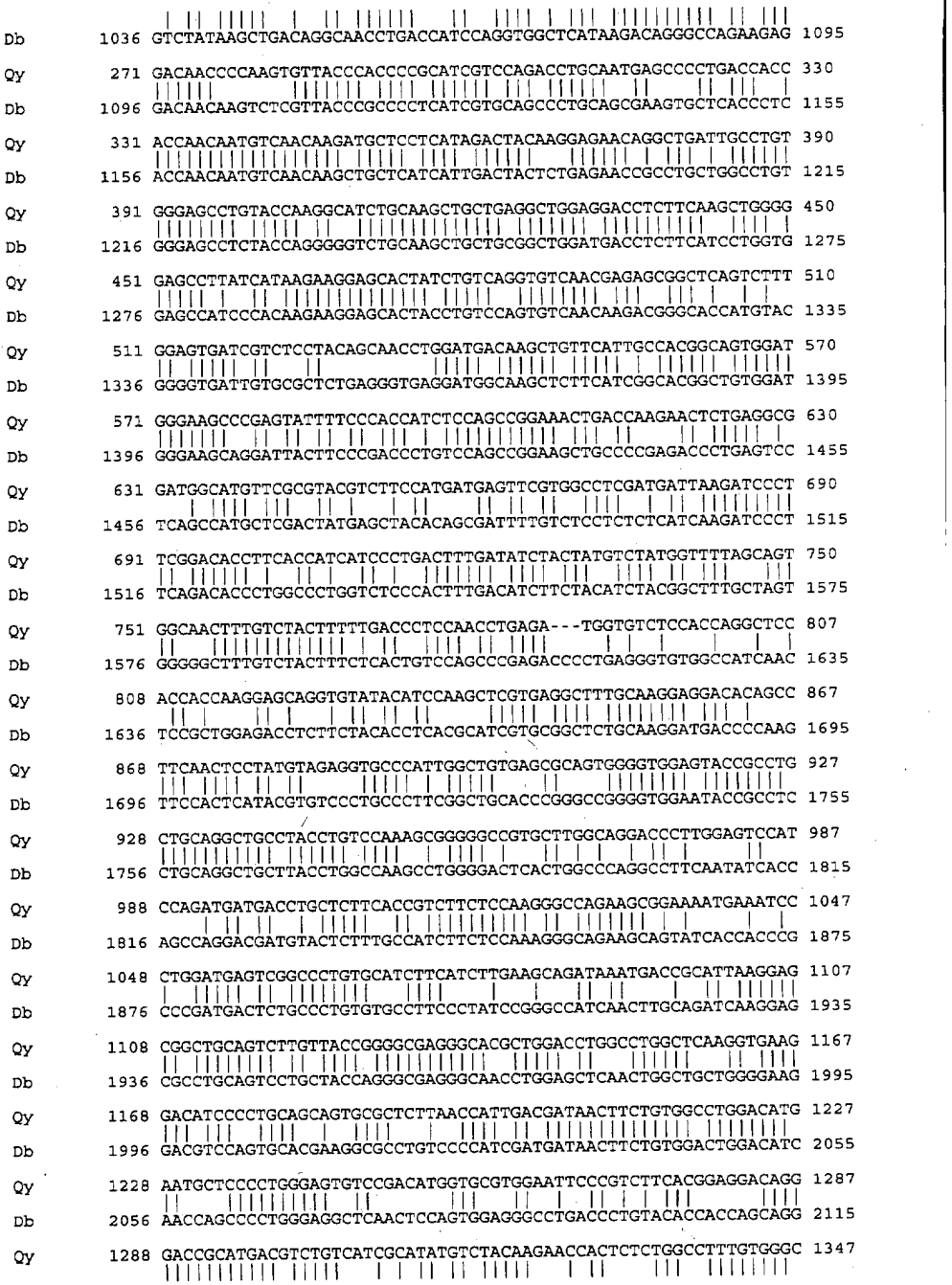
Qy       1348 ACCAAAAGTGGCAAGCTGAAGAAGATCCGGGTGGATGGACCCAGGGGC 1395
              ||  ||  ||||||||||||||  |||  |  ||  |||     |||  ||
Db       2176 ACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTCAGATGC 2223


RESULT 3
US-09-902-775A-169
; Sequence 169, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
```

; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,775A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 169
; LENGTH: 2477
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-902-775A-169

Query Match 10.2%; Score 579.2; DB 4; Length 2477;
Best Local Similarity 67.1%; Pred. No. 1.4e-131;
Matches 837; Conservative 0; Mismatches 408; Indels 3; Gaps 1;





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Db       2116 GACCGCATGACCTCTGTGGCCTCCTACGTTTACAACGGCTACAGCGTGGTTTTTGTGGGG 2175

Qy       1348 ACCAAAAGTGGCAAGCTGAAGAAGATCCGGGTGGATGGACCCAGGGGC 1395
              || || ||||||||||||||| ||| |  | ||  |||    ||| ||
Db       2176 ACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTCAGATGC 2223


RESULT 4
US-09-023-655-603
; Sequence 603, Application US/09023655
; Patent No. 6607879
;  GENERAL INFORMATION:
;    APPLICANT:  Cocks, Benjamin G.
;    APPLICANT:  Susan G. Stuart
;    APPLICANT:  Jeffrey J. Seilhamer
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1508
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/023,655
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0001 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  603:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3458 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  THYMNON04
;      CLONE:  3191066
US-09-023-655-603

  Query Match             5.0%;  Score 284.2;  DB 4;  Length 3458;
  Best Local Similarity   64.4%;  Pred. No. 2e-59;
  Matches  440;  Conservative    0;  Mismatches  237;  Indels    6;  Gaps    1;

Qy       5001 CCGGGGGAGCAAGATGGTGTCTGAAATCTACCTGACCCGACTCCTGGCCACTAAGGGCAC 5060
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Db       1658 CCATCGCAAGAAGGTGCTCCCGGAAATCTACCTGACCCGCCTGCTCTCCACCAAGGGCAC 1717

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Db       1718 GTTGCAGAAGTTTCTGGATGACCTGTTCAAGGCCATTCTGAGTA------TCCGTGAAGA 1771

Qy       5121 TGCCCTGCCCCTGGCCATCAAGTACATGTTTGACTTCCTGGATGAGCAGGCTGATAAACA 5180
                  | || |||||  ||||  || | || ||||||||||| || |||||||| ||
Db       1772 CAAGCCCCCACTGGCTGTCAANNACTTTTTCGACTTCCTGGANGANCAGGCTGAGAAGAG 1831

Qy       5181 TGGCATTCATGACCCGCACGTCCGCCATACCTGGAAGAGCAATTGCCTGCCCCTGAGGTT 5240
                ||  ||    |||||  ||  ||  || | |||||||| |||  |||| || ||  ||||
Db       1832 GGGAATCTCCGACCCCGACACCCTACACATCTGGAAGACCAACAGCCTTCCTCTCCGGTT 1891

Qy       5241 TTGGGTCAACATGATCAAGAACCCGCAGTTTGTGTTTGACATCCATAAGAACAGCATCAC 5300
              |||||  |||||  | |||||||| |||||||| |||||||| | ||||     | ||
Db       1892 CTGGGTGAACATCCTGAAGAACCCCCAGTTTGTCTTTGACATCGACAAGACAGACCACAT 1951

Qy       5301 AGACGCCTGCCTCTCTGTGGTGGCTCAGACCTTCATGGACTCTTGCTCCACGTCAGAGCA 5360
              |||||||||||  || |  || ||| |||||||  ||| | |||||  |  || || |
Db       1952 CGACGCCTGCCTTTCAGTCATCGCGCAGGCCTTCATCGACGCCTGCTCAATCTCTGACCT 2011

Qy       5361 CCGGCTGGGCAAGGACTCGCCCTCCAACAAGCTGCTGTATGCCAAGGACATCCCCAGCTA 5420
              | |||||||||||  |||||  |||||||||  || || ||||||| ||  ||    ||
Db       2012 GCAGCTGGGCAAGGATTCGCCAACCAACAAGCTCCTCTACGCCAAGGAGATTCCTGAGTA 2071

Qy       5421 CAAGAATTGGGTGGAGAGGTATTACTCAGACATAGGGAAGATGCCAGCCATCAGCGACCA 5480
              |  |||     ||| || | || |||     | ||   | | ||| | |  ||||||| ||
Db       2072 CCGGAAGATCGTGCAGCGCTACTACAAGCAGATCCAGGACATGACGCCGCTCAGCGAGCA 2131

Qy       5481 AGACATGAACGCATACCTGGCTGAGCAGTCCCGGATGCACATGAATGAGTTCAACACCAT 5540
              ||| ||||| ||  | ||||| ||| |||| |||    ||  ||||||||||||||||
Db       2132 AGAGATGAATGCCCATCTGGCCGAGGAGTCGAGGAAATACCAGAATGAGTTCAACACCAA 2191

Qy       5541 GAGTGCACTCTCAGAGATCTTCTCCTATGTGGGCAAATACAGCGAGGAGATCCTTGGACC 5600
                 ||  |  |||||| |    || |    | ||  |   | ||||| | |   |
Db       2192 TGTGGCCATGGCAGAGATTTATAAGTACGCCAAGAGGTATCGGCCGCAGATCATGGCCGC 2251

Qy       5601 TCTGGACCACGATGACCAGTGTGGGAAGCAGAAACTGGCCTACAAACTAGAACAAGTCAT 5660
              |||||  | |  |  |  ||| |  |||||   |||| | || || ||  |
Db       2252 GCTGGAGGCCAACCCCACGGCCCGGAGGACACAACTGCAGCACAAGTTTGAGCAGGTGGT 2311

Qy       5661 AACCCTCATGAGCTTAGACAGCT 5683
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Db       2312 GGCTTTGATGGAGGACAACATCT 2334


RESULT 5
US-09-181-706-1
; Sequence 1, Application US/09181706
; Patent No. 6130068
;  GENERAL INFORMATION:
;    APPLICANT:  Melanie K. Spriggs, Michael R. Comeau,
;    APPLICANT:  Robert F. DuBose, Richard S. Johnson
;    TITLE OF INVENTION:  VIRAL ENCODED SEMAPHORIN PROTEIN
;    TITLE OF INVENTION:  RECEPTOR DNA AND POLYPEPTIDES
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Janis C. Henry
;      STREET:  51 University St.
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  US
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/181,706
;      FILING DATE:  October 28, 1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/958,598 (converted to a
;      APPLICATION NUMBER:  Provisional, see below)
;      FILING DATE:  October 28, 1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  --to be assigned-- (USSN 08/958,598
;      APPLICATION NUMBER:  conversion to Provisional application)
;      FILING DATE:  October 26, 1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
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;      NAME:  Henry, Janis C
;      REGISTRATION NUMBER:  34,347
;      REFERENCE/DOCKET NUMBER:  2631-A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)470-4189
;      TELEFAX:  (206)233-0644
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4707 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..4707
US-09-181-706-1

  Query Match             3.5%;  Score 201.2;  DB 3;  Length 4707;
  Best Local Similarity   49.1%;  Pred. No. 4.3e-39;
  Matches  824;  Conservative    0;  Mismatches  728;  Indels  126;  Gaps    6;

Qy       3935 TTCCGTTCCTGGACTATAGAACTTACACCATGCGGGTGCTGTTCCCAGGAATTGAAGACC 3994
Db       3038 TTCCCTTCCTTGACTACAAACATTTTGCTCTGAGAACTTTCTTCCCTGAGTCAGGTGGCT 3097

Qy       3995 ACCCTGTCCTCCGGGACCTTGAGGTCCCGGGCTACCGGCAGGAGCGTGTGGAGAAAGGCC 4054
Db       3098 TCACCCACATCTTCACTGAAGATATGCATAACAGAGACGCCAACGACAAGAATGAAAGTC 3157

Qy       4055 TGAAGCTCTTCGCCCAGCTCATCAACAACAAGGTGTTCCTGCTGTCCTTCATCCGCACGC 4114
Db       3158 TCACAGCTTTGGATGCCCTAATCTGTAATAAAAGCTTTCTTGTTACTGTCATCCACACCC 3217

Qy       4115 TTGAGTCCCAGCGTAGCTTCTCCATGCGCGACCGTGGCAACGTGGCCTCACTCATCATGA 4174
Db       3218 TTGAAAAGCAGAAGAACTTTTCTGTGAAGGACAGGTGTCTGTTTGCCTCCTTCCTAACCA 3277

Qy       4175 CCGTGCTGCAGAGCAAGCTGGAGTACGCCACTGATGTGCTGAAGCAGCTGCTGGCCGACC 4234
Db       3278 TTGCACTGCAAACCAAGCTGGTCTACCTGACCAGCATCCTAGAGGTGCTGACCAGGGACT 3337

Qy       4235 TCATTGACAAGAACCTGGAGAGCAAGAACCACCCTAAGCTGCTGCTCAGGAGGACTGAGT 4294
Db       3338 TGAT------GGAACAGTGTAGTAACATGCAGCCGAAACTCATGCTGAGACGCACGGAGT 3391

Qy       4295 CAGTGGCTGAGAAGATGCTGACCAATTGGTTTACTTTCCTCCTCTACAAGTTCCTCAAGG 4354
Db       3392 CCGTCGTCGAAAAACTCCTCACAAACTGGATGTCCGTCTGCCTTTCTGGATTTCTCCGGG 3451

Qy       4355 AGTGTGCTGGGGAGCCCCTCTTCTCCCTGTTCTGTGCCATCAAGCAGCAGATGGAGAAGG 4414
Db       3452 AGACTGTCGGAGAGCCCTTCTATTTGCTGGTGACGACTCTGAACCAGAAAATTAACAAGG 3511

Qy       4415 GCCCCATTGACGCCATCACGGGCGAGGCCCGCTACTCCTTGAGCGAGGACAAGCTCATCC 4474
Db       3512 GTCCCGTGGATGTAATCACTTGCAAAGCCCTGTACACACTTAATGAAGACTGGCTGTTGT 3571

Qy       4475 GCCAGCAGATTGACTACAAAACCCTGGTCCTGAGCTGTGTCAGCCCAGACAATGCCAACA 4534
Db       3572 GGCAGGTTCCGGAATTCAGTACTGTGGCATTAAACGTCGTCTTTGAAAAAATCCCGGAAA 3631

Qy       4535 GC------------------CCCGAGGTCCCAGTAAAGATCCTCAACTGTGACACCATCA 4576
Db       3632 ACGAGAGTGCAGATGTCTGTCGGAATATTTCAGTCAATGTTCTCGACTGTGACACCATTG 3691

Qy       4577 CTCAGGTCAAGGAGAAGATTCTGGATGCCATCTTCAAGAATGTGCCTTGCTCCCACCGGC 4636
Db       3692 GCCAAGCCAAAGAAAAGATTTTCCAAGCATTCTTAAGCAAAAATGGCTCTCCTTATGGAC 3751

Qy       4637 CCAAAGCTGCAGATATGGATCTGGAGTGGCGACAAGGAAGTGGGGCAAGGATGATCTTGC 4696

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Qy       4697 AGGATGAAGACATCACCACCAAGATTGAGAATGATTGGAAGCGACTGAACACACTGGCCC 4756
Db       3812 ACATCGACAGTTCCTCCGTGATTCTTGAAGATGGAATCACCAAGCTAAACACCATTGGCC 3871

Qy       4757 ACTACCAGGTGCCAGATGGTTCCGTGGTGGCATTAGTGTCCAAGCAGGTGACAGCCTATA 4816
Db       3872 ACTATGAGATATCAAATGGATCCACTATAAAAGTCTTTAAGAAGATAGCAAATTTTACTT 3931

Qy       4817 ACGCAGTGAACAACTCCACCGTCTCCAGGACCTCAGCAAGTAAATATGAAAACATGATCC 4876
Db       3932 CAGATGTGGAGTACTC--------GGATGACCACTGCCATTTGATTTTA---------- 3972

Qy       4877 GGTACACGGGCAGCCCCGACAGCCTCCGCTCACGGACACCTATGATCACTCCTGACCTGG 4936
Db       3973 ------------------------------------------------------------ 3972

Qy       4937 AGAGTGGAGTCAAGATGTGGCACCTAGTGAAGAACCACGAGCACGGAGACCAGAAGGAGG 4996
Db       3973 ----------CCAGATTCGGAAGCATTCCAAGATGTGCAAGGAAAGAGAC-------ATC 4015

Qy       4997 GGGACCGGGGGAGCAAGATGGTGTCTGAAATCTACCTGACCCGACTCCTGGCCACTAAGG 5056
Db       4016 GAGGGAAGCACAAGTTCAAAGTAAAAGAAATGTATCTGACAAAGCTGCTGTCGACCAAGG 4075

Qy       5057 GCACACTGCAGAAGTTTGTGGATGACCTCTTTGAGACCATCTTCAGCACGGCACACCGTG 5116
Db       4076 TGGCAATTCATTCTGTGCTTGAAAAACTTTTTAGAAGCATTTGGAGTTTACCCAACAGCA 4135

Qy       5117 GCTCTGCCCTGCCCCTGGCCATCAAGTACATGTTTGACTTCCTGGATGAGCAGGCTGATA 5176
Db       4136 GAGCT------CCATTTGCTATAAAATACTTTTTTGACTTTTTGGACGCCCAGGCTGAAA 4189

Qy       5177 AACATGGCATTCATGACCCGCACGTCCGCCATACCTGGAAGAGCAATTGCCTGCCCCTGA 5236
Db       4190 ACAAAAAAATCACAGATCCTGACGTCGTACATATTTGGAAAACAAACAGCCTTCCTCTTC 4249

Qy       5237 GGTTTTGGGTCAACATGATCAAGAACCCGCAGTTTGTGTTTGACATCCATAAGAACAGCA 5296
Db       4250 GCTTCTGGGTAAACATCCTGAAGAACCCTCAGTTTGTCTTTGACATTAAGAAGACACCAC 4309

Qy       5297 TCACAGACGCCTGCCTCTCTGTGGTGGCTCAGACCTTCATGGACTCTTGCTCCACGTCAG 5356
Db       4310 ATATAGACGGCTGTTTGTCAGTGATTGCCCAGGCATTCATGGATGCATTTTCTCTCACAG 4369

Qy       5357 AGCACCGGCTGGGCAAGGACTCGCCCTCCAACAAGCTGCTGTATGCCAAGGACATCCCCA 5416
Db       4370 AGCAGCAACTAGGGAAGGAAGCACCAACTAATAAGCTTCTCTATGCCAAGGATATCCCAA 4429

Qy       5417 GCTACAAGAATTGGGTGGAGAGGTATTACTCAGACATAGGGAAGATGCCAGCCATCAGCG 5476
Db       4430 CCTACAAAGAAGAAGTAAAATCTTATTACAAAGCAATCAGGGATTTGCCTCCATTGTCAT 4489

Qy       5477 ACCAAGACATGAACGCATACCTGGCTGAGCAGTCCCGGATGCACATGAATGAGTTCAACA 5536
Db       4490 CCTCAGAAATGGAAGAATTTTTAACTCAGGAATCTAAGAAACATGAAAATGAATTTAATG 4549

Qy       5537 CCATGAGTGCACTCTCAGAGATCTTCTCCTATGTGGGCAAATACAGCGAGGAGATCCT 5594
Db       4550 AAGAAGTGGCCTTGACAGAAATTTACAAATACATCGTAAAATATTTTGATGAGATTCT 4607

RESULT 6
US-09-458-791-1
; Sequence 1, Application US/09458791
; Patent No. 6174689
;   GENERAL INFORMATION:
;       APPLICANT: Spriggs, Melanie
;       TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
;                           RECEPTOR DNA AND POLYPEPTIDES
;       NUMBER OF SEQUENCES: 10
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```
;          CORRESPONDENCE ADDRESS:
;               ADDRESSEE: Janis C. Henry
;               STREET: 51 University St.
;               CITY: Seattle
;               STATE: WA
;               COUNTRY: US
;               ZIP: 98101
;          COMPUTER READABLE FORM:
;               MEDIUM TYPE: Floppy disk
;               COMPUTER: IBM PC compatible
;               OPERATING SYSTEM: MS-DOS/Windows 95
;               SOFTWARE: Word for Windows 95, 7.0a
;          CURRENT APPLICATION DATA:
;               APPLICATION NUMBER: US/09/458,791
;               FILING DATE: 10-Dec-1999
;               CLASSIFICATION: <Unknown>
;          PRIOR APPLICATION DATA:
;               APPLICATION NUMBER: 08/958,598
;               FILING DATE: 28-OCT-1997
;          ATTORNEY/AGENT INFORMATION:
;               NAME: Henry, Janis C
;               REGISTRATION NUMBER: 34,347
;               REFERENCE/DOCKET NUMBER: 2631
;          TELECOMMUNICATION INFORMATION:
;               TELEPHONE: (206)470-4189
;               TELEFAX: (206)233-0644
;   INFORMATION FOR SEQ ID NO: 1:
;          SEQUENCE CHARACTERISTICS:
;               LENGTH: 4707 base pairs
;               TYPE: nucleic acid
;               STRANDEDNESS: double
;               TOPOLOGY: linear
;          MOLECULE TYPE: cDNA
;          HYPOTHETICAL: NO
;          ANTI-SENSE: NO
;          FEATURE:
;               NAME/KEY:  CDS
;               LOCATION:  1..4707
;          SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-458-791-1

  Query Match             3.5%;  Score 201.2;  DB 3;  Length 4707;
  Best Local Similarity   49.1%;  Pred. No. 4.3e-39;
  Matches  824;  Conservative    0;  Mismatches  728;  Indels  126;  Gaps    6;

Qy       3935 TTCCGTTCCTGGACTATAGAACTTACACCATGCGGGTGCTGTTCCCAGGAATTGAAGACC 3994
Db       3038 TTCCCTTCCTTGACTACAAACATTTTGCTCTGAGAACTTTCTTCCCTGAGTCAGGTGGCT 3097

Qy       3995 ACCCTGTCCTCCGGGACCTTGAGGTCCCGGGCTACCGGCAGGAGCGTGTGGAGAAAGGCC 4054
Db       3098 TCACCCACATCTTCACTGAAGATATGCATAACAGAGACGCCAACGACAAGAATGAAAGTC 3157

Qy       4055 TGAAGCTCTTCGCCCAGCTCATCAACAACAAGGTGTTCCTGCTGTCCTTCATCCGCACGC 4114
Db       3158 TCACAGCTTTGGATGCCCTAATCTGTAATAAAAGCTTTCTTGTTACTGTCATCCACACCC 3217

Qy       4115 TTGAGTCCCAGCGTAGCTTCTCCATGCGCGACCGTGGCAACGTGGCCTCACTCATCATGA 4174
Db       3218 TTGAAAAGCAGAAGAACTTTTCTGTGAAGGACAGGTGTCTGTTTGCCTCCTTCCTAACCA 3277

Qy       4175 CCGTGCTGCAGAGCAAGCTGGAGTACGCCACTGATGTGCTGAAGCAGCTGCTGGCCGACC 4234
Db       3278 TTGCACTGCAAACCAAGCTGGTCTACCTGACCAGCATCCTAGAGGTGCTGACCAGGGACT 3337

Qy       4235 TCATTGACAAGAACCTGGAGAGCAAGAACCACCCTAAGCTGCTGCTCAGGAGGACTGAGT 4294
Db       3338 TGAT------GGAACAGTGTAGTAACATGCAGCCGAAACTCATGCTGAGACGCACGGAGT 3391

Qy       4295 CAGTGGCTGAGAAGATGCTGACCAATTGGTTTACTTTCCTCCTCTACAAGTTCCTCAAGG 4354
Db       3392 CCGTCGTCGAAAAACTCCTCACAAACTGGATGTCCGTCTGCCTTTCTGGATTTCTCCGGG 3451

Qy       4355 AGTGTGCTGGGGAGCCCCTCTTCTCCCTGTTCTGTGCCATCAAGCAGCAGATGGAGAAGG 4414
Db       3452 AGACTGTCGGAGAGCCCTTCTATTTGCTGGTGACGACTCTGAACCAGAAAATTAACAAGG 3511

Qy       4415 GCCCCATTGACGCCATCACGGGCGAGGCCCGCTACTCCTTGAGCGAGGACAAGCTCATCC 4474
Db       3512 GTCCCGTGGATGTAATCACTTGCAAAGCCCTGTACACACTTAATGAAGACTGGCTGTTGT 3571

Qy       4475 GCCAGCAGATTGACTACAAAACCCTGGTCCTGAGCTGTGTCAGCCCAGACAATGCCAACA 4534
Db       3572 GGCAGGTTCCGGAATTCAGTACTGTGGCATTAAACGTCGTCTTTGAAAAAATCCCGGAAA 3631

Qy       4535 GC-----------------CCCGAGGTCCCAGTAAAGATCCTCAACTGTGACACCATCA 4576
Db       3632 ACGAGAGTGCAGATGTCTGTCGGAATATTTCAGTCAATGTTCTCGACTGTGACACCATTG 3691

Qy       4577 CTCAGGTCAAGGAGAAGATTCTGGATGCCATCTTCAAGAATGTGCCTTGCTCCCACCGGC 4636
Db       3692 GCCAAGCCAAAGAAAAGATTTCCAAGCATTCTTAAGCAAAAATGGCTCTCCTTATGGAC 3751

Qy       4637 CCAAAGCTGCAGATATGGATCTGGAGTGGCGACAAGGAAGTGGGGCAAGGATGATCTTGC 4696
Db       3752 TTCAGCTTAATGAAATTGGTCTTGAGCTTCAAATGGGCACACGACAGAAAGAACTTCTGG 3811

Qy       4697 AGGATGAAGACATCACCACCAAGATTGAGAATGATTGGAAGCGACTGAACACACTGGCCC 4756
Db       3812 ACATCGACAGTTCCTCCGTGATTCTTGAAGATGGAATCACCAAGCTAAACACCATTGGCC 3871

Qy       4757 ACTACCAGGTGCCAGATGGTTCCGTGGTGGCATTAGTGTCCAAGCAGGTGACAGCCTATA 4816
Db       3872 ACTATGAGATATCAAATGGATCCACTATAAAAGTCTTTAAGAAGATAGCAAATTTTACTT 3931

Qy       4817 ACGCAGTGAACAACTCCACCGTCTCCAGGACCTCAGCAAGTAAATATGAAAACATGATCC 4876
Db       3932 CAGATGTGGAGTACTC--------GGATGACCACTGCCATTTGATTTTA----------- 3972

Qy       4877 GGTACACGGGCAGCCCCGACAGCCTCCGCTCACGGACACCTATGATCACTCCTGACCTGG 4936
Db       3973 ------------------------------------------------------------ 3972

Qy       4937 AGAGTGGAGTCAAGATGTGGCACCTAGTGAAGAACCACGAGCACGGAGACCAGAAGGAGG 4996
Db       3973 ----------CCAGATTCGGAAGCATTCCAAGATGTGCAAGGAAAGAGAC-------ATC 4015

Qy       4997 GGGACCGGGGGAGCAAGATGGTGTCTGAAATCTACCTGACCCGACTCCTGGCCACTAAGG 5056
Db       4016 GAGGGAAGCACAAGTTCAAAGTAAAAGAAATGTATCTGACAAAGCTGCTGTCGACCAAGG 4075

Qy       5057 GCACACTGCAGAAGTTTGTGGATGACCTCTTTGAGACCATCTTCAGCACGGCACACCGTG 5116
Db       4076 TGGCAATTCATTCTGTGCTTGAAAAACTTTTTAGAAGCATTTGGAGTTTACCCAACAGCA 4135

Qy       5117 GCTCTGCCCTGCCCCTGGCCATCAAGTACATGTTTGACTTCCTGGATGAGCAGGCTGATA 5176
Db       4136 GAGCT------CCATTTGCTATAAAATACTTTTTTGACTTTTTGGACGCCCAGGCTGAAA 4189

Qy       5177 AACATGGCATTCATGACCCGCACGTCCGCCATACCTGGAAGAGCAATTGCCTGCCCCTGA 5236
Db       4190 ACAAAAAAATCACAGATCCTGACGTCGTACATATTTGGAAAACAAACAGCCTTCCTCTTC 4249

Qy       5237 GGTTTTGGGTCAACATGATCAAGAACCCGCAGTTTGTGTTTGACATCCATAAGAACAGCA 5296
Db       4250 GCTTCTGGGTAAACATCCTGAAGAACCCTCAGTTTGTCTTTGACATTAAGAAGACACCAC 4309

Qy       5297 TCACAGACGCCTGCCTCTCTGTGGTGGCTCAGACCTTCATGGACTCTTGCTCCACGTCAG 5356
Db       4310 ATATAGACGGCTGTTTGTCAGTGATTGCCCAGGCATTCATGGATGCATTTTCTCTCACAG 4369

Qy       5357 AGCACCGGCTGGGCAAGGACTCGCCCTCCAACAAGCTGCTGTATGCCAAGGACATCCCCA 5416
Db       4370 AGCAGCAACTAGGGAAGGAAGCACCAACTAATAAGCTTCTCTATGCCAAGGATATCCCAA 4429

Qy       5417 GCTACAAGAATTGGGTGGAGAGGTATTACTCAGACATAGGGAAGATGCCAGCCATCAGCG 5476
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Db       4430 CCTACAAAGAAGAAGTAAAATCTTATTACAAAGCAATCAGGGATTTGCCTCCATTGTCAT 4489

Qy       5477 ACCAAGACATGAACGCATACCTGGCTGAGCAGTCCCGGATGCACATGAATGAGTTCAACA 5536

Db       4490 CCTCAGAAATGGAAGAATTTTTAACTCAGGAATCTAAGAAACATGAAAATGAATTTAATG 4549

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Db       4550 AAGAAGTGGCCTTGACAGAAATTTACAAATACATCGTAAAATATTTTGATGAGATTCT 4607
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RESULT 7
US-09-459-066-1
; Sequence 1, Application US/09459066
; Patent No. 6187909
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
; TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry
; STREET: 51 University St.
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/Windows 95
; SOFTWARE: Word for Windows 95, 7.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/459,066
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/958,598
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4707 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..4707
US-09-459-066-1

Query Match 3.5%; Score 201.2; DB 3; Length 4707;
Best Local Similarity 49.1%; Pred. No. 4.3e-39;
Matches 824; Conservative 0; Mismatches 728; Indels 126; Gaps 6;

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Qy       3935 TTCCGTTCCTGGACTATAGAACTTACACCATGCGGGTGCTGTTCCCAGGAATTGAAGACC 3994

Db       3038 TTCCCTTCCTTGACTACAAACATTTTGCTCTGAGAACTTTCTTCCCTGAGTCAGGTGGCT 3097

Qy       3995 ACCCTGTCCTCCGGGACCTTGAGGTCCCGGGCTACCGGCAGGAGCGTGTGGAGAAAGGCC 4054

Db       3098 TCACCCACATCTTCACTGAAGATATGCATAACAGAGACGCCAACGACAAGAATGAAAGTC 3157

Qy       4055 TGAAGCTCTTCGCCCAGCTCATCAACAACAAGGTGTTCCTGCTGTCCTTCATCCGCACGC 4114

Db       3158 TCACAGCTTTGGATGCCCTAATCTGTAATAAAAGCTTTCTTGTTACTGTCATCCACACCC 3217

Qy       4115 TTGAGTCCCAGCGTAGCTTCTCCATGCGCGACCGTGGCAACGTGGCCTCACTCATCATGA 4174

Db       3218 TTGAAAAGCAGAAGAACTTTTCTGTGAAGGACAGGTGTCTGTTTGCCTCCTTCCTAACCA 3277

Qy       4175 CCGTGCTGCAGAGCAAGCTGGAGTACGCCACTGATGTGCTGAAGCAGCTGCTGGCCGACC 4234

Db       3278 TTGCACTGCAAACCAAGCTGGTCTACCTGACCAGCATCCTAGAGGTGCTGACCAGGGACT 3337

Qy       4235 TCATTGACAAGAACCTGGAGAGCAAGAACCACCCTAAGCTGCTGCTCAGGAGGACTGAGT 4294

Db       3338 TGAT------GGAACAGTGTAGTAACATGCAGCCGAAACTCATGCTGAGACGCACGGAGT 3391

Qy       4295 CAGTGGCTGAGAAGATGCTGACCAATTGGTTTACTTTCCTCCTCTACAAGTTCCTCAAGG 4354

Db       3392 CCGTCGTCGAAAAACTCCTCACAAACTGGATGTCCGTCTGCCTTTCTGGATTTCTCCGGG 3451

Qy       4355 AGTGTGCTGGGGAGCCCCTCTTCTCCCTGTTCTGTGCCATCAAGCAGCAGATGGAGAAGG 4414

Db       3452 AGACTGTCGGAGAGCCCTTCTATTTGCTGGTGACGACTCTGAACCAGAAAATTAACAAGG 3511

Qy       4415 GCCCCATTGACGCCATCACGGGCGAGGCCCGCTACTCCTTGAGCGAGGACAAGCTCATCC 4474

Db       3512 GTCCCGTGGATGTAATCACTTGCAAAGCCCTGTACACACTTAATGAAGACTGGCTGTTGT 3571

Qy       4475 GCCAGCAGATTGACTACAAAACCCTGGTCCTGAGCTGTGTCAGCCCAGACAATGCCAACA 4534

Db       3572 GGCAGGTTCCGGAATTCAGTACTGTGGCATTAAACGTCGTCTTTGAAAAAATCCCGGAAA 3631

Qy       4535 GC------------------CCCGAGGTCCCAGTAAAGATCCTCAACTGTGACACCATCA 4576

Db       3632 ACGAGAGTGCAGATGTCTGTCGGAATATTTCAGTCAATGTTCTCGACTGTGACACCATTG 3691

Qy       4577 CTCAGGTCAAGGAGAAGATTCTGGATGCCATCTTCAAGAATGTGCCTTGCTCCCACCGGC 4636

Db       3692 GCCAAGCCAAAGAAAAGATTTTCCAAGCATTCTTAAGCAAAAATGGCTCTCCTTATGGAC 3751

Qy       4637 CCAAAGCTGCAGATATGGATCTGGAGTGGCGACAAGGAAGTGGGGCAAGGATGATCTTGC 4696

Db       3752 TTCAGCTTAATGAAATTGGTCTTGAGCTTCAAATGGGCACACGACAGAAAGAACTTCTGG 3811

Qy       4697 AGGATGAAGACATCACCACCAAGATTGAGAATGATTGGAAGCGACTGAACACACTGGCCC 4756

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Qy       4757 ACTACCAGGTGCCAGATGGTTCCGTGGTGGCATTAGTGTCCAAGCAGGTGACAGCCTATA 4816

Db       3872 ACTATGAGATATCAAATGGATCCACTATAAAAGTCTTTAAGAAGATAGCAAATTTTACTT 3931

Qy       4817 ACGCAGTGAACAACTCCACCGTCTCCAGGACCTCAGCAAGTAAATATGAAAACATGATCC 4876

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Qy       4877 GGTACACGGGCAGCCCCGACAGCCTCCGCTCACGGACACCTATGATCACTCCTGACCTGG 4936

Db       3973 ------------------------------------------------------------ 3972

Qy       4937 AGAGTGGAGTCAAGATGTGGCACCTAGTGAAGAACCACGAGCACGGAGACCAGAAGGAGG 4996

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Qy       5057 GCACACTGCAGAAGTTTGTGGATGACCTCTTTGAGACCATCTTCAGCACGGCACACCGTG 5116

Db       4076 TGGCAATTCATTCTGTGCTTGAAAAACTTTTTAGAAGCATTTGGAGTTTACCCAACAGCA 4135

Qy       5117 GCTCTGCCCTGCCCCTGGCCATCAAGTACATGTTTGACTTCCTGGATGAGCAGGCTGATA 5176
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Db       4136 GAGCT------CCATTTGCTATAAAATACTTTTTTGACTTTTTGGACGCCCAGGCTGAAA 4189

Qy       5177 AACATGGCATTCATGACCCGCACGTCCGCCATACCTGGAAGAGCAATTGCCTGCCCCTGA 5236

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Qy       5417 GCTACAAGAATTGGGTGGAGAGGTATTACTCAGACATAGGGAAGATGCCAGCCATCAGCG 5476

Db       4430 CCTACAAAGAAGAAGTAAAATCTTATTACAAAGCAATCAGGGATTTGCCTCCATTGTCAT 4489

Qy       5477 ACCAAGACATGAACGCATACCTGGCTGAGCAGTCCCGGATGCACATGAATGAGTTCAACA 5536

Db       4490 CCTCAGAAATGGAAGAATTTTTAACTCAGGAATCTAAGAAACATGAAAATGAATTTAATG 4549

Qy       5537 CCATGAGTGCACTCTCAGAGATCTTCTCCTATGTGGGCAAATACAGCGAGGAGATCCT 5594

Db       4550 AAGAAGTGGCCTTGACAGAAATTTACAAATACATCGTAAAATATTTTGATGAGATTCT 4607
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RESULT 8
US-09-459-065-1
; Sequence 1, Application US/09459065
; Patent No. 6562949
;  GENERAL INFORMATION:
;    APPLICANT:  Spriggs, Melanie
;    TITLE OF INVENTION:  VIRAL ENCODED SEMAPHORIN PROTEIN
;    TITLE OF INVENTION:  RECEPTOR DNA AND POLYPEPTIDES
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Janis C. Henry
;      STREET:  51 University St.
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  US
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  MS-DOS/Windows 95
;      SOFTWARE:  Word for Windows 95, 7.0a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/459,065
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/958,598
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Henry, Janis C
;      REGISTRATION NUMBER:  34,347
;      REFERENCE/DOCKET NUMBER:  2631
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)470-4189
;      TELEFAX:  (206)233-0644
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4707 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..4707
US-09-459-065-1

  Query Match             3.5%;  Score 201.2;  DB 4;  Length 4707;
  Best Local Similarity   49.1%;  Pred. No. 4.3e-39;
  Matches  824;  Conservative    0;  Mismatches  728;  Indels  126;  Gaps    6;

Qy       3935 TTCCGTTCCTGGACTATAGAACTTACACCATGCGGGTGCTGTTCCCAGGAATTGAAGACC 3994

Db       3038 TTCCCTTCCTTGACTACAAACATTTTGCTCTGAGAACTTTCTTCCCTGAGTCAGGTGGCT 3097

Qy       3995 ACCCTGTCCTCCGGGACCTTGAGGTCCCGGGCTACCGGCAGGAGCGTGTGGAGAAAGGCC 4054

Db       3098 TCACCCACATCTTCACTGAAGATATGCATAACAGAGACGCCAACGACAAGAATGAAAGTC 3157

Qy       4055 TGAAGCTCTTCGCCCAGCTCATCAACAACAAGGTGTTCCTGCTGTCCTTCATCCGCACGC 4114

Db       3158 TCACAGCTTTGGATGCCCTAATCTGTAATAAAAGCTTTCTTGTTACTGTCATCCACACCC 3217

Qy       4115 TTGAGTCCCAGCGTAGCTTCTCCATGCGCGACCGTGGCAACGTGGCCTCACTCATCATGA 4174

Db       3218 TTGAAAAGCAGAAGAACTTTTCTGTGAAGGACAGGTGTCTGTTTGCCTCCTTCCTAACCA 3277

Qy       4175 CCGTGCTGCAGAGCAAGCTGGAGTACGCCACTGATGTGCTGAAGCAGCTGCTGGCCGACC 4234

Db       3278 TTGCACTGCAAACCAAGCTGGTCTACCTGACCAGCATCCTAGAGGTGCTGACCAGGGACT 3337

Qy       4235 TCATTGACAAGAACCTGGAGAGCAAGAACCACCCTAAGCTGCTGCTCAGGAGGACTGAGT 4294

Db       3338 TGAT------GGAACAGTGTAGTAACATGCAGCCGAAACTCATGCTGAGACGCACGGAGT 3391

Qy       4295 CAGTGGCTGAGAAGATGCTGACCAATTGGTTTACTTTCCTCCTCTACAAGTTCCTCAAGG 4354

Db       3392 CCGTCGTCGAAAAACTCCTCACAAACTGGATGTCCGTCTGCCTTTCTGGATTTCTCCGGG 3451

Qy       4355 AGTGTGCTGGGGAGCCCCTCTTCTCCCTGTTCTGTGCCATCAAGCAGCAGATGGAGAAGG 4414

Db       3452 AGACTGTCGGAGAGCCCTTCTATTTGCTGGTGACGACTCTGAACCAGAAAATTAACAAGG 3511

Qy       4415 GCCCCATTGACGCCATCACGGGCGAGGCCCGCTACTCCTTGAGCGAGGACAAGCTCATCC 4474

Db       3512 GTCCCGTGGATGTAATCACTTGCAAAGCCCTGTACACACTTAATGAAGACTGGCTGTTGT 3571

Qy       4475 GCCAGCAGATTGACTACAAAACCCTGGTCCTGAGCTGTGTCAGCCCAGACAATGCCAACA 4534

Db       3572 GGCAGGTTCCGGAATTCAGTACTGTGGCATTAAACGTCGTCTTTGAAAAAATCCCGGAAA 3631

Qy       4535 GC------------------CCCGAGGTCCCAGTAAAGATCCTCAACTGTGACACCATCA 4576

Db       3632 ACGAGAGTGCAGATGTCTGTCGGAATATTTCAGTCAATGTTCTCGACTGTGACACCATTG 3691

Qy       4577 CTCAGGTCAAGGAGAAGATTCTGGATGCCATCTTCAAGAATGTGCCTTGCTCCCACCGGC 4636

Db       3692 GCCAAGCCAAAGAAAAGATTTTCCAAGCATTCTTAAGCAAAAATGGCTCTCCTTATGGAC 3751

Qy       4637 CCAAAGCTGCAGATATGGATCTGGAGTGGCGACAAGGAAGTGGGGCAAGGATGATCTTGC 4696

Db       3752 TTCAGCTTAATGAAATTGGTCTTGAGCTTCAAATGGGCACACGACAGAAAGAACTTCTGG 3811

Qy       4697 AGGATGAAGACATCACCACCAAGATTGAGAATGATTGGAAGCGACTGAACACACTGGCCC 4756

Db       3812 ACATCGACAGTTCCTCCGTGATTCTTGAAGATGGAATCACCAAGCTAAACACCATTGGCC 3871

Qy       4757 ACTACCAGGTGCCAGATGGTTCCGTGGTGGCATTAGTGTCCAAGCAGGTGACAGCCTATA 4816

Db       3872 ACTATGAGATATCAAATGGATCCACTATAAAAGTCTTTAAGAAGATAGCAAATTTTACTT 3931

Qy       4817 ACGCAGTGAACAACTCCACCGTCTCCAGGACCTCAGCAAGTAAATATGAAAACATGATCC 4876
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Db       3932 CAGATGTGGAGTACTC--------GGATGACCACTGCCATTTGATTTTA---------- 3972

Qy       4877 GGTACACGGGCAGCCCCGACAGCCTCCGCTCACGGACACCTATGATCACTCCTGACCTGG 4936

Db       3973 ------------------------------------------------------------ 3972

Qy       4937 AGAGTGGAGTCAAGATGTGGCACCTAGTGAAGAACCACGAGCACGGAGACCAGAAGGAGG 4996

Db       3973 ----------CCAGATTCGGAAGCATTCCAAGATGTGCAAGGAAAGAGAC-------ATC 4015

Qy       4997 GGGACCGGGGGAGCAAGATGGTGTCTGAAATCTACCTGACCCGACTCCTGGCCACTAAGG 5056

Db       4016 GAGGGAAGCACAAGTTCAAAGTAAAAGAAATGTATCTGACAAAGCTGCTGTCGACCAAGG 4075

Qy       5057 GCACACTGCAGAAGTTTGTGGATGACCTCTTTGAGACCATCTTCAGCACGGCACACCGTG 5116

Db       4076 TGGCAATTCATTCTGTGCTTGAAAAACTTTTTAGAAGCATTTGGAGTTTACCCAACAGCA 4135

Qy       5117 GCTCTGCCCTGCCCCTGGCCATCAAGTACATGTTTGACTTCCTGGATGAGCAGGCTGATA 5176

Db       4136 GAGCT------CCATTTGCTATAAAATACTTTTTTGACTTTTTGGACGCCCAGGCTGAAA 4189

Qy       5177 AACATGGCATTCATGACCCGCACGTCCGCCATACCTGGAAGAGCAATTGCCTGCCCCTGA 5236

Db       4190 ACAAAAAAATCACAGATCCTGACGTCGTACATATTTGGAAAACAAACAGCCTTCCTCTTC 4249

Qy       5237 GGTTTTGGGTCAACATGATCAAGAACCCGCAGTTTGTGTTTGACATCCATAAGAACAGCA 5296

Db       4250 GCTTCTGGGTAAACATCCTGAAGAACCCTCAGTTTGTCTTTGACATTAAGAAGACACCAC 4309

Qy       5297 TCACAGACGCCTGCCTCTCTGTGGTGGCTCAGACCTTCATGGACTCTTGCTCCACGTCAG 5356

Db       4310 ATATAGACGGCTGTTTGTCAGTGATTGCCCAGGCATTCATGGATGCATTTTCTCTCACAG 4369

Qy       5357 AGCACCGGCTGGGCAAGGACTCGCCCTCCAACAAGCTGCTGTATGCCAAGGACATCCCCA 5416

Db       4370 AGCAGCAACTAGGGAAGGAAGCACCAACTAATAAGCTTCTCTATGCCAAGGATATCCCAA 4429

Qy       5417 GCTACAAGAATTGGGTGGAGAGGTATTACTCAGACATAGGGAAGATGCCAGCCATCAGCG 5476

Db       4430 CCTACAAAGAAGAAGTAAAATCTTATTACAAAGCAATCAGGGATTTGCCTCCATTGTCAT 4489

Qy       5477 ACCAAGACATGAACGCATACCTGGCTGAGCAGTCCCGGATGCACATGAATGAGTTCAACA 5536

Db       4490 CCTCAGAAATGGAAGAATTTTTAACTCAGGAATCTAAGAAACATGAAAATGAATTTAATG 4549

Qy       5537 CCATGAGTGCACTCTCAGAGATCTTCTCCTATGTGGGCAAATACAGCGAGGAGATCCT 5594

Db       4550 AAGAAGTGGCCTTGACAGAAATTTACAAATACATCGTAAAATATTTTGATGAGATTCT 4607
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RESULT 9
US-09-328-475C-37/c
; Sequence 37, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-37

Query Match 1.5%; Score 86.4; DB 4; Length 1024;
Best Local Similarity 67.9%; Pred. No. 2.4e-11;
Matches 148; Conservative 0; Mismatches 68; Indels 2; Gaps 2;

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Qy       5472 CAGCGACCAAGACATGAACGCATA-CCTGGCTGAGCAGTCCCGGATGCACATGAATGAG- 5529

Db        780 CAGTGACCAGGCCATGAATGCCTACCCTCGCCGAGCAGTCCCGCCTGCACNCCGTGGAGT 721

Qy       5530 TTCAACACCATGAGTGCACTCTCAGAGATCTTCTCCTATGTGGGCAAATACAGCGAGGAG 5589

Db        720 TTCAACATGTTGAGTGCCCCCAATGAGATCTACTCCTATGTCAGCAAGTATAGTGAGGAG 661

Qy       5590 ATCCTTGGACCTCTGGACCACGATGACCAGTGTGGGAAGCAGAAACTGGCCTACAAACTA 5649

Db        660 CTCATCGGGGCCCTAGAGCAGGATGAGCAGGCACGGCGGCANCGGCTGGCTTATAAGGTG 601

Qy       5650 GAACAAGTCATAACCCTCATGAGCTTAGACAGCTGAAA 5687

Db        600 GAGCAGCTCATTAATGCCATGTCCATTGAGAGCTGAGA 563
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RESULT 10
US-09-313-294A-6281
; Sequence 6281, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 6281
; LENGTH: 288
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6476212 700351536H1
; NAME/KEY: unsure
; LOCATION: 9, 19, 26, 50, 82, 109, 135, 175-176, 186, 197, 208, 217, 244
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-6281

Query Match 1.0%; Score 57.8; DB 4; Length 288;
Best Local Similarity 73.2%; Pred. No. 0.00013;
Matches 71; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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Qy       4685 GGATGATCTTGCAGGATGAAGACATCACCACCAAGATTGAGAATGATTGGAAGCGACTGA 4744

Db         12 GGGTCGTNCTGCAANATGAGGACATCACCACCAAGATTNAGGGTGACTGGAAGCGGCTCA 71

Qy       4745 ACACACTGGCCCACTACCAGGTGCCAGATGGTTCCGT 4781

Db         72 ACACACTGATNCATTATCAGGTGAGAGGGGGTGTCTT 108
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RESULT 11
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367

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;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7218 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  pTZgpt-F1s
US-08-232-463-14

  Query Match             0.9%;  Score 49.6;  DB 1;  Length 7218;
  Best Local Similarity   4.0%;  Pred. No. 0.058;
  Matches   16;  Conservative  219;  Mismatches  163;  Indels    0;  Gaps    0;

Qy       4649 ATATGGATCTGGAGTGGCGACAAGGAAGTGGGGCAAGGATGATCTTGCAGGATGAAGACA 4708
Db       1443 ATTTGGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1384

Qy       4709 TCACCACCAAGATTGAGAATGATTGGAAGCGACTGAACACACTGGCCCACTACCAGGTGC 4768
Db       1383 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1324

Qy       4769 CAGATGGTTCCGTGGTGGCATTAGTGTCCAAGCAGGTGACAGCCTATAACGCAGTGAACA 4828
Db       1323 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1264

Qy       4829 ACTCCACCGTCTCCAGGACCTCAGCAAGTAAATATGAAAACATGATCCGGTACACGGGCA 4888
Db       1263 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1204

Qy       4889 GCCCCGACAGCCTCCGCTCACGGACACCTATGATCACTCCTGACCTGGAGAGTGGAGTCA 4948
Db       1203 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1144

Qy       4949 AGATGTGGCACCTAGTGAAGAACCACGAGCACGGAGACCAGAAGGAGGGGGACCGGGGGA 5008
Db       1143 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1084

Qy       5009 GCAAGATGGTGTCTGAAATCTACCTGACCCGACTCCTG 5046
Db       1083 RRRRRRRRRRRRRRRRRATCGCAAGCTCCCTCGACCTG 1046


RESULT 12
US-08-607-509-3
; Sequence 3, Application US/08607509
; Patent No. 5876735
;  GENERAL INFORMATION:
;    APPLICANT:  Reed, Steven G.
;    TITLE OF INVENTION:  METHODS FOR ENHANCEMENT OF PROTECTIVE IMMUNE RESPONSES
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/607,509
;      FILING DATE:  16-FEB-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  210121.404C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206)682-6031
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1867 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  117..1325
US-08-607-509-3

  Query Match             0.9%;  Score 49.4;  DB 2;  Length 1867;
  Best Local Similarity   45.3%;  Pred. No. 0.034;
  Matches  179;  Conservative    0;  Mismatches  216;  Indels    0;  Gaps    0;

Qy       4049 AAGGCCTGAAGCTCTTCGCCCAGCTCATCAACAACAAGGTGTTCCTGCTGTCCTTCATCC 4108
Db        403 AGGGCCTCGTGCTCTCCCCCACTCGCGAGCTGGCCCTGCAGACGGCGGAGGTGATCAGCC 462

Qy       4109 GCACGCTTGAGTCCCAGCGTAGCTTCTCCATGCGCGACCGTGGCAACGTGGCCTCACTCA 4168
Db        463 GCATCGGTGAGTTCCTGTCGAACAGCTCCAAGTTCTGCGAGACCTTTGTCGGCGGCACGC 522

Qy       4169 TCATGACCGTGCTGCAGAGCAAGCTGGAGTACGCCACTGATGTGCTGAAGCAGCTGCTGG 4228
Db        523 GCGTGCAGGATGACCTGCGCAAGCTGCAGGCCGGCGTCATCGTTGCCGTGGGCACGCCGG 582

Qy       4229 CCGACCTCATTGACAAGAACCTGGAGAGCAAGAACCACCCTAAGCTGCTGCTCAGGAGGA 4288
Db        583 GCCGCGTGTCCGACGTGATCAAGCGTGGCGCGCTGCGCACAGAGTCGCTGCGCGTGCTGG 642

Qy       4289 CTGAGTCAGTGGCTGAGAAGATGCTGACCAATTGGTTTACTTTCCTCCTCTACAAGTTCC 4348
Db        643 TGCTCGACGAGGCTGATGAGATGCTGTCTCAGGGCTTCGCGGACCAGATTTACGAGATCT 702

Qy       4349 TCAAGGAGTGTGCTGGGGAGCCCCTCTTCTCCCTGTTCTGTGCCATCAAGCAGCAGATGG 4408
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Db         703 TCCGCTTCCTGCCGAAGGACATCCAGGTCGCGCTCTTCTCCGCCACGATGCCGGAGGAGG 762

Qy        4409 AGAAGGGCCCCATTGACGCCATCACGGGCGAGGCC 4443

Db         763 TACTGGAGCTGACGAAGAAGTTCATGCGCGACCCC 797
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RESULT 13
US-08-634-642-3
; Sequence 3, Application US/08634642
; Patent No. 5879687
; GENERAL INFORMATION:
;   APPLICANT: Reed, Steven G.
;   TITLE OF INVENTION: METHODS FOR ENHANCEMENT OF
;   TITLE OF INVENTION: PROTECTIVE IMMUNE RESPONSES
;   NUMBER OF SEQUENCES: 15
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: SEED and BERRY LLP
;   STREET: 6300 Columbia Center, 701 Fifth Avenue
;   CITY: Seattle
;   STATE: Washington
;   COUNTRY: USA
;   ZIP: 98104-7092
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/634,642
;   FILING DATE: 18-APR-1996
;   CLASSIFICATION: 424
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Maki, David J.
;   REGISTRATION NUMBER: 31,392
;   REFERENCE/DOCKET NUMBER: 210121.404C4
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (206) 622-4900
;   TELEFAX: (206)682-6031
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1867 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 117..1325
US-08-634-642-3

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  Query Match              0.9%;  Score 49.4;  DB 2;  Length 1867;
  Best Local Similarity   45.3%;  Pred. No. 0.034;
  Matches  179;  Conservative    0;  Mismatches  216;  Indels    0;  Gaps    0;

Qy        4049 AAGGCCTGAAGCTCTTCGCCCAGCTCATCAACAACAAGGTGTTCCTGCTGTCCTTCATCC 4108

Db         403 AGGGCCTCGTGCTCTCCCCCACTCGCGAGCTGGCCCTGCAGACGGCGGAGGTGATCAGCC 462

Qy        4109 GCACGCTTGAGTCCCAGCGTAGCTTCTCCATGCGCGACCGTGGCAACGTGGCCTCACTCA 4168

Db         463 GCATCGGTGAGTTCCTGTCGAACAGCTCCAAGTTCTGCGAGACCTTTGTCGGCGGCACGC 522

Qy        4169 TCATGACCGTGCTGCAGAGCAAGCTGGAGTACGCCACTGATGTGCTGAAGCAGCTGCTGG 4228

Db         523 GCGTGCAGGATGACCTGCGCAAGCTGCAGGCCGGCGTCATCGTTGCCGTGGGCACGCCGG 582

Qy        4229 CCGACCTCATTGACAAGAACCTGGAGAGCAAGAACCACCCTAAGCTGCTGCTCAGGAGGA 4288

Db         583 GCCGCGTGTCCGACGTGATCAAGCGTGGCGCGCTGCGCACAGAGTCGCTGCGCGTGCTGG 642

Qy        4289 CTGAGTCAGTGGCTGAGAAGATGCTGACCAATTGGTTTACTTTCCTCCTCTACAAGTTCC 4348

Db         643 TGCTCGACGAGGCTGATGAGATGCTGTCTCAGGGCTTCGCGGACCAGATTTACGAGATCT 702
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Qy        4349 TCAAGGAGTGTGCTGGGGAGCCCCTCTTCTCCCTGTTCTGTGCCATCAAGCAGCAGATGG 4408

Db         703 TCCGCTTCCTGCCGAAGGACATCCAGGTCGCGCTCTTCTCCGCCACGATGCCGGAGGAGG 762

Qy        4409 AGAAGGGCCCCATTGACGCCATCACGGGCGAGGCC 4443

Db         763 TACTGGAGCTGACGAAGAAGTTCATGCGCGACCCC 797
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RESULT 14
US-08-989-370-3
; Sequence 3, Application US/08989370
; Patent No. 6013268
; GENERAL INFORMATION:
;   APPLICANT: Reed, Steven G.
;   TITLE OF INVENTION: METHODS FOR ENHANCEMENT OF PROTECTIVE IMMUNE RESPONSES
;   NUMBER OF SEQUENCES: 14
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: SEED and BERRY
;   STREET: 6300 Columbia Center, 701 Fifth Avenue
;   CITY: Seattle
;   STATE: Washington
;   COUNTRY: USA
;   ZIP: 98104-7092
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/989,370
;   FILING DATE: 12-DEC-1997
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Maki, David J.
;   REGISTRATION NUMBER: 31,392
;   REFERENCE/DOCKET NUMBER: 210121.404C5
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (206) 622-4900
;   TELEFAX: (206)682-6031
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1867 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 117..1325
US-08-989-370-3

```
  Query Match              0.9%;  Score 49.4;  DB 3;  Length 1867;
  Best Local Similarity   45.3%;  Pred. No. 0.034;
  Matches  179;  Conservative    0;  Mismatches  216;  Indels    0;  Gaps    0;

Qy        4049 AAGGCCTGAAGCTCTTCGCCCAGCTCATCAACAACAAGGTGTTCCTGCTGTCCTTCATCC 4108

Db         403 AGGGCCTCGTGCTCTCCCCCACTCGCGAGCTGGCCCTGCAGACGGCGGAGGTGATCAGCC 462

Qy        4109 GCACGCTTGAGTCCCAGCGTAGCTTCTCCATGCGCGACCGTGGCAACGTGGCCTCACTCA 4168

Db         463 GCATCGGTGAGTTCCTGTCGAACAGCTCCAAGTTCTGCGAGACCTTTGTCGGCGGCACGC 522

Qy        4169 TCATGACCGTGCTGCAGAGCAAGCTGGAGTACGCCACTGATGTGCTGAAGCAGCTGCTGG 4228

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RESULT 15
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; Sequence 3, Application US/09398169
; Patent No. 6660840
;   GENERAL INFORMATION:
;        APPLICANT: Reed, Steven G.
;        TITLE OF INVENTION: METHODS FOR ENHANCEMENT OF PROTECTIVE IMMUNE RESPONSES
;        NUMBER OF SEQUENCES: 14
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: SEED and BERRY
;             STREET: 6300 Columbia Center, 701 Fifth Avenue
;             CITY: Seattle
;             STATE: Washington
;             COUNTRY: USA
;             ZIP: 98104-7092
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/398,169
;             FILING DATE: 17-Sep-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/989,370
;             FILING DATE: 12-DEC-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Maki, David J.
;             REGISTRATION NUMBER: 31,392
;             REFERENCE/DOCKET NUMBER: 210121.404C5
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (206) 622-4900
;             TELEFAX: (206)682-6031
;    INFORMATION FOR SEQ ID NO: 3:
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;             LENGTH: 1867 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  117..1325
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Job time : 272 secs
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Searched: 2308684 seqs, 1750822206 residues

Total number of hits satisfying chosen parameters: 4617368

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2533.8	44.5	5895	12	US-10-087-684-31	Sequence 31, Appl
3	2533.8	44.5	5895	12	US-10-218-779-31	Sequence 31, Appl
4	1157.8	20.3	3666	15	US-10-108-260A-802	Sequence 802, App
5	793.8	13.9	2597	14	US-10-245-103-91	Sequence 91, Appl
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ALIGNMENTS

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; Sequence 95, Application US/10175523
; Publication No. US20030096264A1
; GENERAL INFORMATION:
;  APPLICANT: Brockman, Jeffrey
;  APPLICANT:  Evans, David
;  APPLICANT:  Hook, Derek
;  APPLICANT:  Klimczak, Leszek
;  APPLICANT:  Laeng, Pascal
;  APPLICANT:  Palfreyman, Michael
;  APPLICANT:  Rajan, Prithi
;  TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
;  FILE REFERENCE: 3235/1J795-US3
;  CURRENT APPLICATION NUMBER: US/10/175,523
;  CURRENT FILING DATE:  2002-06-18
;  PRIOR APPLICATION NUMBER: US 60/299,151
;  PRIOR FILING DATE: 2001-06-18
;  PRIOR APPLICATION NUMBER: US 60/317,828
;  PRIOR FILING DATE: 2001-09-07
;  PRIOR APPLICATION NUMBER: US 60/325,150
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: US 60/333,047
;  PRIOR FILING DATE: 2001-11-14
;  PRIOR APPLICATION NUMBER: US 60/349,936
;  PRIOR FILING DATE: 2002-01-18
;  PRIOR APPLICATION NUMBER: US 60/361,834
;  PRIOR FILING DATE: 2002-03-04
;  NUMBER OF SEQ ID NOS: 197
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;   ORGANISM: Mus musculus
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;   NAME/KEY: misc_feature
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;   OTHER INFORMATION: where n may be a or g or c or t/u, unknown, or other
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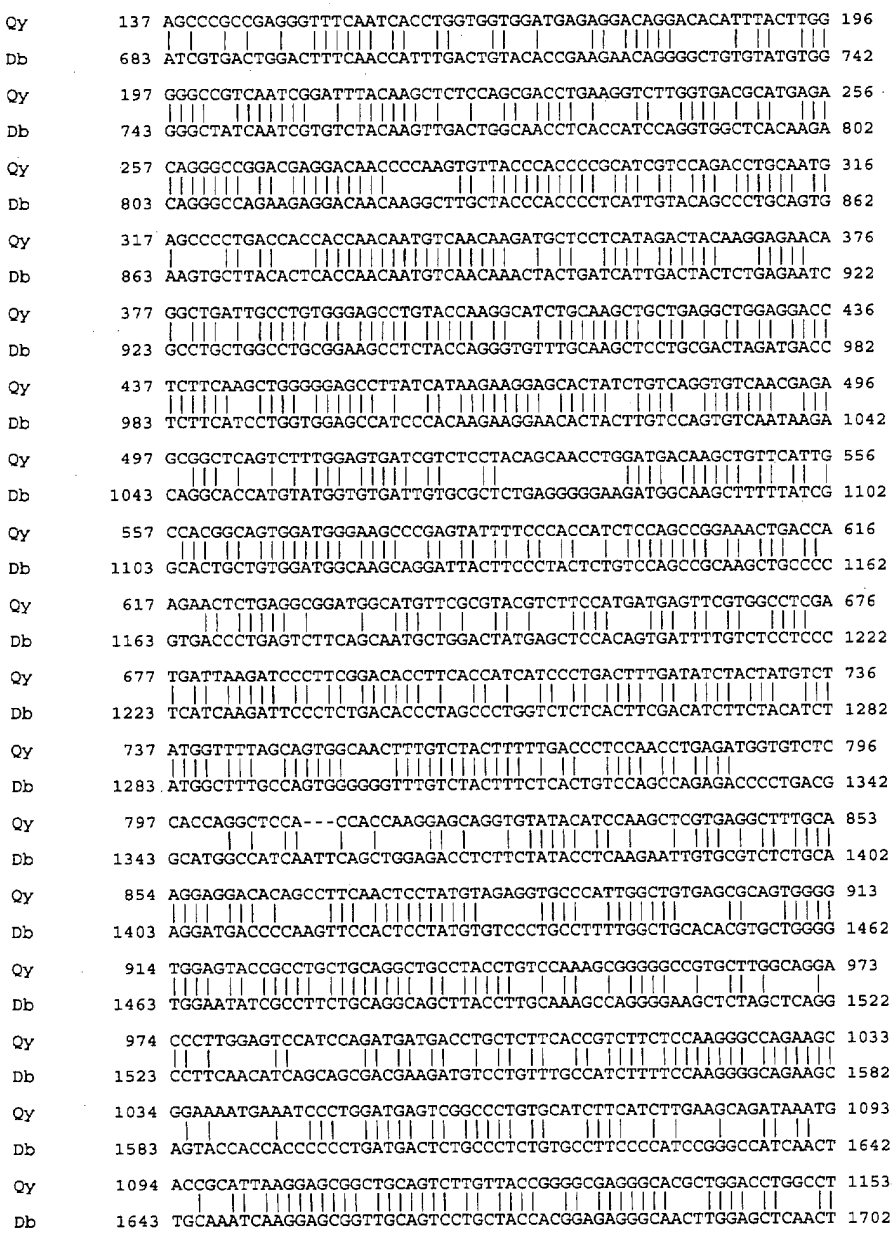

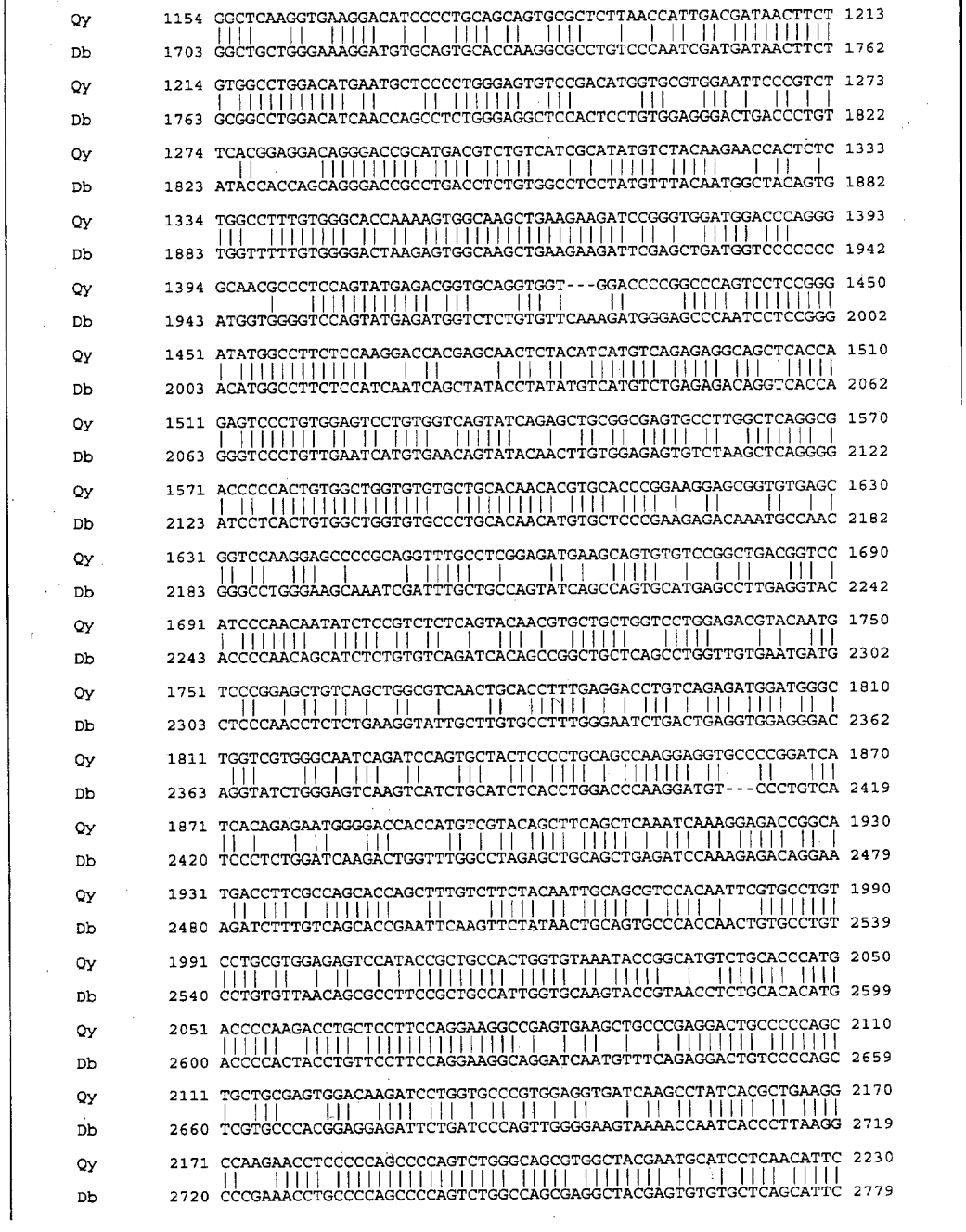

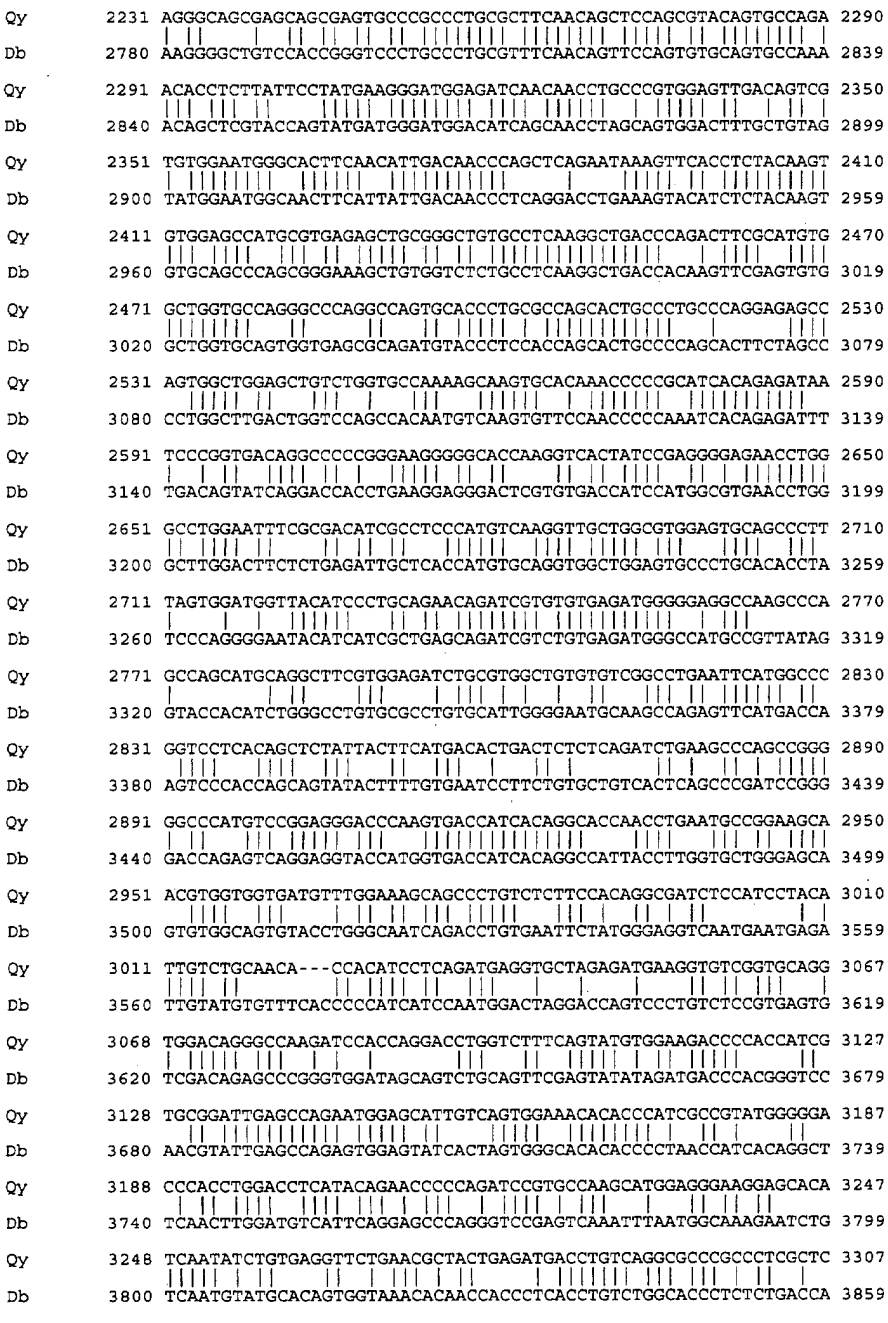
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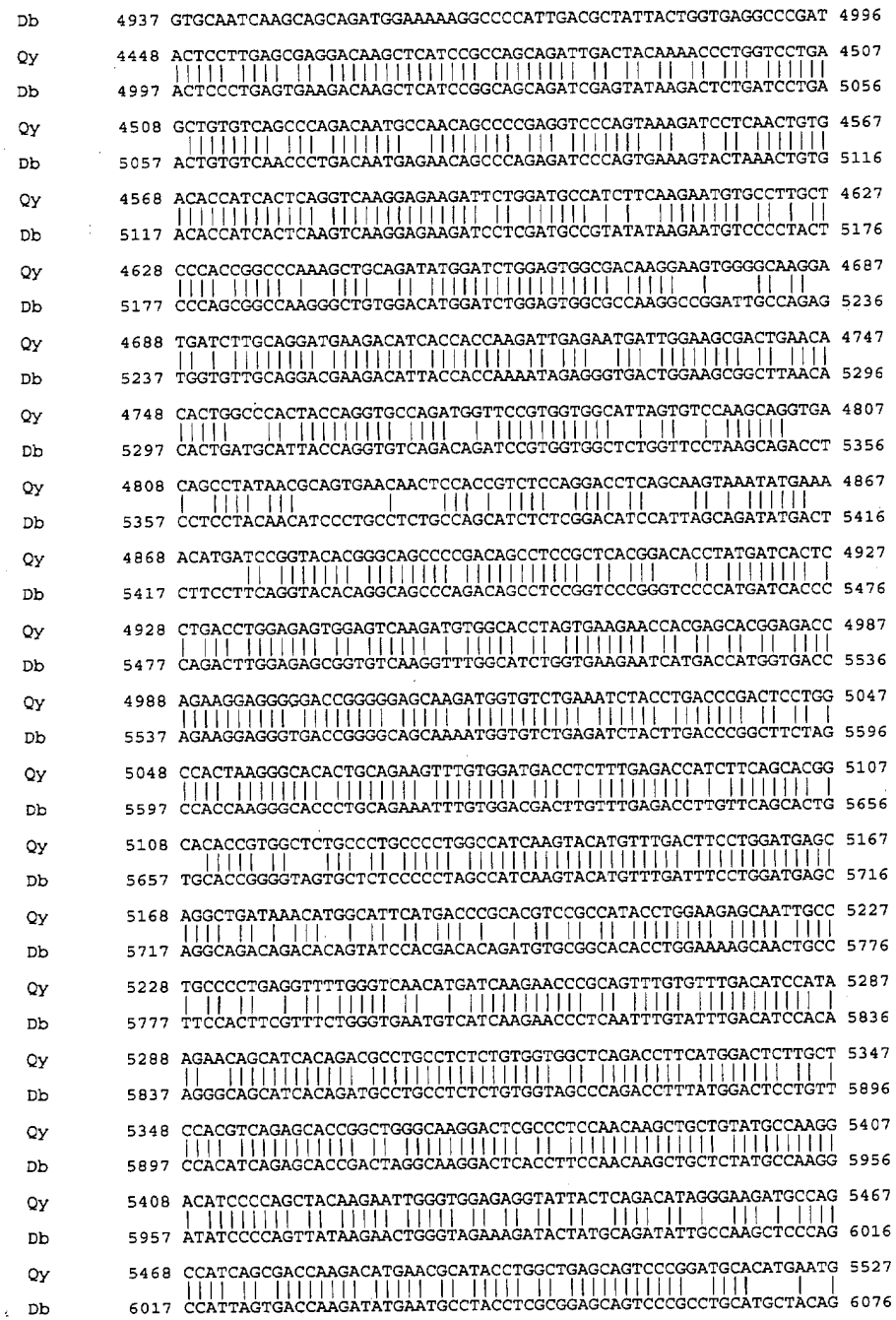

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;  APPLICANT: Edinger, Shlomit R.
;  APPLICANT:  MacDougall, John R.
;  APPLICANT:  Millet, Isabelle
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Stone, David J.
;  APPLICANT:  Grosse, William M.
;  APPLICANT:  Lepley, Denise M.
;  APPLICANT:  Rieger, Daniel K.
;  APPLICANT:  Burgess, Cathereine E.
;  APPLICANT:  Casman, Stacie, J.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Boldog, Ferenc L.
;  APPLICANT:  Li, Li
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Mishra, Vishnu
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Tchernev, Velizar T.
;  APPLICANT:  Vernet, Corine A.M.
;  APPLICANT:  Zerhusen, Bryan D.
;  APPLICANT:  Malyankar, Uriel M.
;  APPLICANT:  Guo, Xiaojia
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Gangolli, Esha A.
;  TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-214 CIP
;  CURRENT APPLICATION NUMBER: US/10/087,684
;  CURRENT FILING DATE:  2003-03-10
;  PRIOR APPLICATION NUMBER: 60/253,834
;  PRIOR FILING DATE: 2000-11-29
;  PRIOR APPLICATION NUMBER: 60/250,926
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: 60/264,180
;  PRIOR FILING DATE: 2001-01-25
;  PRIOR APPLICATION NUMBER: 60/274,194
;  PRIOR FILING DATE: 2001-03-08
;  PRIOR APPLICATION NUMBER: 60/313,656
;  PRIOR FILING DATE: 2001-08-20
;  PRIOR APPLICATION NUMBER: 60/327,456
;  PRIOR FILING DATE: 2001-10-05
;  NUMBER OF SEQ ID NOS: 220
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;   LOCATION: (23)..(5797)
US-10-087-684-31

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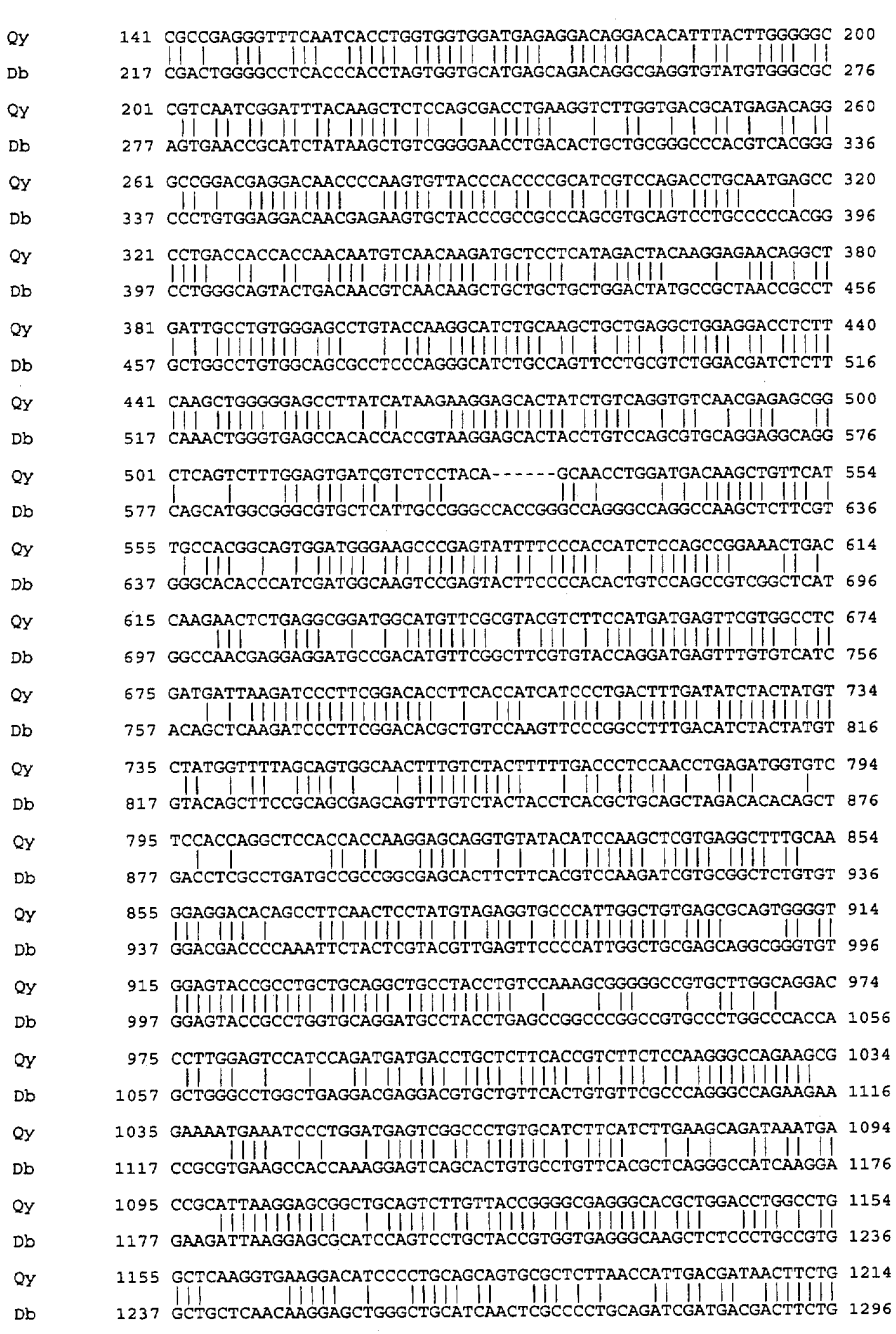
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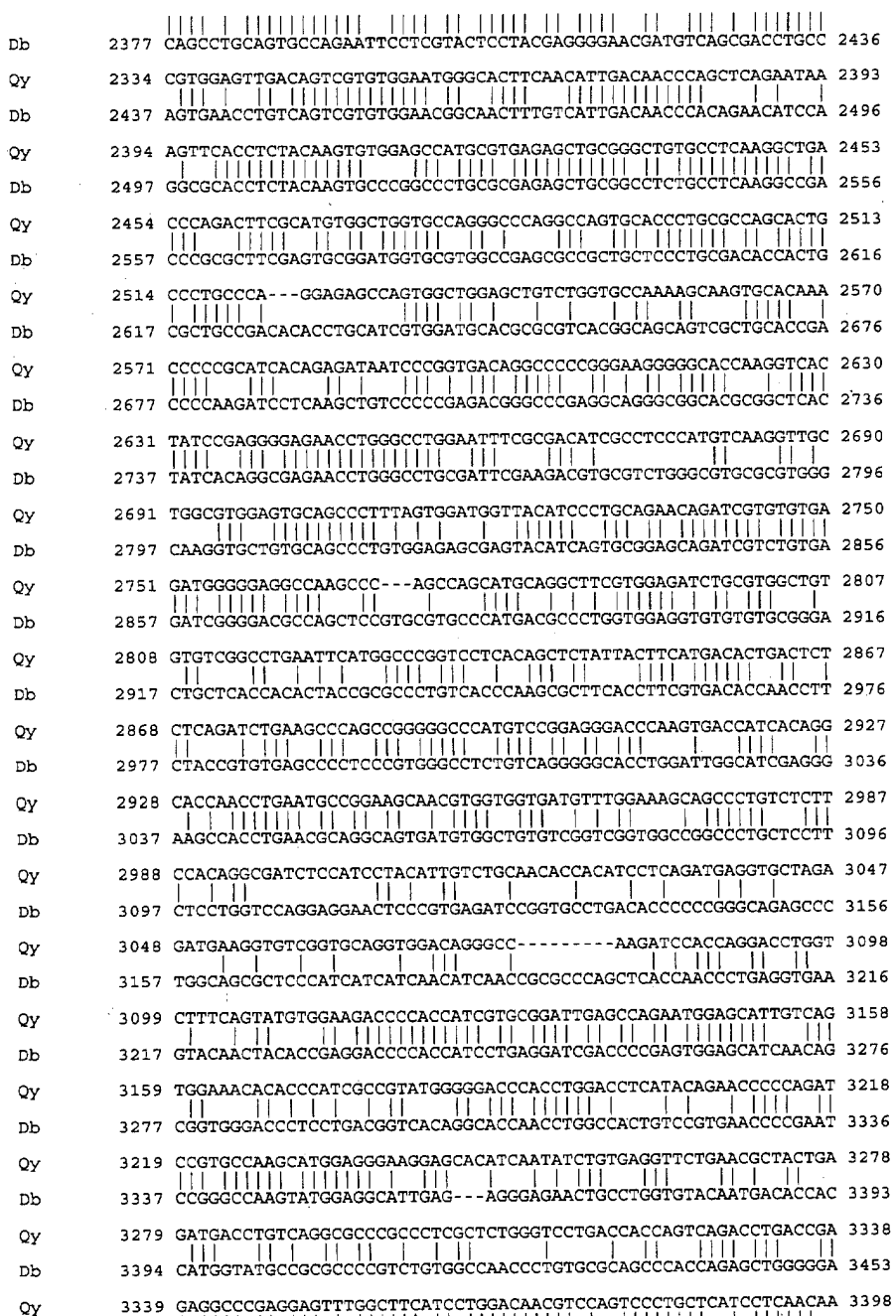

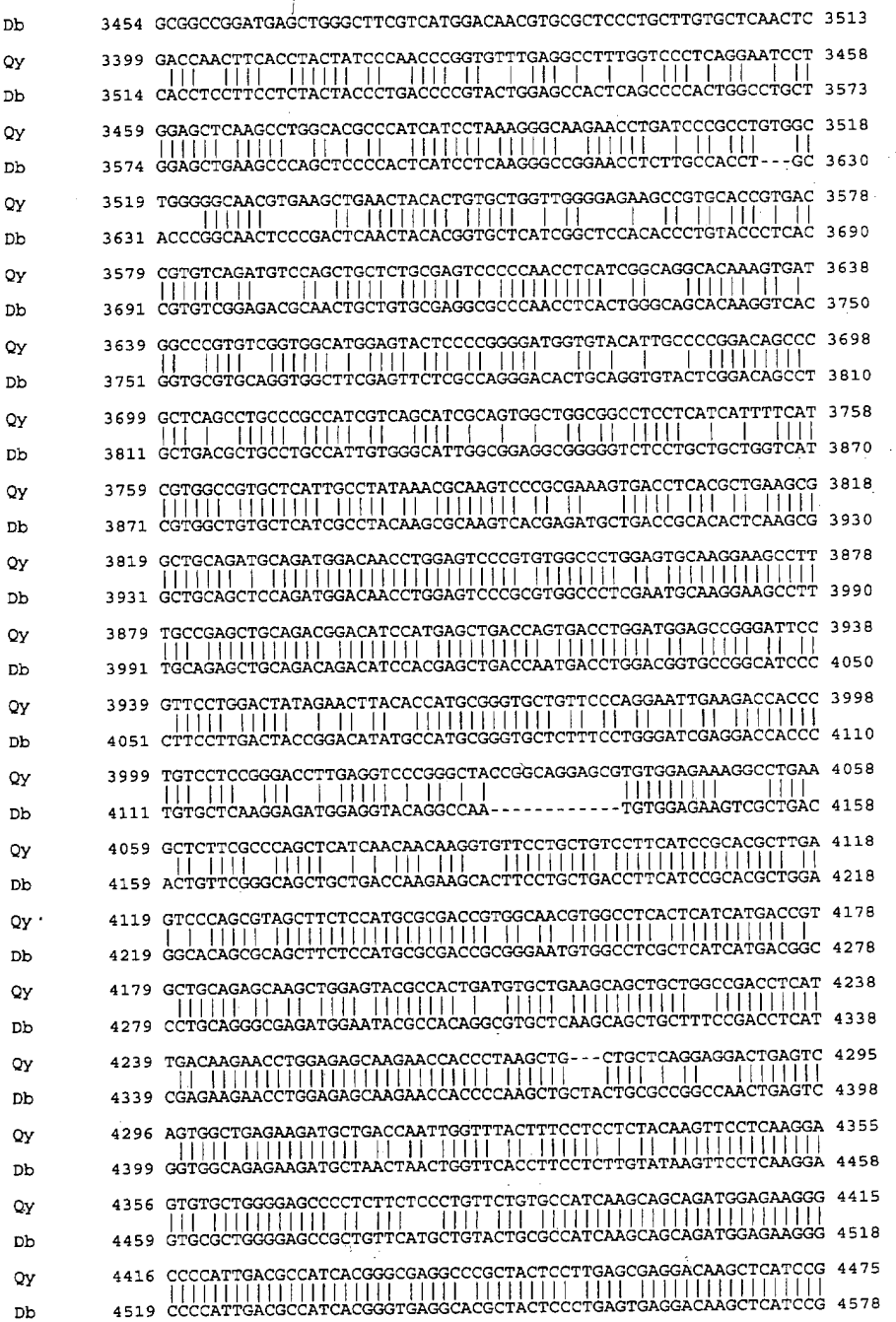

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; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David
; APPLICANT: Gerlach, Valerie
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook II, John
; APPLICANT: Lepley, Denise
; APPLICANT: Rieger, Daniel
; APPLICANT: Burgess, Catherine
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; APPLICANT: Patturajan, Meera
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; APPLICANT: Tchernev, Velizar
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Malyankar, Uriel
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles
; APPLICANT: Gangolli, Esha
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; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,-926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 5895
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-218-779-31

Query Match 44.5%; Score 2533.8; DB 12; Length 5895;
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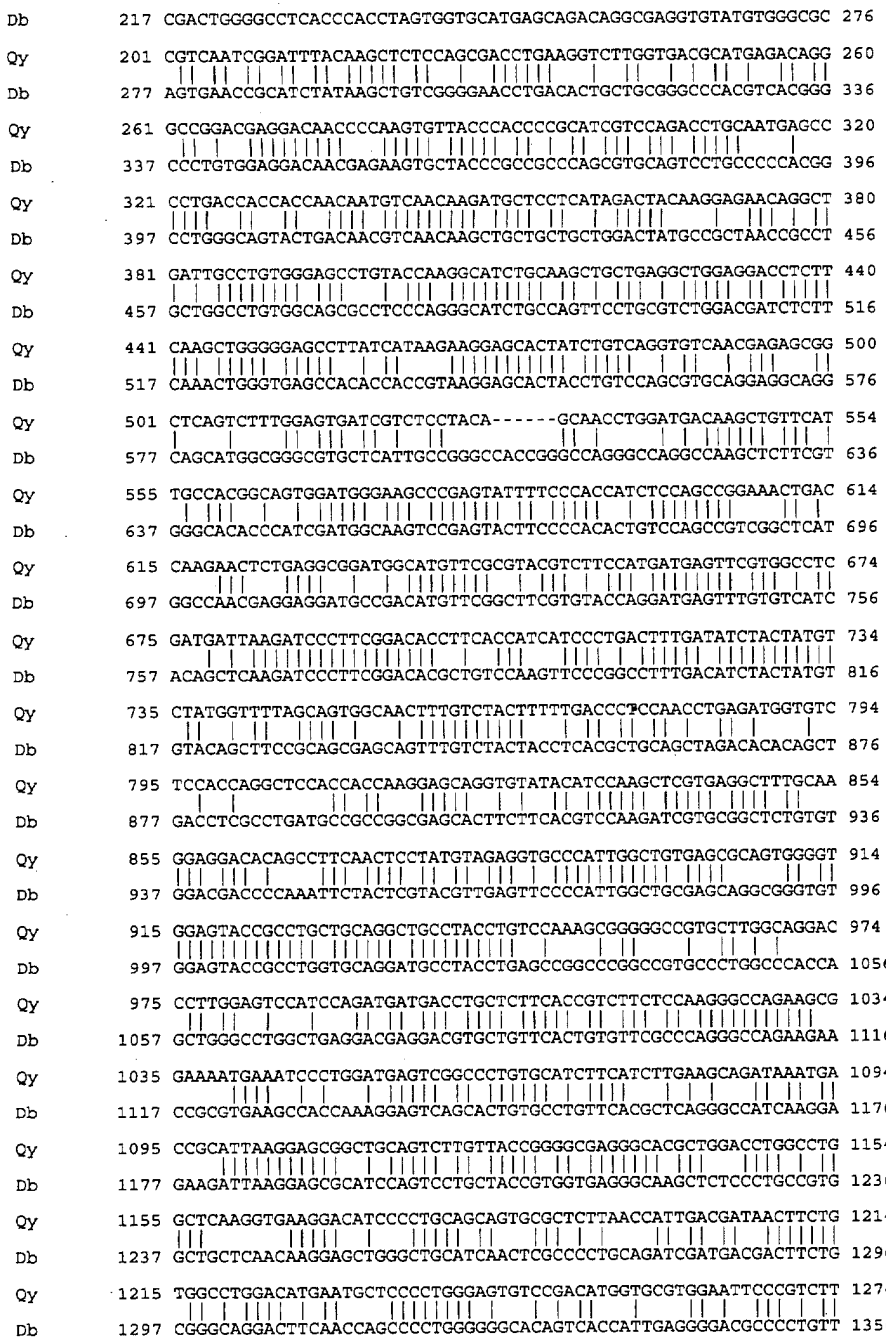
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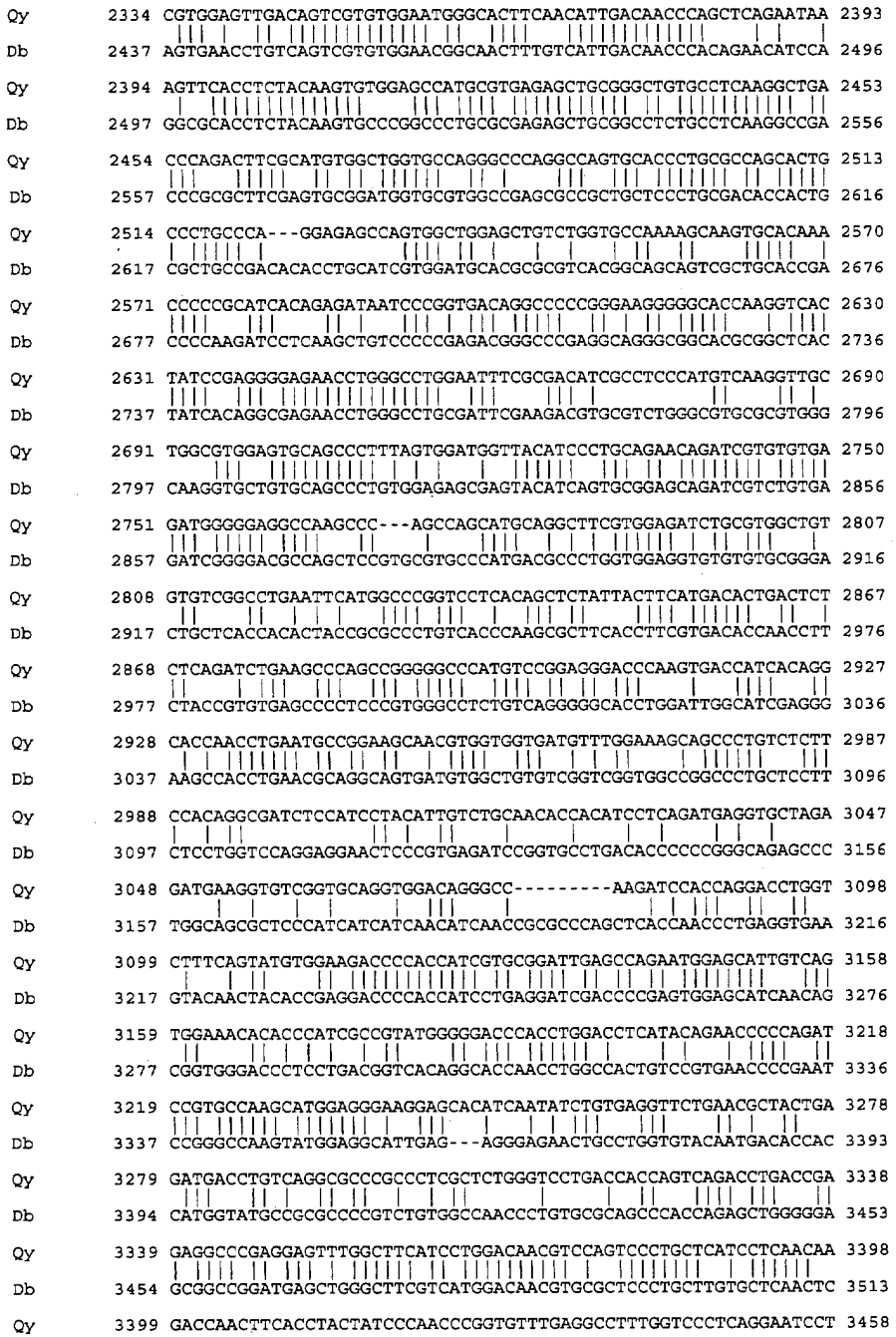
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Qy 2394 AGTTCACCTCTACAAGTGTGGAGCCATGCGTGAGAGCTGCGGGCTGTGCCTCAAGGCTGA 2453
Db 2497 GGCGCACCTCTACAAGTGCCCGGCCCTGCGCGAGAGCTGCGGCCTCTGCCTCAAGGCCGA 2556
Qy 2454 CCCAGACTTCGCATGTGGCTGGTGCCAGGGCCAGGCCAGTGCACCCTGCGCCAGCACTG 2513
Db 2557 CCCGCGCTTCGAGTGCGGATGGTGCGTGGCCGAGCGCCGCTGCTCCCTGCGACACCACTG 2616
Qy 2514 CCCTGCCCA---GGAGAGCCAGTGGCTGGAGCTGTCTGGTGCCAAAAGCAAGTGCACAAA 2570
Db 2617 CGCTGCCGACACACCTGCATCGTGGATGCACGCGCGTCACGGCAGCAGTCGCTGCACCGA 2676
Qy 2571 CCCCCGCATCACAGAGATAATCCCGGTGACAGGCCCCCGGGAAGGGGGCACCAAGGTCAC 2630
Db 2677 CCCCAAGATCCTCAAGCTGTCCCCCGAGACGGGCCCGAGGCAGGGCGGCACGCGGCTCAC 2736
Qy 2631 TATCCGAGGGGAGAACCTGGGCCTGGAATTTCGCGACATCGCCTCCCATGTCAAGGTTGC 2690
Db 2737 TATCACAGGCGAGAACCTGGGCCTGCGATTCGAAGACGTGCGTCTGGGCGTGCGCGTGGG 2796
Qy 2691 TGGCGTGGAGTGCAGCCCTTTAGTGGATGGTTACATCCCTGCAGAACAGATCGTGTGTGA 2750
Db 2797 CAAGGTGCTGTGCAGCCCTGTGGAGAGCGAGTACATCAGTGCGGAGCAGATCGTCTGTGA 2856
Qy 2751 GATGGGGGAGGCCAAGCCC---AGCCAGCATGCAGGCTTCGTGGAGATCTGCGTGGCTGT 2807
Db 2857 GATCGGGGACGCCAGCTCCGTGCGTGCCCATGACGCCCTGGTGGAGGTGTGTGTGCGGGA 2916
Qy 2808 GTGTCGGCCTGAATTCATGGCCCGGTCCTCACAGCTCTATTACTTCATGACACTGACTCT 2867
Db 2917 CTGCTCACCACACTACCGCGCCCTGTCACCCAAGCGCTTCACCTTCGTGACACCAACCTT 2976
Qy 2868 CTCAGATCTGAAGCCCAGCCGGGGGCCCATGTCCGGAGGGACCCAAGTGACCATCACAGG 2927
Db 2977 CTACCGTGTGAGCCCCTCCCGTGGGCCTCTGTCAGGGGGCACCTGGATTGGCATCGAGGG 3036
Qy 2928 CACCAACCTGAATGCCGGAAGCAACGTGGTGGTGATGTTTGGAAAGCAGCCCTGTCTCTT 2987
Db 3037 AAGCCACCTGAACGCAGGCAGTGATGTGGCTGTGTCGGTCGGTGGCCGGCCCTGCTCCTT 3096
Qy 2988 CCACAGGCGATCTCCATCCTACATTGTCTGCAACACCACATCCTCAGATGAGGTGCTAGA 3047
Db 3097 CTCCTGGTCCAGGAGGAACTCCCGTGAGATCCGGTGCCTGACACCCCCCGGGCAGAGCCC 3156
Qy 3048 GATGAAGGTGTCGGTGCAGGTGGACAGGGCC---------AAGATCCACCAGGACCTGGT 3098
Db 3157 TGGCAGCGCTCCCATCATCATCAACATCAACCGCGCCCAGCTCACCAACCCTGAGGTGAA 3216
Qy 3099 CTTTCAGTATGTGGAAGACCCCACCATCGTGCGGATTGAGCCAGAATGGAGCATTGTCAG 3158
Db 3217 GTACAACTACACCGAGGACCCCACCATCCTGAGGATCGACCCCGAGTGGAGCATCAACAG 3276
Qy 3159 TGGAAACACACCCATCGCCGTATGGGGGACCCACCTGGACCTCATACAGAACCCCCAGAT 3218
Db 3277 CGGTGGGACCCTCCTGACGGTCACAGGCACCAACCTGGCCACTGTCCGTGAACCCCGAAT 3336
Qy 3219 CCGTGCCAAGCATGGAGGGAAGGAGCACATCAATATCTGTGAGGTTCTGAACGCTACTGA 3278
Db 3337 CCGGGCCAAGTATGGAGGCATTGAG---AGGGAGAACTGCCTGGTGTACAATGACACCAC 3393
Qy 3279 GATGACCTGTCAGGCGCCCGCCCTCGCTCTGGGTCCTGACCACCAGTCAGACCTGACCGA 3338
Db 3394 CATGGTATGCCGCGCCCCGTCTGTGGCCAACCCTGTGCGCAGCCCACCAGAGCTGGGGGA 3453
Qy 3339 GAGGCCCGAGGAGTTTGGCTTCATCCTGGACAACGTCCAGTCCCTGCTCATCCTCAACAA 3398
Db 3454 GCGGCCGGATGAGCTGGGCTTCGTCATGGACAACGTGCGCTCCCTGCTTGTGCTCAACTC 3513
Qy 3399 GACCAACTTCACCTACTATCCCAACCCGGTGTTTGAGGCCTTTGGTCCCTCAGGAATCCT 3458
Db 3514 CACCTCCTTCCTCTACTACCCTGACCCCGTACTGGAGCCACTCAGCCCCACTGGCCTGCT 3573
Qy 3459 GGAGCTCAAGCCTGGCACGCCCATCATCCTAAAGGGCAAGAACCTGATCCCGCCTGTGGC 3518
Db 3574 GGAGCTGAAGCCCAGCTCCCCACTCATCCTCAAGGGCCGGAACCTCTTGCCACCT---GC 3630
Qy 3519 TGGGGGCAACGTGAAGCTGAACTACACTGTGCTGGTTGGGGAGAAGCCGTGCACCGTGAC 3578
Db 3631 ACCCGGCAACTCCCGACTCAACTACACGGTGCTCATCGGCTCCACACCCTGTACCCTCAC 3690
Qy 3579 CGTGTCAGATGTCCAGCTGCTCTGCGAGTCCCCCAACCTCATCGGCAGGCACAAAGTGAT 3638
Db 3691 CGTGTCGGAGACGCAACTGCTGTGCGAGGCGCCCAACCTCACTGGGCAGCACAAGGTCAC 3750
Qy 3639 GGCCCGTGTCGGTGGCATGGAGTACTCCCCGGGGATGGTGTACATTGCCCCGGACAGCCC 3698
Db 3751 GGTGCGTGCAGGTGGCTTCGAGTTCTCGCCAGGGACACTGCAGGTGTACTCGGACAGCCT 3810
Qy 3699 GCTCAGCCTGCCCGCCATCGTCAGCATCGCAGTGGCTGGCGGCCTCCTCATCATTTTCAT 3758
Db 3811 GCTGACGCTGCCTGCCATTGTGGGCATTGGCGGAGGCGGGGGTCTCCTGCTGCTGGTCAT 3870
Qy 3759 CGTGGCCGTGCTCATTGCCTATAAACGCAAGTCCCGCGAAAGTGACCTCACGCTGAAGCG 3818
Db 3871 CGTGGCTGTGCTCATCGCCTACAAGCGCAAGTCACGAGATGCTGACCGCACACTCAAGCG 3930
Qy 3819 GCTGCAGATGCAGATGGACAACCTGGAGTCCCGTGTGGCCCTGGAGTGCAAGGAAGCCTT 3878
Db 3931 GCTGCAGCTCCAGATGGACAACCTGGAGTCCCGCGTGGCCCTCGAATGCAAGGAAGCCTT 3990
Qy 3879 TGCCGAGCTGCAGACGGACATCCATGAGCTGACCAGTGACCTGGATGGAGCCGGGATTCC 3938
Db 3991 TGCAGAGCTGCAGACAGACATCCACGAGCTGACCAATGACCTGGACGGTGCCGGCATCCC 4050
Qy 3939 GTTCCTGGACTATAGAACTTACACCATGCGGGTGCTGTTCCCAGGAATTGAAGACCACCC 3998
Db 4051 CTTCCTTGACTACCGGACATATGCCATGCGGGTGCTCTTTCCTGGGATCGAGGACCACCC 4110
Qy 3999 TGTCCTCCGGGACCTTGAGGTCCCGGGCTACCGGCAGGAGCGTGTGGAGAAAGGCCTGAA 4058
Db 4111 TGTGCTCAAGGAGATGGAGGTACAGGCCAA----------TGTGGAGAAGTCGCTGAC 4158
Qy 4059 GCTCTTCGCCCAGCTCATCAACAACAAGGTGTTCCTGCTGTCCTTCATCCGCACGCTTGA 4118
Db 4159 ACTGTTCGGGCAGCTGCTGACCAAGAAGCACTTCCTGCTGACCTTCATCCGCACGCTGGA 4218
Qy 4119 GTCCCAGCGTAGCTTCTCCATGCGCGACCGTGGCAACGTGGCCTCACTCATCATGACCGT 4178
Db 4219 GGCACAGCGCAGCTTCTCCATGCGCGACCGCGGGAATGTGGCCTCGCTCATCATGACGGC 4278
Qy 4179 GCTGCAGAGCAAGCTGGAGTACGCCACTGATGTGCTGAAGCAGCTGCTGGCCGACCTCAT 4238
Db 4279 CCTGCAGGGCGAGATGGAATACGCCACAGGCGTGCTCAAGCAGCTGCTTTCCGACCTCAT 4338
Qy 4239 TGACAAGAACCTGGAGAGCAAGAACCACCCTAAGCTG---CTGCTCAGGAGGACTGAGTC 4295
Db 4339 CGAGAAGAACCTGGAGAGCAAGAACCACCCCAAGCTGCTACTGCGCCGGCCAACTGAGTC 4398
Qy 4296 AGTGGCTGAGAAGATGCTGACCAATTGGTTTACTTTCCTCCTCTACAAGTTCCTCAAGGA 4355
Db 4399 GGTGGCAGAGAAGATGCTAACTAACTGGTTCACCTTCCTCTTGTATAAGTTCCTCAAGGA 4458
Qy 4356 GTGTGCTGGGGAGCCCCTCTTCTCCCTGTTCTGTGCCATCAAGCAGCAGATGGAGAAGGG 4415
Db 4459 GTGCGCTGGGGAGCCGCTGTTCATGCTGTACTGCGCCATCAAGCAGCAGATGGAGAAGGG 4518
Qy 4416 CCCCATTGACGCCATCACGGGCGAGGCCCGCTACTCCTTGAGCGAGGACAAGCTCATCCG 4475
Db 4519 CCCCATTGACGCCATCACGGGTGAGGCACGCTACTCCCTGAGTGAGGACAAGCTCATCCG 4578
Qy 4476 CCAGCAGATTGACTACAAAACCCTGGTCCTGAGCTGTGTCAGCCCAGACAATGCCAACAG 4535

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Db       4579 GCAGCAGATTGACTACAAGACACTGACCCTGAACTGTGTGAACCCTGAGAATGAGAATGC 4638
Qy       4536 CCCCGAGGTCCCAGTAAAGATCCTCAACTGTGACACCATCACTCAGGTCAAGGAGAAGAT 4595
Db       4639 ACCTGAGGTGCCGGTGAAGGGGCTGGACTGTGACACGGTCACCCAGGCCAAGGAGAAGCT 4698
Qy       4596 TCTGGATGCCATCTTCAAGAATGTGCCTTGCTCCCACCGGCCCAAAGCTGCAGATATGGA 4655
Db       4699 GCTGGACGCTGCCTACAAGGGCGTGCCCTACTCCCAGCGGCCCAAGGCCGCGGACATGGA 4758
Qy       4656 TCTGGAGTGGCGACAAGGAAGTGGGGCAAGGATGATCTTGCAGGATGAAGACATCACCAC 4715
Db       4759 CCTGGAGTGGCGCCAGGGCCGCATGGCGCGCATCATCCTGCAGGACGAGGACGTCACCAC 4818
Qy       4716 CAAGATTGAGAATGATTGGAAGCGACTGAACACACTGGCCCACTACCAGGTGCCAGATGG 4775
Db       4819 CAAGATTGACAACGATTGGAAGAGGCTGAACACACTGGCTCACTACCAGGTGACAGACGG 4878
Qy       4776 TTCCGTGGTGGCATTAGTGTCCAAGCAGGTGACAGCCTATAACGCAGTGAACAACTCCAC 4835
Db       4879 GTCCTCGGTGGCACTGGTGCCCAAGCAGACGTCCGCCTACAACATCTCCAACTCCTCCAC 4938
Qy       4836 CGTCTCCAGGACCTCAGCAAGTAAATATGAAAACATGATCCGGTACACGGGCAGCCCCGA 4895
Db       4939 CTTCACCAAG---TCCCTCAGCAGATACGAGAGCATGCTGCGCACGGCCAGCAGCCCCGA 4995
Qy       4896 CAGCCTCCGCTCACGGACACCTATGATCACTCCTGACCTGGAGAGTGGAGTCAAGATGTG 4955
Db       4996 CAGCCTGCGCTCGCGCACGCCCATGATCACGCCCGACCTGGAGAGCGGCACCAAGCTGTG 5055
Qy       4956 GCACCTAGTGAAGAACCACGAGCACGGAGACCAGAAGGAGGGGGACCGGGGGAGCAAGAT 5015
Db       5056 GCACCTGGTGAAGAACCACGACCACCTGGACCAGCGTGAGGGTGACCGCGGCAGCAAGAT 5115
Qy       5016 GGTGTCTGAAATCTACCTGACCCGACTCCTGGCCACTA---AGGGCACACTGCAGAAGTT 5072
Db       5116 GGTCTCGGAGATCTACTTGACACGGCTACTGGCCACCAAGCAGGGCACACTGCAGAAGTT 5175
Qy       5073 TGTGGATGACCTCTTTGAGACCATCTTCAGCACGGCACACCGTGGCTCTGCCCTGCCCCT 5132
Db       5176 TGTGGACGACCTGTTTGAGACCATCTTCAGCACGGCACACCGGGGCTCAGCCCTGCCGCT 5235
Qy       5133 GGCCATCAAGTACATGTTTGACTTCCTGGATGAGCAGGCTGATAAACATGGCATTCATGA 5192
Db       5236 GGCCATCAAGTACATGTTCGACTTCCTGGATGAGCAGGCCGACAAGCACCAGATCCACGA 5295
Qy       5193 CCCGCACGTCCGCCATACCTGGAAGAGCAATT---GCCTGCCCCTGAGGTTTTGGGTCAA 5249
Db       5296 TGCTGACGTGCGCCACACCTGGAAGAGCAACTGCAGCCTGCCCCTGCGCTTCTGGGTGAA 5355
Qy       5250 CATGATCAAGAACCCGCAGTTTGTGTTTGACATCCATAAGAACAGCATCACAGACGCCTG 5309
Db       5356 CGTGATCAAGAACCCACAGTTTGTGTTCGACATTCACAAGAACAGCATCACGGACGCCTG 5415
Qy       5310 CCTCTCTGTGGTGGCTCAGACCTTCATGGACTCTTGCTCCACGTCAGAGCACCGGCTGGG 5369
Db       5416 CTTGTCGGTGGTGGCCCAGACCTTCATGGACTCCTGCTCCACCTCTGAGCACAAGCTGGG 5475
Qy       5370 CAAGGACTCGCCCTCCAACAAGCTGCTGTATGCCAAGGACATCCCCAGCTACAAGAATTG 5429
Db       5476 CAAGGACTCACCCTCCAACAAGCTGCTCTACGCCAAGGACATCCCCAACTACAAGAGCTG 5535
Qy       5430 GGTGGA---GAGGTATTACTCAGACATAGGGAAGATGCCAGCCATCAGCGACCAAGACAT 5486
Db       5536 GGTGGAGAGGAGGTACTATGCAGACATCGCCAAGATGCCAGCCATCAGCGACCAGGACAT 5595
Qy       5487 GAACGCATACCTGGCTGAGCAGTCCCGGATGCACATGAATGAGTTCAACACCATGAGTGC 5546
Db       5596 GAGTGCGTATCTGGCTGAGCAGTCCCGCCTGCACCTGAGCCAGTTCAACAGCATGAGCGC 5655
Qy       5547 ACTCTCAGAGATCTTCTCCTATGTGGGCAAATACAGCGA------GGAGATCCTTGGACC 5600
Db       5656 CTTGCACGAGATCTACTCCTACATCACCAAGTACAAGGATGAGGTGCAGATCCTGGCAGC 5715
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Qy       5601 TCTGGACCACGATGACCAGTGTGGGAAGCAGAAACTGGCCTACAAACTAGAACAAGTCAT 5660
Db       5716 CCTGGAGAAGGATGAGCAGGCGCGGCGGCAGCGGCTGCGGAGCAAGCTGGAGCAGGTGGT 5775
Qy       5661 AACCCTCATGAGCTTAGACAGCTGA 5685
Db       5776 GGACACGATGGCCCTGAGCAGCTGA 5800
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RESULT 4
US-10-108-260A-802
; Sequence 802, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 802
; LENGTH: 3666
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-802

Query Match 20.3%; Score 1157.8; DB 15; Length 3666;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1159; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       4527 TGCCAACAGCCCCGAGGTCCCAGTAAAGATCCTCAACTGTGACACCATCACTCAGGTCAA 4586
Db          1 TGCCAACAGCCCCGAGGTCCCAGTAAAGATCCTCAACTGTGACACCATCACTCAGGTCAA 60
Qy       4587 GGAGAAGATTCTGGATGCCATCTTCAAGAATGTGCCTTGCTCCCACCGGCCCAAAGCTGC 4646
Db          61 GGAGAAGATTCTGGATGCCATCTTCAAGAATGTGCCTTGCTCCCACCGGCCCAAAGCTGC 120
Qy       4647 AGATATGGATCTGGAGTGGCGACAAGGAAGTGGGGCAAGGATGATCTTGCAGGATGAAGA 4706
Db         121 AGATATGGATCTGGAGTGGCGACAAGGAAGTGGGGCAAGGATGATCTTGCAGGATGAAGA 180
Qy       4707 CATCACCACCAAGATTGAGAATGATTGGAAGCGACTGAACACACTGGCCCACTACCAGGT 4766
Db         181 CATCACCACCAAGATTGAGAATGATTGGAAGCGACTGAACACACTGGCCCACTACCAGGT 240
Qy       4767 GCCAGATGGTTCCGTGGTGGCATTAGTGTCCAAGCAGGTGACAGCCTATAACGCAGTGAA 4826
Db         241 GCCAGATGGTTCCGTGGTGGCATTAGTGTCCAAGCAGGTGACAGCCTATAACGCAGTGAA 300
Qy       4827 CAACTCCACCGTCTCCAGGACCTCAGCAAGTAAATATGAAAACATGATCCGGTACACGGG 4886
Db         301 CAACTCCACCGTCTCCAGGACCTCAGCAAGTAAATATGAAAACATGATCCGGTACACGGG 360
Qy       4887 CAGCCCCGACAGCCTCCGCTCACGGACACCTATGATCACTCCTGACCTGGAGAGTGGAGT 4946
Db         361 CAGCCCCGACAGCCTCCGCTCACGGACACCTATGATCACTCCTGACCTGGAGAGTGGAGT 420
Qy       4947 CAAGATGTGGCACCTAGTGAAGAACCACGAGCACGGAGACCAGAAGGAGGGGGACCGGGG 5006
Db         421 CAAGATGTGGCACCTAGTGAAGAACCACGAGCACGGAGACCAGAAGGAGGGGGACCGGGG 480
Qy       5007 GAGCAAGATGGTGTCTGAAATCTACCTGACCCGACTCCTGGCCACTAAGGGCACACTGCA 5066
Db         481 GAGCAAGATGGTGTCTGAAATCTACCTGACCCGACTCCTGGCCACTAAGGGCACACTGCA 540
Qy       5067 GAAGTTTGTGGATGACCTCTTTGAGACCATCTTCAGCACGGCACACCGTGGCTCTGCCCT 5126
Db         541 GAAGTTTGTGGATGACCTCTTTGAGACCATCTTCAGCACGGCACACCGTGGCTCTGCCCT 600
Qy       5127 GCCCCTGGCCATCAAGTACATGTTTGACTTCCTGGATGAGCAGGCTGATAAACATGGCAT 5186
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCCCCTGGCCATCAAGTACATGTTTGACTTCCTGGATGAGCAGGCTGATAAACATGGCAT 660

Qy       5187 TCATGACCCGCACGTCCGCCATACCTGGAAGAGCAATTGCCTGCCCCTGAGGTTTTGGGT 5246
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TCATGACCCGCACGTCCGCCATACCTGGAAGAGCAATTGCCTGCCCCTGAGGTTTTGGGT 720

Qy       5247 CAACATGATCAAGAACCCGCAGTTTGTGTTTGACATCCATAAGAACAGCATCACAGACGC 5306
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CAACATGATCAAGAACCCGCAGTTTGTGTTTGACATCCATAAGAACAGCATCACAGACGC 780

Qy       5307 CTGCCTCTCTGTGGTGGCTCAGACCTTCATGGACTCTTGCTCCACGTCAGAGCACCGGCT 5366
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CTGCCTCTCTGTGGTGGCTCAGACCTTCATGGACTCTTGCTCCACGTCAGAGCACCGGCT 840

Qy       5367 GGGCAAGGACTCGCCCTCCAACAAGCTGCTGTATGCCAAGGACATCCCCAGCTACAAGAA 5426
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGGCAAGGACTCGCCCTCCAACAAGCTGCTGTATGCCAAGGACATCCCCAGCTACAAGAA 900

Qy       5427 TTGGGTGGAGAGGTATTACTCAGACATAGGGAAGATGCCAGCCATCAGCGACCAAGACAT 5486
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGGGTGGAGAGGTATTACTCAGACATAGGGAAGATGCCAGCCATCAGCGACCAAGACAT 960

Qy       5487 GAACGCATACCTGGCTGAGCAGTCCCGGATGCACATGAATGAGTTCAACACCATGAGTGC 5546
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAACGCATACCTGGCTGAGCAGTCCCGGATGCACATGAATGAGTTCAACACCATGAGTGC 1020

Qy       5547 ACTCTCAGAGATCTTCTCCTATGTGGGCAAATACAGCGAGGAGATCCTTGGACCTCTGGA 5606
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACTCTCAGAGATCTTCTCCTATGTGGGCAAATACAGCGAGGAGATCCTTGGACCTCTGGA 1080

Qy       5607 CCACGATGACCAGTGTGGGAAGCAGAAACTGGCCTACAAACTAGAACAAGTCATAACCCT 5666
                 |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CCACGACGACCAGTGTGGGAAGCAGAAACTGGCCTACAAACTAGAACAAGTCATAACCCT 1140

Qy       5667 CATGAGCTTAGACAGCTGAAA 5687
                 |||||||||||||||||| |
Db       1141 CATGAGCTTAGACAGCTGAGA 1161


RESULT 5
US-10-245-103-91
; Sequence 91, Application US/10245103
; Publication No. US20030068778A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin
;  APPLICANT:  Eaton,Dan
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Grimaldi,J. Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stephan,Jean-Phillippe
;  APPLICANT:  Watanbe,Colin
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang,Zemin
;  APPLICANT:  Fong,Sherman
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3630R1C112
;  CURRENT APPLICATION NUMBER: US/10/245,103
;  CURRENT FILING DATE:  2002-09-17
;  PRIOR APPLICATION NUMBER: 10/197942
;  PRIOR FILING DATE: 2002-07-18
;  PRIOR APPLICATION NUMBER: 60/059114
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/063046
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/065027
;  PRIOR FILING DATE: 1997-11-10
;  PRIOR APPLICATION NUMBER: 60/079689
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: 60/086478
;  PRIOR FILING DATE: 1998-05-22
;  PRIOR APPLICATION NUMBER: 60/087607
;  PRIOR FILING DATE: 1998-06-02
;  PRIOR APPLICATION NUMBER: 60/089801
;  PRIOR FILING DATE: 1998-06-18
;  PRIOR APPLICATION NUMBER: 60/090557
;  PRIOR FILING DATE: 1998-06-24
;  PRIOR APPLICATION NUMBER: 60/090689
;  PRIOR FILING DATE: 1998-06-25
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 91
;   LENGTH: 2597
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-245-103-91

  Query Match             13.9%;  Score 793.8;  DB 14;  Length 2597;
  Best Local Similarity   99.7%;  Pred. No. 1.6e-215;
  Matches  795;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        579 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 638
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 60

Qy        639 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 698
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 120

Qy        699 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 758
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 180

Qy        759 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 818
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 240

Qy        819 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 878
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 300

Qy        879 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 938
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 360

Qy        939 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 998
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 420

Qy        999 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 1058
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 480

Qy       1059 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 1118
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 540

Qy       1119 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 1178
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 600

Qy       1179 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 1238
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 660

Qy       1239 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 1298
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 720

Qy       1299 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 1358
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 780
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Qy       1359 CAAGCTGAAGAAGATCC 1375
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Db        781 CAAGCTGAAGAAGGTGC 797
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RESULT 6
US-10-245-107-91
; Sequence 91, Application US/10245107
; Publication No. US20030068779A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin
; APPLICANT: Eaton,Dan
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Goddard,Audrey
; APPLICANT: Grimaldi,J. Christopher
; APPLICANT: Gurney,Austin
; APPLICANT: Smith,Victoria
; APPLICANT: Stephan,Jean-Phillippe
; APPLICANT: Watanbe,Colin
; APPLICANT: Wood,William
; APPLICANT: Zhang,Zemin
; APPLICANT: Fong,Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630R1C71
; CURRENT APPLICATION NUMBER: US/10/245,107
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 91
; LENGTH: 2597
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-245-107-91

Query Match 13.9%; Score 793.8; DB 14; Length 2597;
Best Local Similarity 99.7%; Pred. No. 1.6e-215;
Matches 795; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy        579 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 60

Qy        639 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 120

Qy        699 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 180

Qy        759 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 240

Qy        819 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 300

Qy        879 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 938
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 360

Qy        939 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 420

Qy        999 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 480

Qy       1059 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 540

Qy       1119 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 1178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 600

Qy       1179 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 1238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 660

Qy       1239 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 1298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 720

Qy       1299 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 1358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 780

Qy       1359 CAAGCTGAAGAAGATCC 1375
              ||||||||||||| | |
Db        781 CAAGCTGAAGAAGGTGC 797
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RESULT 7
US-10-245-143-91
; Sequence 91, Application US/10245143
; Publication No. US20030068780A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin
; APPLICANT: Eaton,Dan
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Goddard,Audrey
; APPLICANT: Grimaldi,J. Christopher
; APPLICANT: Gurney,Austin
; APPLICANT: Smith,Victoria
; APPLICANT: Stephan,Jean-Phillippe
; APPLICANT: Watanbe,Colin
; APPLICANT: Wood,William
; APPLICANT: Zhang,Zemin
; APPLICANT: Fong,Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630R1C90
; CURRENT APPLICATION NUMBER: US/10/245,143
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10

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;  PRIOR APPLICATION NUMBER: 60/079689
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: 60/086478
;  PRIOR FILING DATE: 1998-05-22
;  PRIOR APPLICATION NUMBER: 60/087607
;  PRIOR FILING DATE: 1998-06-02
;  PRIOR APPLICATION NUMBER: 60/089801
;  PRIOR FILING DATE: 1998-06-18
;  PRIOR APPLICATION NUMBER: 60/090557
;  PRIOR FILING DATE: 1998-06-24
;  PRIOR APPLICATION NUMBER: 60/090689
;  PRIOR FILING DATE: 1998-06-25
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 91
;   LENGTH: 2597
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-245-143-91

  Query Match             13.9%;  Score 793.8;  DB 14;  Length 2597;
  Best Local Similarity   99.7%;  Pred. No. 1.6e-215;
  Matches  795;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        579 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 60

Qy        639 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 120

Qy        699 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 180

Qy        759 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 240

Qy        819 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 300

Qy        879 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 938
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 360

Qy        939 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 420

Qy        999 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 480

Qy       1059 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 540

Qy       1119 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 1178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 600

Qy       1179 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 1238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 660

Qy       1239 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 1298
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Db        661 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 720

Qy       1299 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 1358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 780

Qy       1359 CAAGCTGAAGAAGATCC 1375
              ||||||||||||||| |||
Db        781 CAAGCTGAAGAAGGTGC 797


RESULT 8
US-10-245-771-91
; Sequence 91, Application US/10245771
; Publication No. US20030068781A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin
;  APPLICANT:  Eaton,Dan
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Grimaldi,J. Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stephan,Jean-Phillippe
;  APPLICANT:  Watanbe,Colin
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang,Zemin
;  APPLICANT:  Fong,Sherman
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3630R1C98
;  CURRENT APPLICATION NUMBER: US/10/245,771
;  CURRENT FILING DATE:  2002-09-16
;  PRIOR APPLICATION NUMBER: 10/197942
;  PRIOR FILING DATE: 2002-07-18
;  PRIOR APPLICATION NUMBER: 60/059114
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/063046
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/065027
;  PRIOR FILING DATE: 1997-11-10
;  PRIOR APPLICATION NUMBER: 60/079689
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: 60/086478
;  PRIOR FILING DATE: 1998-05-22
;  PRIOR APPLICATION NUMBER: 60/087607
;  PRIOR FILING DATE: 1998-06-02
;  PRIOR APPLICATION NUMBER: 60/089801
;  PRIOR FILING DATE: 1998-06-18
;  PRIOR APPLICATION NUMBER: 60/090557
;  PRIOR FILING DATE: 1998-06-24
;  PRIOR APPLICATION NUMBER: 60/090689
;  PRIOR FILING DATE: 1998-06-25
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 91
;   LENGTH: 2597
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-245-771-91

  Query Match             13.9%;  Score 793.8;  DB 14;  Length 2597;
  Best Local Similarity   99.7%;  Pred. No. 1.6e-215;
  Matches  795;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        579 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 60

Qy        639 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 120

Qy        699 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 180
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Qy        759 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 240

Qy        819 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 300

Qy        879 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 938
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 360

Qy        939 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 420

Qy        999 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 480

Qy       1059 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 540

Qy       1119 TTGTTACCGGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 1178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTGTTACCGGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 600

Qy       1179 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 1238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 660

Qy       1239 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 1298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 720

Qy       1299 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 1358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 780

Qy       1359 CAAGCTGAAGAAGATCC 1375
              ||||||||||||| | |
Db        781 CAAGCTGAAGAAGGTGC 797
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RESULT 9
US-10-245-851-91
; Sequence 91, Application US/10245851
; Publication No. US20030068782A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin
; APPLICANT: Eaton,Dan
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Goddard,Audrey
; APPLICANT: Grimaldi,J. Christopher
; APPLICANT: Gurney,Austin
; APPLICANT: Smith,Victoria
; APPLICANT: Stephan,Jean-Phillippe
; APPLICANT: Watanbe,Colin
; APPLICANT: Wood,William
; APPLICANT: Zhang,Zemin
; APPLICANT: Fong,Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630R1C93
; CURRENT APPLICATION NUMBER: US/10/245,851
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 91
; LENGTH: 2597
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-245-851-91

Query Match 13.9%; Score 793.8; DB 14; Length 2597;
Best Local Similarity 99.7%; Pred. No. 1.6e-215;
Matches 795; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy        579 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 60

Qy        639 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 120

Qy        699 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 180

Qy        759 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 240

Qy        819 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 300

Qy        879 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 938
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 360

Qy        939 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 420

Qy        999 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 480

Qy       1059 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 540

Qy       1119 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 1178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 600

Qy       1179 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 1238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 660

Qy       1239 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 1298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        661 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 720

Qy       1299 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 1358
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 780

Qy       1359 CAAGCTGAAGAAGATCC 1375
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Db        781 CAAGCTGAAGAAGGTGC 797


RESULT 10
US-10-245-883-91
; Sequence 91, Application US/10245883
; Publication No. US20030068783A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin
;  APPLICANT:  Eaton,Dan
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Grimaldi,J. Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stephan,Jean-Phillippe
;  APPLICANT:  Watanbe,Colin
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang,Zemin
;  APPLICANT:  Fong,Sherman
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3630R1C70
;  CURRENT APPLICATION NUMBER: US/10/245,883
;  CURRENT FILING DATE:  2002-09-16
;  PRIOR APPLICATION NUMBER: 10/197942
;  PRIOR FILING DATE: 2002-07-18
;  PRIOR APPLICATION NUMBER: 60/059114
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/063046
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/065027
;  PRIOR FILING DATE: 1997-11-10
;  PRIOR APPLICATION NUMBER: 60/079689
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: 60/086478
;  PRIOR FILING DATE: 1998-05-22
;  PRIOR APPLICATION NUMBER: 60/087607
;  PRIOR FILING DATE: 1998-06-02
;  PRIOR APPLICATION NUMBER: 60/089801
;  PRIOR FILING DATE: 1998-06-18
;  PRIOR APPLICATION NUMBER: 60/090557
;  PRIOR FILING DATE: 1998-06-24
;  PRIOR APPLICATION NUMBER: 60/090689
;  PRIOR FILING DATE: 1998-06-25
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 91
;   LENGTH: 2597
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-245-883-91

  Query Match             13.9%;  Score 793.8;  DB 14;  Length 2597;
  Best Local Similarity   99.7%;  Pred. No. 1.6e-215;
  Matches  795;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        579 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 60

Qy        639 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 120

Qy        699 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 180

Qy        759 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 240

Qy        819 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 300

Qy        879 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 938
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 360

Qy        939 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 420

Qy        999 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 480

Qy       1059 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 540

Qy       1119 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 1178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 600

Qy       1179 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 1238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 660

Qy       1239 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 1298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 720

Qy       1299 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 1358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGTGGCCTTTGTGGGCACCAAAAGTGG 780

Qy       1359 CAAGCTGAAGAAGATCC 1375
              ||||||||||||||| | |
Db        781 CAAGCTGAAGAAGGTGC 797


RESULT 11
US-10-237-535-91
; Sequence 91, Application US/10237535
; Publication No. US20030073188A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin
;  APPLICANT:  Eaton,Dan
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Grimaldi,J. Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stephan,Jean-Phillippe
;  APPLICANT:  Watanbe,Colin
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang,Zemin
;  APPLICANT:  Fong,Sherman
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3630R1C3
;  CURRENT APPLICATION NUMBER: US/10/237,535
;  CURRENT FILING DATE:  2002-09-06
;  PRIOR APPLICATION NUMBER: 10/197942
;  PRIOR FILING DATE: 2002-07-18
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; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/091358
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
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; PRIOR APPLICATION NUMBER: 60/115554
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; PRIOR APPLICATION NUMBER: 60/119342
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: 60/123957
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; PRIOR APPLICATION NUMBER: 60/123972
; PRIOR FILING DATE: 1999-03-11
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; PRIOR APPLICATION NUMBER: 60/131271
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/133459
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/135725
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; PRIOR APPLICATION NUMBER: 60/135729
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; PRIOR APPLICATION NUMBER: 60/138385
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; PRIOR APPLICATION NUMBER: 60/140653
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; PRIOR APPLICATION NUMBER: 60/145228
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; PRIOR APPLICATION NUMBER: 60/232887
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/235147
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/261878
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/261910
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/261939
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/262150
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/264395
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/266421
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/267623
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/274399
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/280982
; PRIOR FILING DATE: 2001-04-03
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; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/282199
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/290589
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 09/180997
; PRIOR FILING DATE: 1998-11-19
; PRIOR APPLICATION NUMBER: 09/267213
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; PRIOR APPLICATION NUMBER: 09/403297
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; PRIOR APPLICATION NUMBER: 09/423741
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; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 09/802706
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; PRIOR APPLICATION NUMBER: 09/872035
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; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/924419
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/927796
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/929404
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/931836
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 09/941992
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 09/946374
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 10/001054
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 10/081056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 10/119480
; PRIOR FILING DATE: 2002-04-09

Query Match 13.9%; Score 793.8; DB 14; Length 2597;
Best Local Similarity 99.7%; Pred. No. 1.6e-215;
Matches 795; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy        579 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 60

Qy        639 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 120

Qy        699 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 180

Qy        759 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 240

Qy        819 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 300

Qy        879 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 938
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 360

Qy        939 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 420

Qy        999 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 480

Qy       1059 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 540

Qy       1119 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 1178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 600

Qy       1179 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 1238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 660

Qy       1239 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 1298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 720

Qy       1299 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 1358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 780

Qy       1359 CAAGCTGAAGAAGATCC 1375
              ||||||||||||| | |
Db         781 CAAGCTGAAGAAGGTGC 797
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RESULT 12
US-10-238-183-91
; Sequence 91, Application US/10238183
; Publication No. US20030073189A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin
; APPLICANT: Eaton,Dan
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Goddard,Audrey
; APPLICANT: Grimaldi,J. Christopher
; APPLICANT: Gurney,Austin
; APPLICANT: Smith,Victoria
; APPLICANT: Stephan,Jean-Phillippe
; APPLICANT: Watanbe,Colin
; APPLICANT: Wood,William
; APPLICANT: Zhang,Zemin
; APPLICANT: Fong,Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630R1C11
; CURRENT APPLICATION NUMBER: US/10/238,183
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
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; PRIOR APPLICATION NUMBER: 60/091978
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; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
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; PRIOR APPLICATION NUMBER: 60/119342
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: 60/123957
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123972
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: 60/127372
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/131271
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/133459
; PRIOR FILING DATE: 1999-05-11
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; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/138385
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; PRIOR APPLICATION NUMBER: 60/145698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 60/146222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 60/146843
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/148188
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/148513
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/149327
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149395
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/150114
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: 60/151700
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/151734
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/162506
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; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/177118
; PRIOR FILING DATE: 2000-01-20
; PRIOR APPLICATION NUMBER: 60/179851
; PRIOR FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 60/180921
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/187202
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/198587
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 60/199614
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 60/206330
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/206368
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/209832
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: 60/218371
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 60/222695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/229896
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/230621
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/232887
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/235147
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/261878
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/261910
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/261939
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/262150
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/264395
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/266421
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/267623
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/274399
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/280982
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/282129
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/282199
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/290589
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 09/180997
; PRIOR FILING DATE: 1998-11-19
; PRIOR APPLICATION NUMBER: 09/267213
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380138
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/403297
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/423741
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: 09/709238
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 09/802706
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 09/872035
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/924419
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/927796
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/929404
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/931836
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 09/941992
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 09/946374
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 10/001054
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15

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;  PRIOR APPLICATION NUMBER: 10/081056
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: 10/119480
;  PRIOR FILING DATE: 2002-04-09

  Query Match             13.9%;  Score 793.8;  DB 14;  Length 2597;
  Best Local Similarity   99.7%;  Pred. No. 1.6e-215;
  Matches  795;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        579 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 60

Qy        639 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 120

Qy        699 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 180

Qy        759 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 240

Qy        819 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 300

Qy        879 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 938
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 360

Qy        939 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 420

Qy        999 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 480

Qy       1059 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 540

Qy       1119 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 1178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 600

Qy       1179 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 1238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 660

Qy       1239 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 1298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 720

Qy       1299 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 1358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 780

Qy       1359 CAAGCTGAAGAAGATCC 1375
              ||||||||||||| | |
Db        781 CAAGCTGAAGAAGGTGC 797


RESULT 13
US-10-238-283-91
; Sequence 91, Application US/10238283
; Publication No. US20030073190A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin
;  APPLICANT:  Eaton,Dan
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Grimaldi,J. Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stephan,Jean-Phillippe
;  APPLICANT:  Watanbe,Colin
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang,Zemin
;  APPLICANT:  Fong,Sherman
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3630R1C15
;  CURRENT APPLICATION NUMBER: US/10/238,283
;  CURRENT FILING DATE:  2002-09-09
;  PRIOR APPLICATION NUMBER: 10/197942
;  PRIOR FILING DATE: 2002-07-18
;  PRIOR APPLICATION NUMBER: 60/059114
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/063046
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/065027
;  PRIOR FILING DATE: 1997-11-10
;  PRIOR APPLICATION NUMBER: 60/079689
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: 60/086478
;  PRIOR FILING DATE: 1998-05-22
;  PRIOR APPLICATION NUMBER: 60/087607
;  PRIOR FILING DATE: 1998-06-02
;  PRIOR APPLICATION NUMBER: 60/089801
;  PRIOR FILING DATE: 1998-06-18
;  PRIOR APPLICATION NUMBER: 60/090557
;  PRIOR FILING DATE: 1998-06-24
;  PRIOR APPLICATION NUMBER: 60/090689
;  PRIOR FILING DATE: 1998-06-25
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 91
;   LENGTH: 2597
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-238-283-91

  Query Match             13.9%;  Score 793.8;  DB 14;  Length 2597;
  Best Local Similarity   99.7%;  Pred. No. 1.6e-215;
  Matches  795;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        579 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 60

Qy        639 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 120

Qy        699 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 180

Qy        759 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 240

Qy        819 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 300

Qy        879 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 938
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 360

Qy        939 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        361 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 420

Qy        999 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 480

Qy       1059 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 540

Qy       1119 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 1178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 600

Qy       1179 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 1238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 660

Qy       1239 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 1298
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Db        661 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 720

Qy       1299 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 1358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 780

Qy       1359 CAAGCTGAAGAAGATCC 1375
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Db        781 CAAGCTGAAGAAGGTGC 797


RESULT 14
US-10-238-370-91
; Sequence 91, Application US/10238370
; Publication No. US20030073191A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin
;  APPLICANT:  Eaton,Dan
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Grimaldi,J. Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stephan,Jean-Phillippe
;  APPLICANT:  Watanbe,Colin
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang,Zemin
;  APPLICANT:  Fong,Sherman
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3630R1C10
;  CURRENT APPLICATION NUMBER: US/10/238,370
;  CURRENT FILING DATE:  2002-09-09
;  PRIOR APPLICATION NUMBER: 10/197942
;  PRIOR FILING DATE: 2002-07-18
;  PRIOR APPLICATION NUMBER: 60/059114
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/063046
;  PRIOR FILING DATE: 1997-10-24
;  PRIOR APPLICATION NUMBER: 60/065027
;  PRIOR FILING DATE: 1997-11-10
;  PRIOR APPLICATION NUMBER: 60/079689
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: 60/086478
;  PRIOR FILING DATE: 1998-05-22
;  PRIOR APPLICATION NUMBER: 60/087607
;  PRIOR FILING DATE: 1998-06-02
;  PRIOR APPLICATION NUMBER: 60/089801
;  PRIOR FILING DATE: 1998-06-18
;  PRIOR APPLICATION NUMBER: 60/090557
;  PRIOR FILING DATE: 1998-06-24
;  PRIOR APPLICATION NUMBER: 60/090689
;  PRIOR FILING DATE: 1998-06-25
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 91
;   LENGTH: 2597
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-238-370-91

  Query Match             13.9%;  Score 793.8;  DB 14;  Length 2597;
  Best Local Similarity   99.7%;  Pred. No. 1.6e-215;
  Matches  795;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        579 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 60

Qy        639 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 120

Qy        699 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 180

Qy        759 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 240

Qy        819 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 300

Qy        879 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 938
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 360

Qy        939 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 420

Qy        999 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 480

Qy       1059 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 540

Qy       1119 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 1178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 600

Qy       1179 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 1238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 660

Qy       1239 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 1298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 720

Qy       1299 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 1358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 780

Qy       1359 CAAGCTGAAGAAGATCC 1375
              ||||||||||||| | |
Db        781 CAAGCTGAAGAAGGTGC 797


RESULT 15
US-10-245-055-91
; Sequence 91, Application US/10245055
; Publication No. US20030073192A1
```

; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin
; APPLICANT: Eaton,Dan
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Goddard,Audrey
; APPLICANT: Grimaldi,J. Christopher
; APPLICANT: Gurney,Austin
; APPLICANT: Smith,Victoria
; APPLICANT: Stephan,Jean-Phillippe
; APPLICANT: Watanbe,Colin
; APPLICANT: Wood,William
; APPLICANT: Zhang,Zemin
; APPLICANT: Fong,Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630R1C88
; CURRENT APPLICATION NUMBER: US/10/245,055
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 91
; LENGTH: 2597
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-245-055-91

Query Match 13.9%; Score 793.8; DB 14; Length 2597;
Best Local Similarity 99.7%; Pred. No. 1.6e-215;
Matches 795; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy        639 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 698
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Search completed: February 20, 2004, 02:47:35
Job time : 1250 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 19, 2004, 16:15:27 ; Search time 8735 Seconds
(without alignments)
19455.715 Million cell updates/sec

Title: US-09-964-956-12
Perfect score: 5691
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
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20: em_gss_vrt:*
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25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	3	2111.4	37.1	5564	29	AY420221	AY420221 Mus muscu
	4	2017.2	35.4	5520	29	AY420666	AY420666 Homo sapi
	5	1767.2	31.1	5447	29	AY420668	AY420668 Mus muscu
	6	1681.4	29.5	5520	29	AY420667	AY420667 Pan trogl
	7	1552.6	27.3	5341	29	AY420220	AY420220 Pan trogl
	8	1221.2	21.5	3355	11	AK049319	AK049319 Mus muscu
	9	743.8	13.1	838	14	CD653539	CD653539 AGENCOURT
	10	658.8	11.6	1059	12	BM547417	BM547417 AGENCOURT
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	12	638.4	11.2	745	14	CA316867	CA316867 UI-M-FW0-
	13	613	10.8	618	13	BX470595	BX470595 DKFZp686G
	14	599.2	10.5	1027	12	BM544169	BM544169 AGENCOURT
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ALIGNMENTS

RESULT 1
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DEFINITION Homo sapiens HCM7151 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY420219
VERSION AY420219.1 GI:39776176
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 5691)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 5691)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence as made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

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ORIGIN

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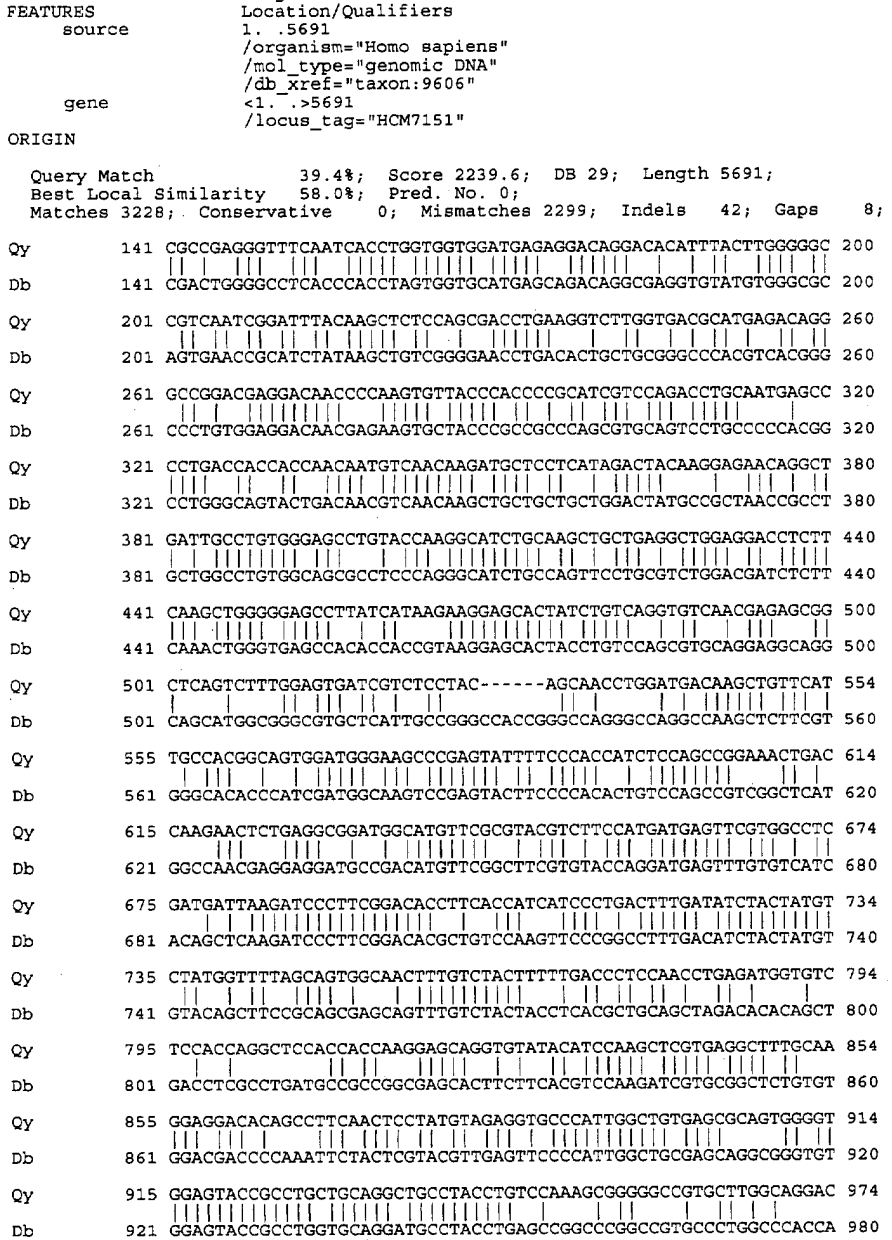

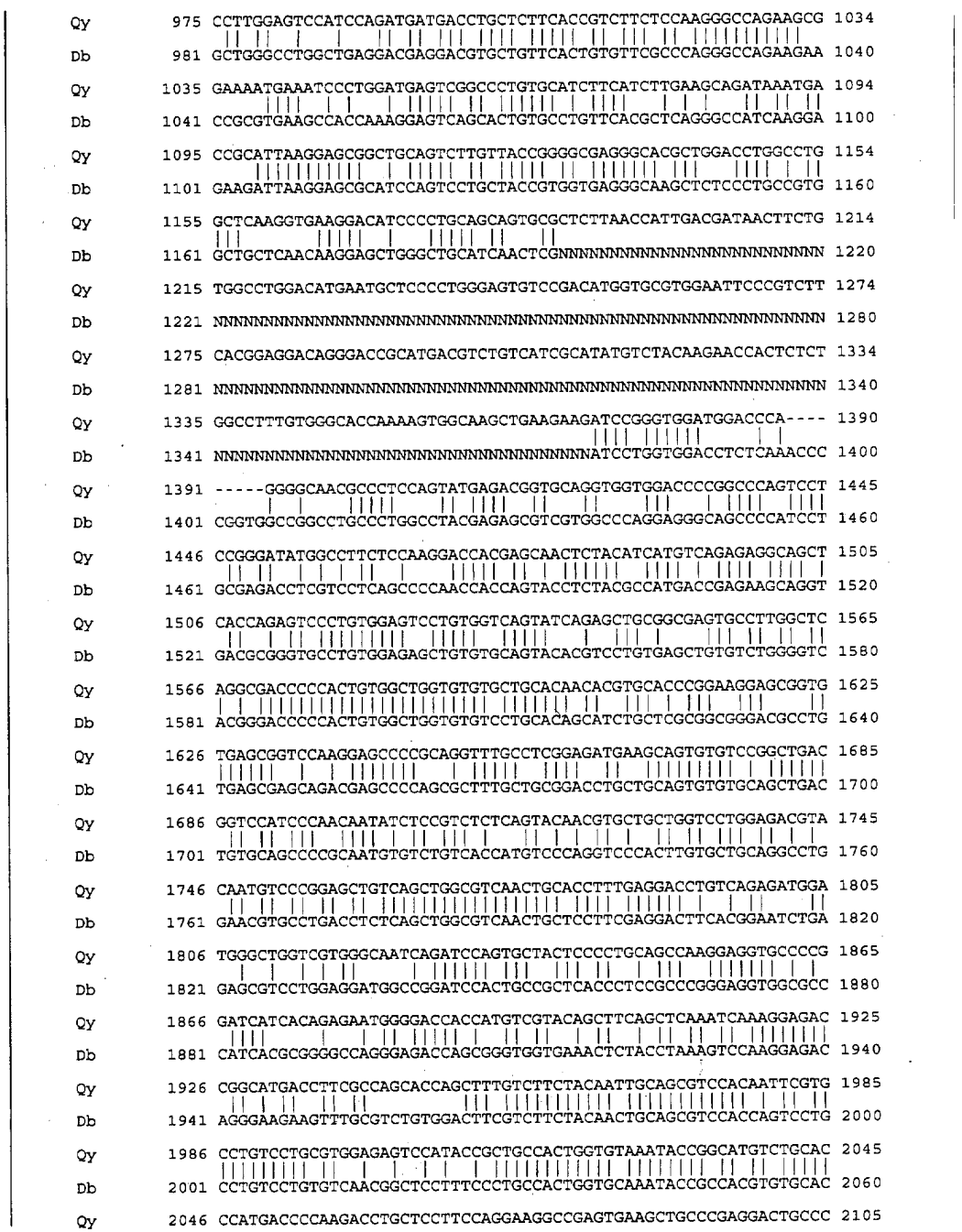

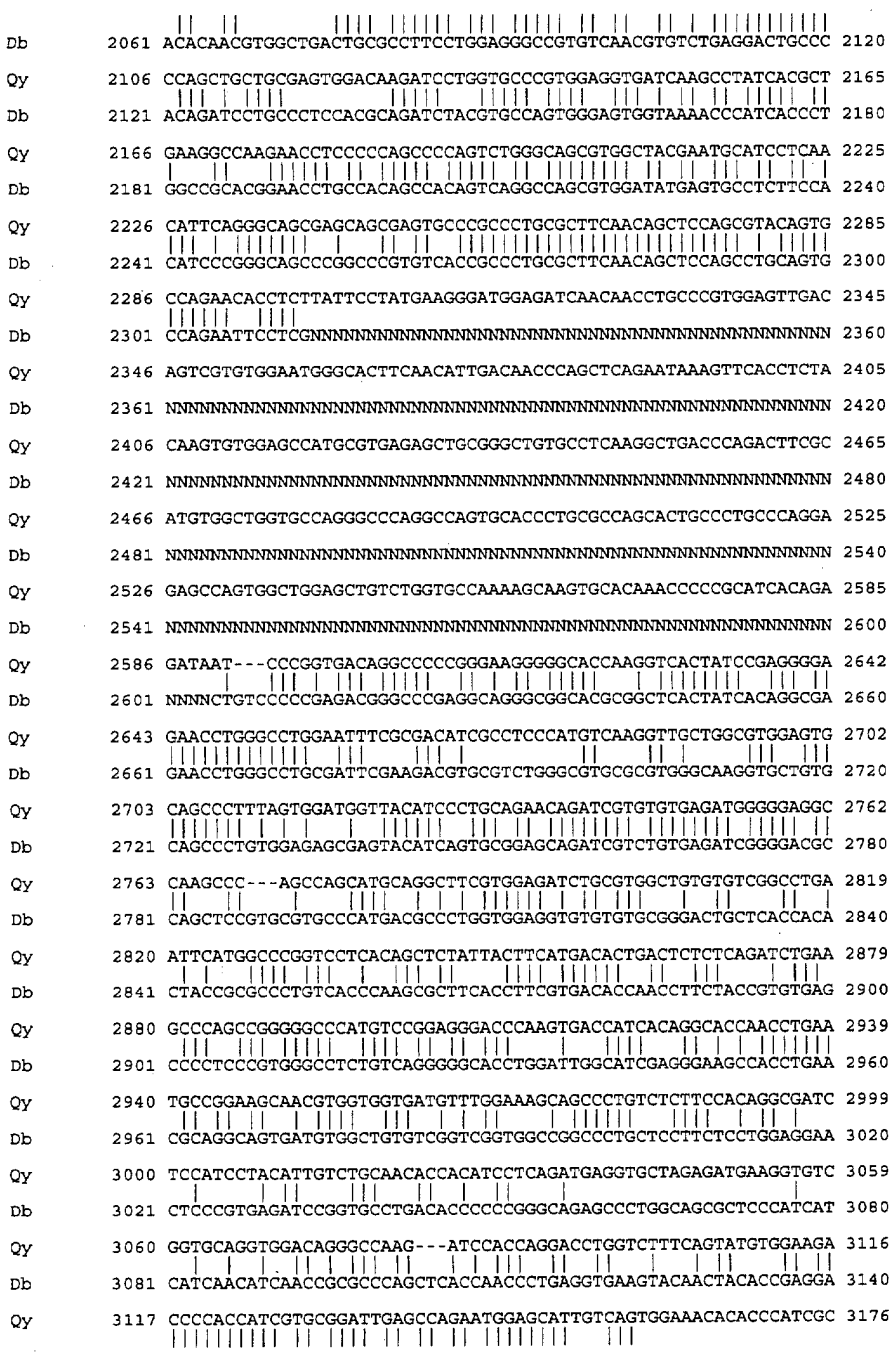
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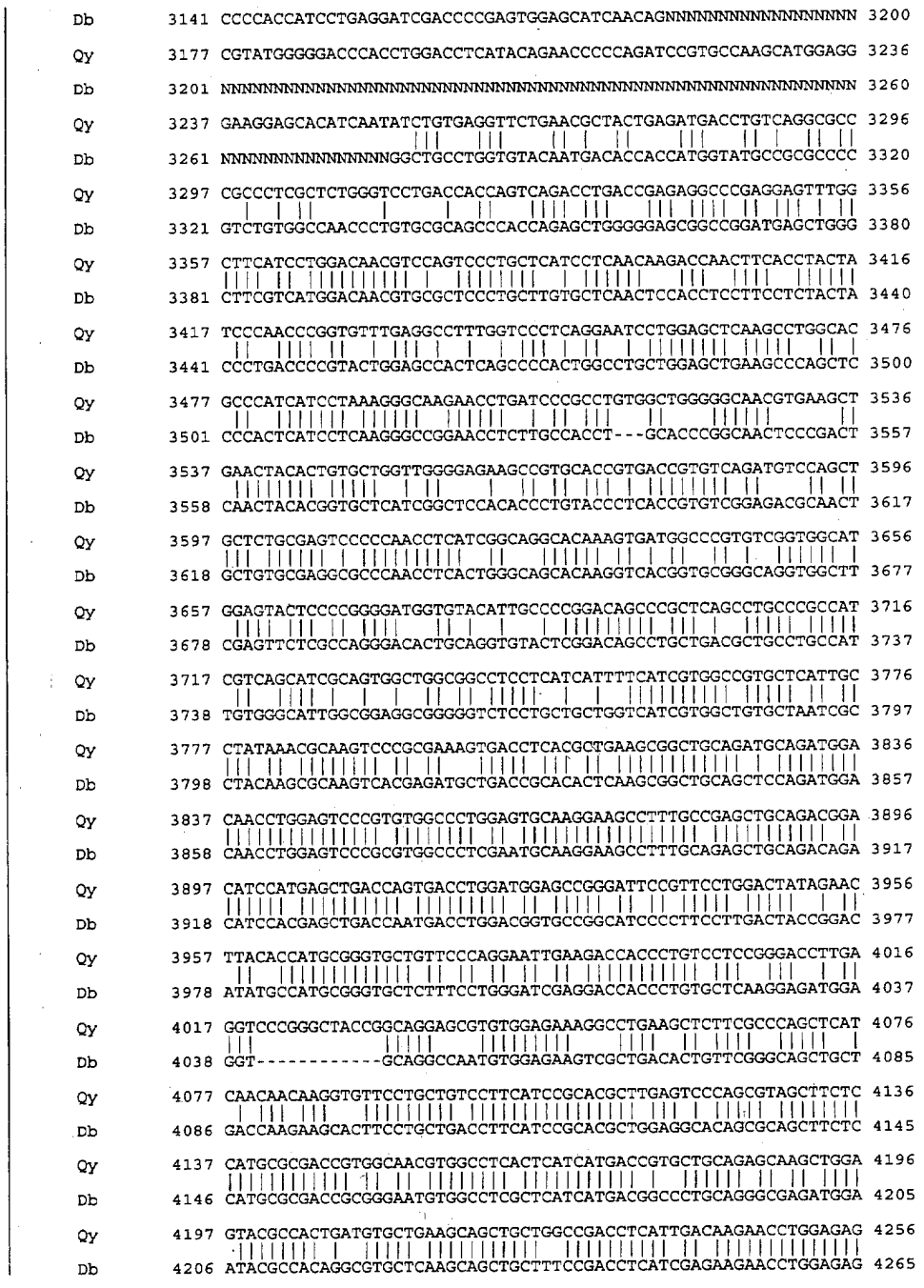
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Qy       5097 CTTCAGCACGGCACACCGTGGCTCTGCCCTGCCCCTGGCCATCAAGTACATGTTTGACTT 5156
Db       5103 CTTCAGCACGGCACACCGGGGCTCAGCCCTGCCGCTGGCCATCAAGTACATGTTCGACTT 5162

Qy       5157 CCTGGATGAGCAGGCTGATAAACATGGCATTCATGACCCGCACGTCCGCCATACCTGGAA 5216
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Qy       5217 GAGCAATTGCCTGCCCCTGAGGTTTTGGGTCAACATGATCAAGAACCCGCAGTTTGTGTT 5276
Db       5223 GAGCAACTGCCTGCCCCTGCGCTTCTGGGTGAACGTGATCAAGAACCCACAGTTTGTGTT 5282

Qy       5277 TGACATCCATAAGAACAGCATCACAGACGCCTGCCTCTCTGTGGTGGCTCAGACCTTCAT 5336
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Qy       5337 GGACTCTTGCTCCACGTCAGAGCACCGGCTGGGCAAGGACTCGCCCTCCAACAAGCTGCT 5396
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Qy       5457 GAAGATGCCAGCCATCAGCGACCAAGACATGAACGCATACCTGGCTGAGCAGTCCCGGAT 5516
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Qy       5517 GCACATGAATGAGTTCAACACCATGAGTGCACTCTCAGAGATCTTCTCCTATGTGGGCAA 5576
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Qy       5637 GGCCTACAAACTAGAACAAGTCATAACCCTCATGAGCTTAGACAGCTGA 5685
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RESULT 2
AK051614

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LOCUS       AK051614               3361 bp    mRNA    linear   HTC 20-SEP-2003
DEFINITION  Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length
            enriched library, clone:D130060F15 product:similar to PLEXIN 2 [Mus
            musculus], full insert sequence.
ACCESSION   AK051614
VERSION     AK051614.1  GI:26342059
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
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            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
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  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 3361)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
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            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.go.jp/
            URL:http://fantom.gsc.riken.go.jp/.
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                     /db_xref="MGI:2419923"
                     /db_xref="taxon:10090"
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                     SPNLIGRHKVMARVGGMEYSPGMVYIAPDSPLSLPAIVSIAVAGGLLIIFIVAVLIAY
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                     QQIEYKTLVLSCVSPDNVNSPEVPVKILNCDTITQVKEKILDAIFKNVPCSHRPKAAD
                     MDLEWRQGSGARMILQDEDITTKIENDWKRLNTVAHYQVPDGSVVALVSKQVTAYNAE
                     NNSTVSRTSASKYENMIRYTGSPDSLRSRTPMITPDLESGVKLWHLVKNHEHGDQKEG
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ORIGIN

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Db         61 ACTCACCTGGACCTCATACAGAACCCACAGATCCGTGCCAAGCATGGAGGAAAAGAACAC 120

Qy       3247 ATCAATATCTGTGAGGTTCTGAACGCTACTGAGATGACCTGTCAGGCGCCCGCCCTCGCT 3306

Db        121 ATCAACATCTGTGAGGTCCTAAATGCTACAGAGATGACCTGCCAGGCTCCAGCCCTTGCC 180

Qy       3307 CTGGGTCCTGACCACCAGTCAGACCTGACCGAGAGGCCCGAGGAGTTTGGCTTCATCCTG 3366

Db        181 CTGGGTCCCGACCACCAGTCAGATCTCACTGAGAGGCCTGAAGAATTTGGTTTCATCCTG 240

Qy       3367 GACAACGTCCAGTCCCTGCTCATCCTCAACAAGACCAACTTCACCTACTATCCCAACCCG 3426

Db        241 GACAATGTCCAGTCTCTGCTAATTCTCAACAAGACCAACTTCACCTATTATCCTAACCCC 300

Qy       3427 GTGTTTGAGGCCTTTGGTCCCTCAGGAATCCTGGAGCTCAAGCCTGGCACGCCCATCATC 3486

Db        301 GTGTTTGAGGCTTTCAGTCCCTCGGGAATCCTGGAGCTCAAGCCGGGCACCCCCATTATC 360

Qy       3487 CTAAAGGGCAAGAACCTGATCCCGCCTGTGGCTGGGGGCAACGTGAAGCTGAACTACACT 3546

Db        361 CTAAAGGGCAAGAACTTGATCCCGCCTGTGGCCGGAGGCAATGTGAAGCTGAACTACACC 420

Qy       3547 GTGCTGGTTGGGGAGAAGCCGTGCACCGTGACCGTGTCAGATGTCCAGCTGCTCTGCGAG 3606

Db        421 GTGCTGGTTGGGGAGAAACCATGCACCGTGACAGTATCAGATGTGCAGCTGCTCTGCGAG 480

Qy       3607 TCCCCCAACCTCATCGGCAGGCACAAAGTGATGGCCCGTGTCGGTGGCATGGAGTACTCC 3666

Db        481 TCTCCCAACCTCATCGGCAGGCACAAAGTGATGGCACGGGTGGGTGGCATGGAGTATTCC 540

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Db        541 CCTGGGATGGTATACATCGCCCCAGACAGCCCGCTCAGCCTGCCCGCCATTGTCAGCATC 600

Qy       3727 GCAGTGGCTGGCGGCCTCCTCATCATTTTCATCGTGGCCGTGCTCATTGCCTATAAACGC 3786

Db        601 GCGGTGGCTGGTGGCCTCCTCATCATCTTCATCGTGGCCGTACTCATCGCCTACAAACGC 660

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Qy       3847 TCCCGTGTGGCCCTGGAGTGCAAGGAAGCCTTTGCCGAGCTGCAGACGGACATCCATGAG 3906

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Qy       3907 CTGACCAGTGACCTGGATGGAGCCGGGATTCCGTTCCTGGACTATAGAACTTACACCATG 3966

Db        781 CTTACCAGTGACCTGGATGGAGCTGGGATTCCCTTTCTGGACTACAGAACCTATACCATG 840

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Qy       4027 TACCGGCAGGAGCGTGTGGAGAAAGGCCTGAAGCTCTTCGCCCAGCTCATCAACAACAAG 4086

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Qy       4087 GTGTTCCTGCTGTCCTTCATCCGCACGCTTGAGTCCCAGCGTAGCTTCTCCATGCGCGAC 4146

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Qy       4207 GATGTGCTGAAGCAGCTGCTGGCCGACCTCATTGACAAGAACCTGGAGAGCAAGAACCAC 4266
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Qy       4567 GACACCATCACTCAGGTCAAGGAGAAGATTCTGGATGCCATCTTCAAGAATGTGCCTTGC 4626
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Db       1621 ACAGTAGCCCACTACCAGGTACCAGATGGTTCTGTGGTGGCTTTAGTGTCCAAGCAAGTG 1680
Qy       4807 ACAGCCTATAACGCAGTGAACAACTCCACCGTCTCCAGGACCTCAGCAAGTAAATATGAA 4866
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Qy       4867 AACATGATCCGGTACACGGGCAGCCCCGACAGCCTCCGCTCACGGACACCTATGATCACT 4926
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Qy       5047 GCCACTAAGGGCACACTGCAGAAGTTTGTGGATGACCTCTTTGAGACCATCTTCAGCACG 5106
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Qy       5107 GCACACCGTGGCTCTGCCCTGCCCCTGGCCATCAAGTACATGTTTGACTTCCTGGATGAG 5166
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RESULT 3
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LOCUS       AY420221               5564 bp    DNA     linear   GSS 12-DEC-2003
DEFINITION  Mus musculus HCM7151 gene, VIRTUAL TRANSCRIPT, partial sequence,
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ACCESSION   AY420221
VERSION     AY420221.1  GI:39776178
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 5564)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 5564)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence as made by sequencing genomic exons and ordering them
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ORIGIN
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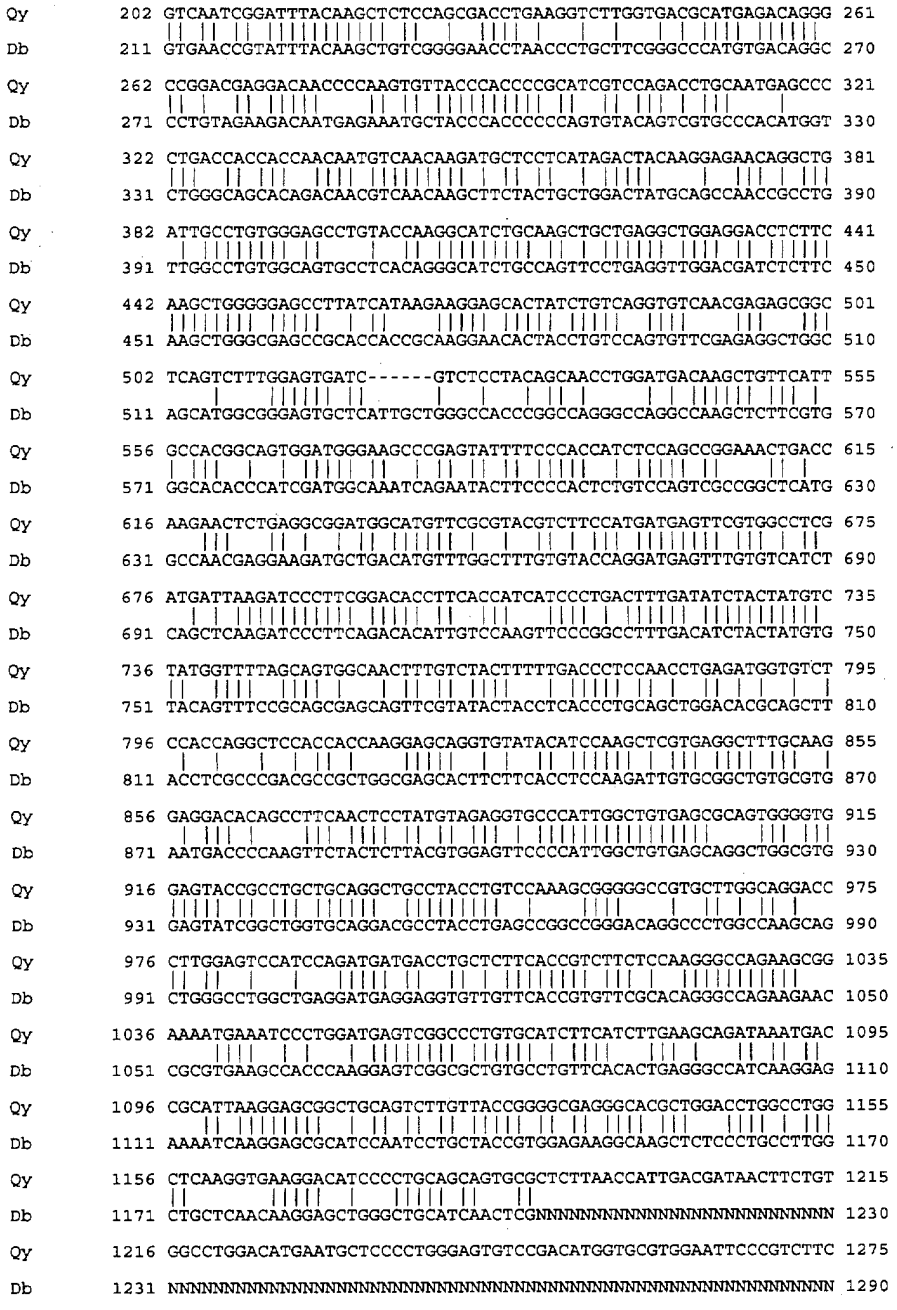

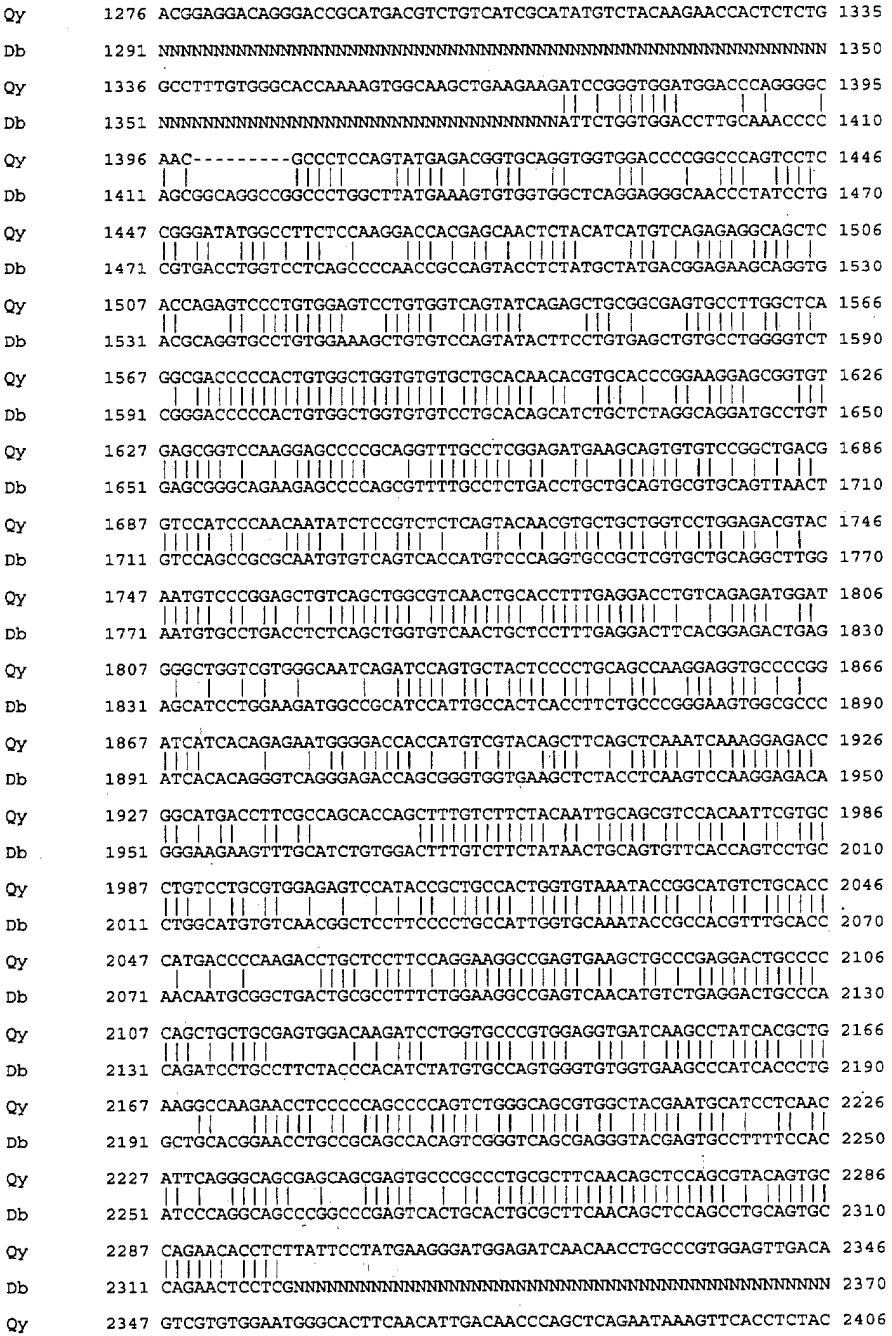

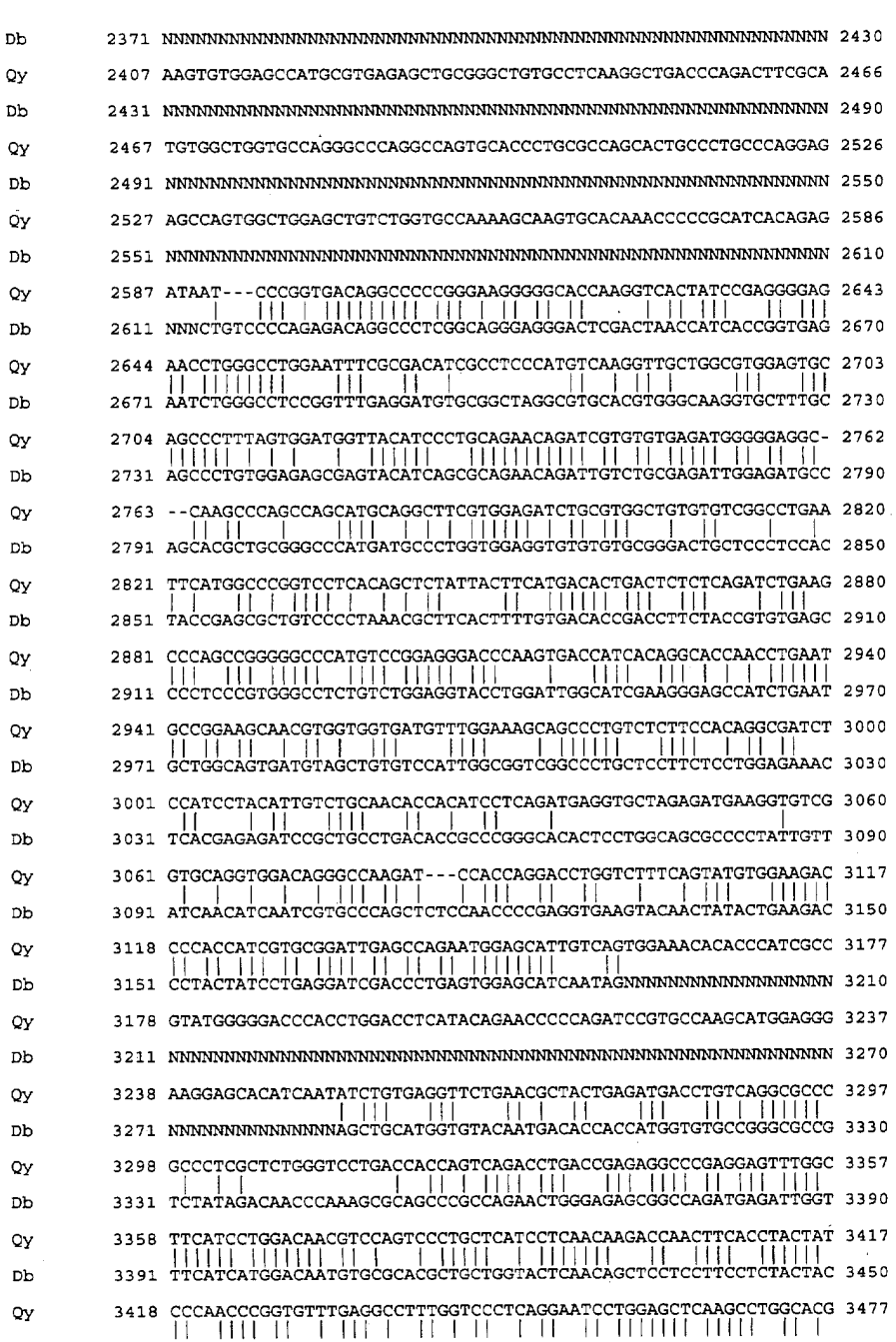

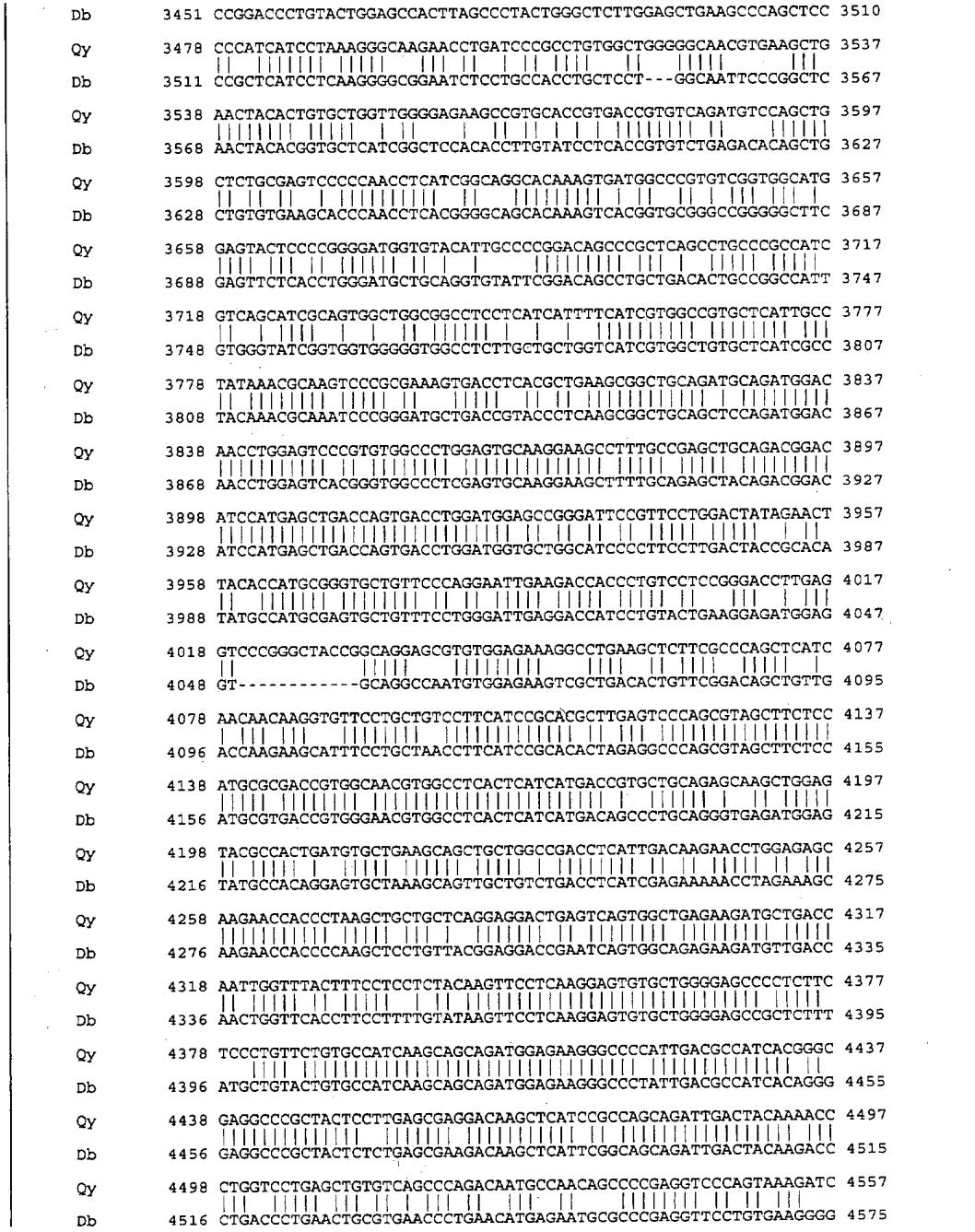

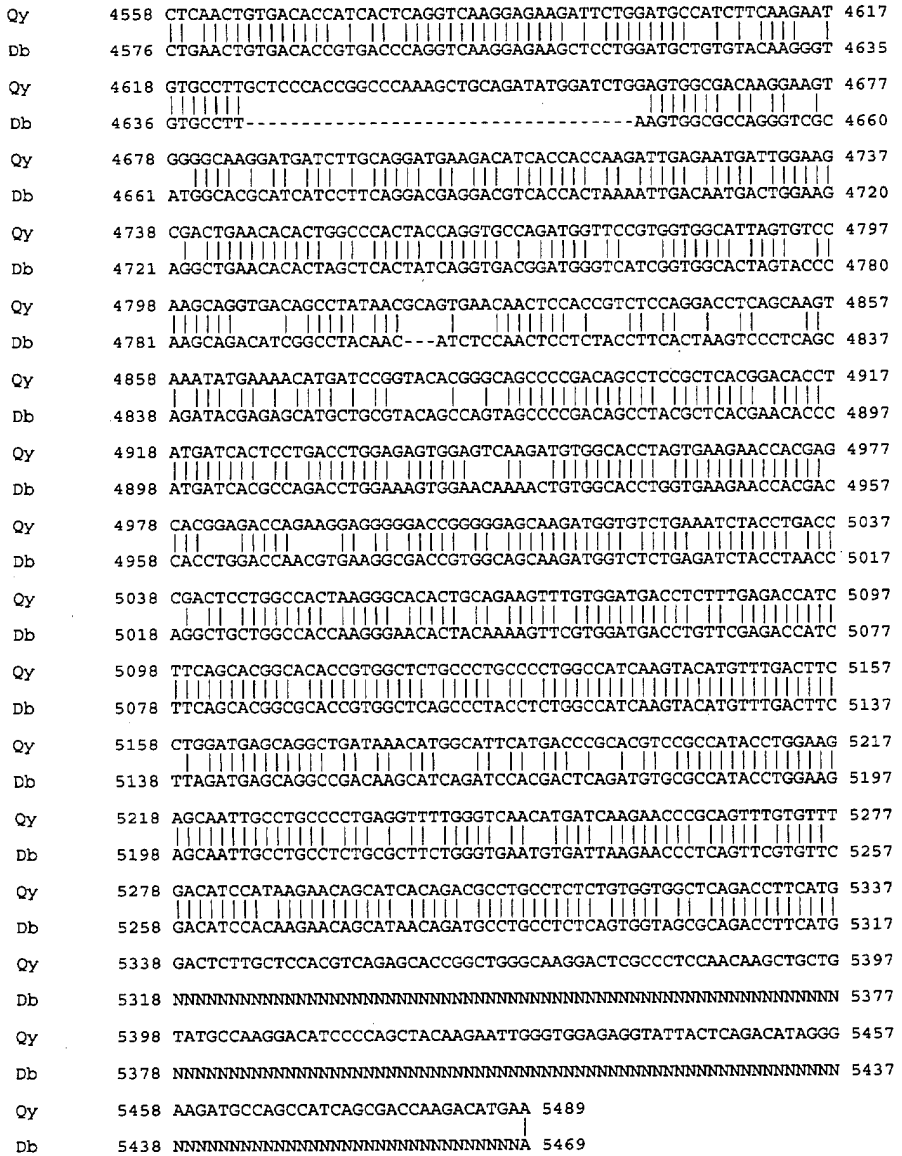

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RESULT 4
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LOCUS       AY420666                5520 bp    DNA     linear   GSS 12-DEC-2003
DEFINITION  Homo sapiens HCM7300 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY420666
VERSION     AY420666.1  GI:39776623
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 5520)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 5520)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
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            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence as made by sequencing genomic exons and ordering them
            based on alignment.
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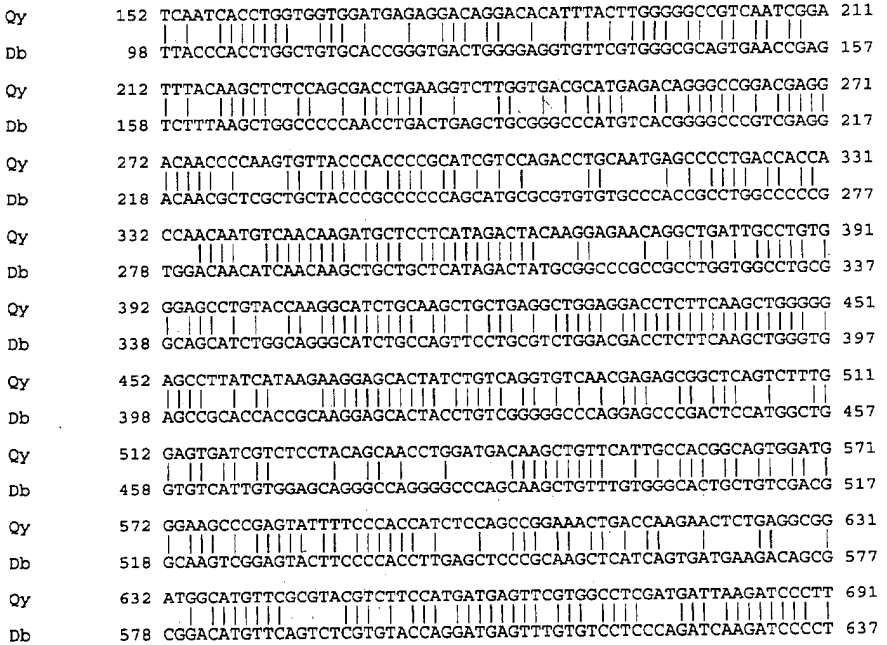

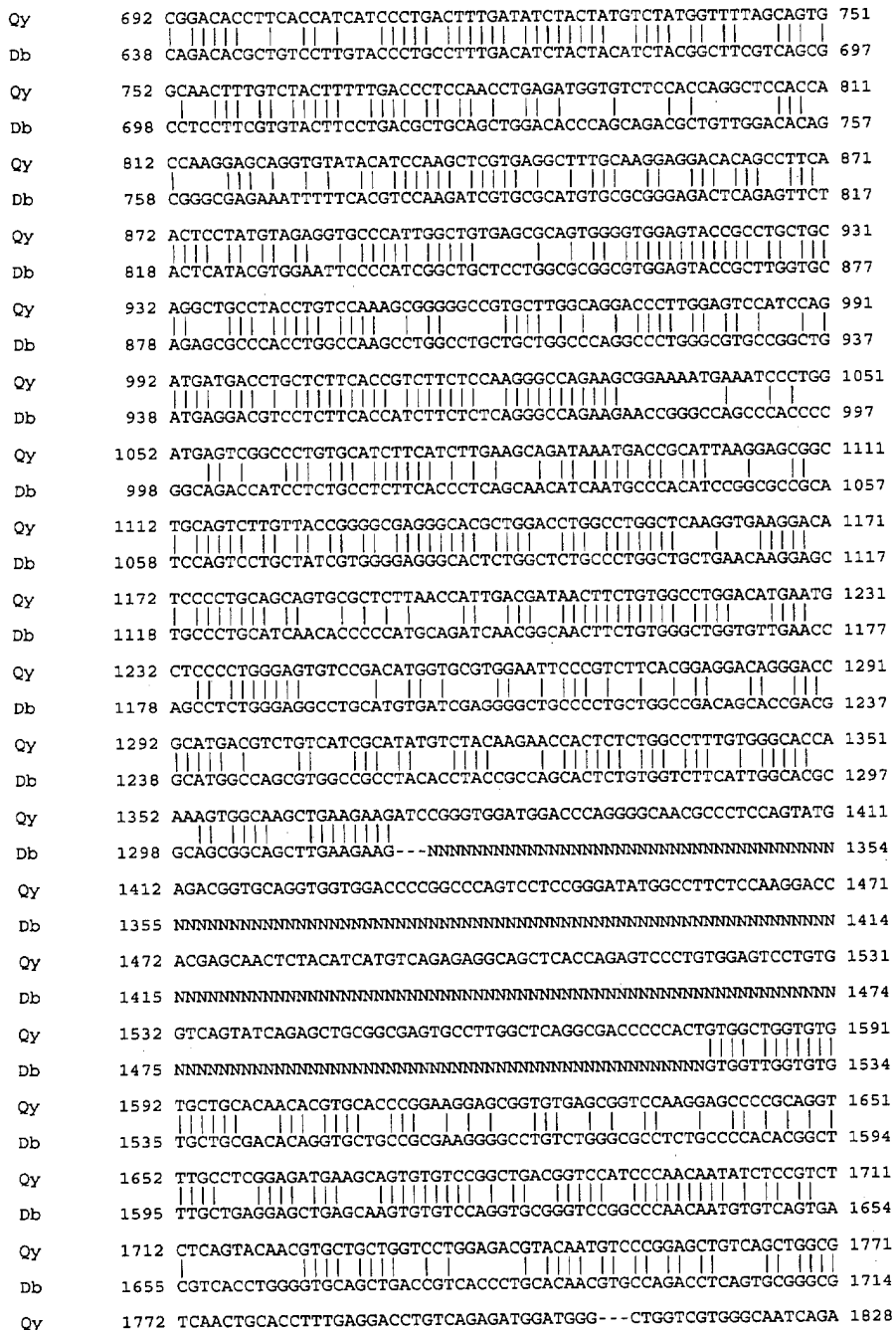
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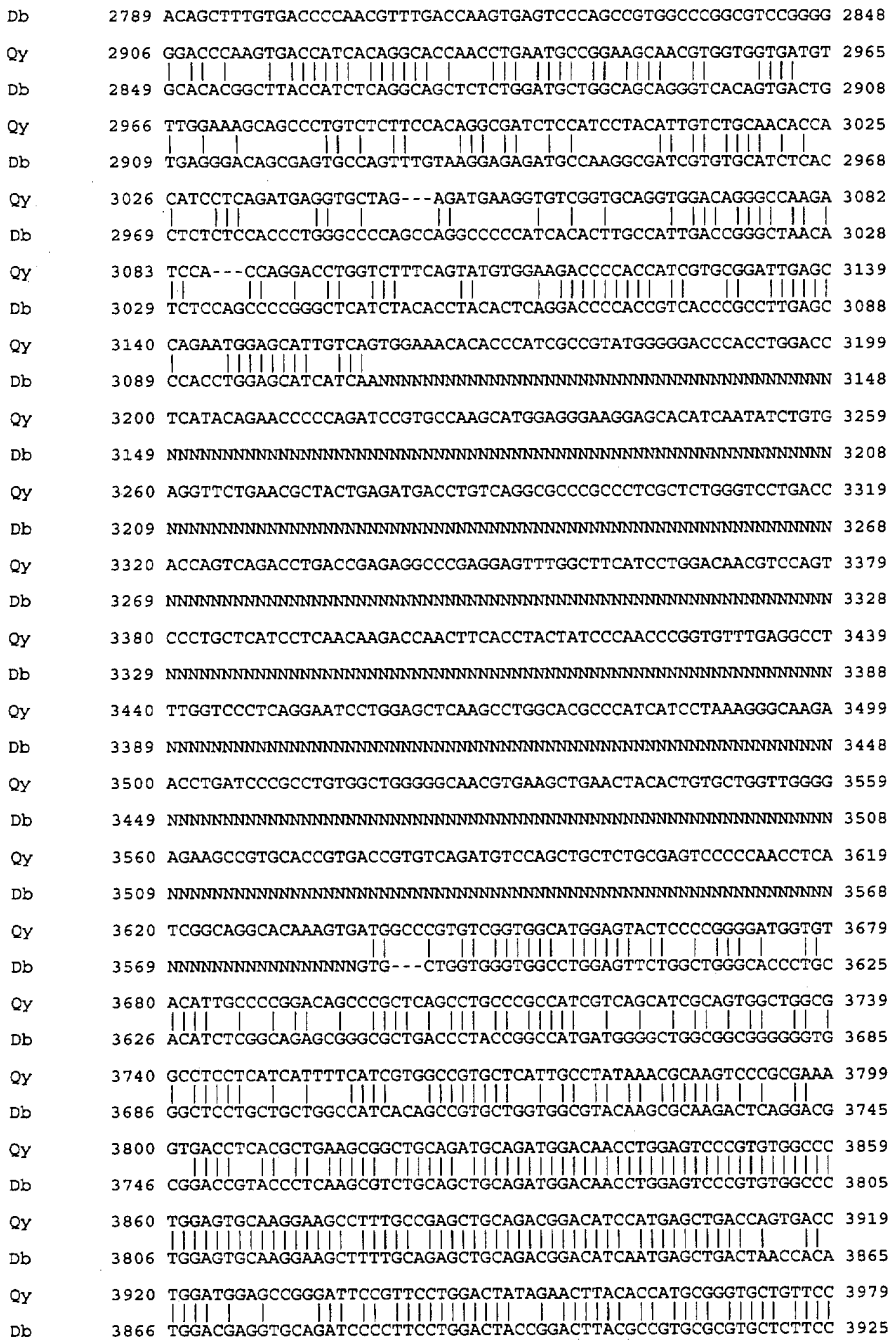

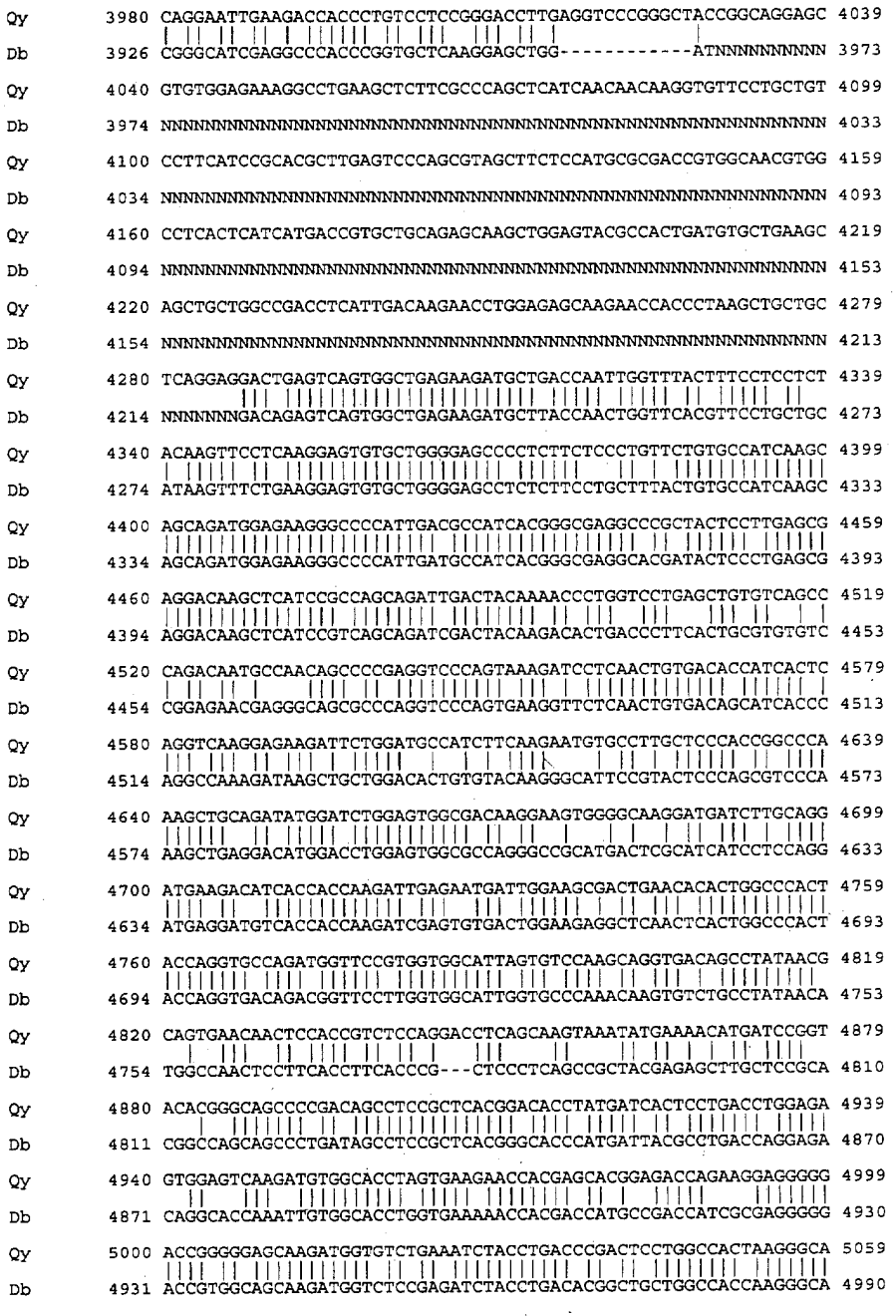

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VERSION     AY420668.1  GI:39776625
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SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
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  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
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            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
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  JOURNAL   Science 302 (5652), 1960-1963 (2003)
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REFERENCE   2  (bases 1 to 5447)
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  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
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COMMENT     This sequence as made by sequencing genomic exons and ordering them
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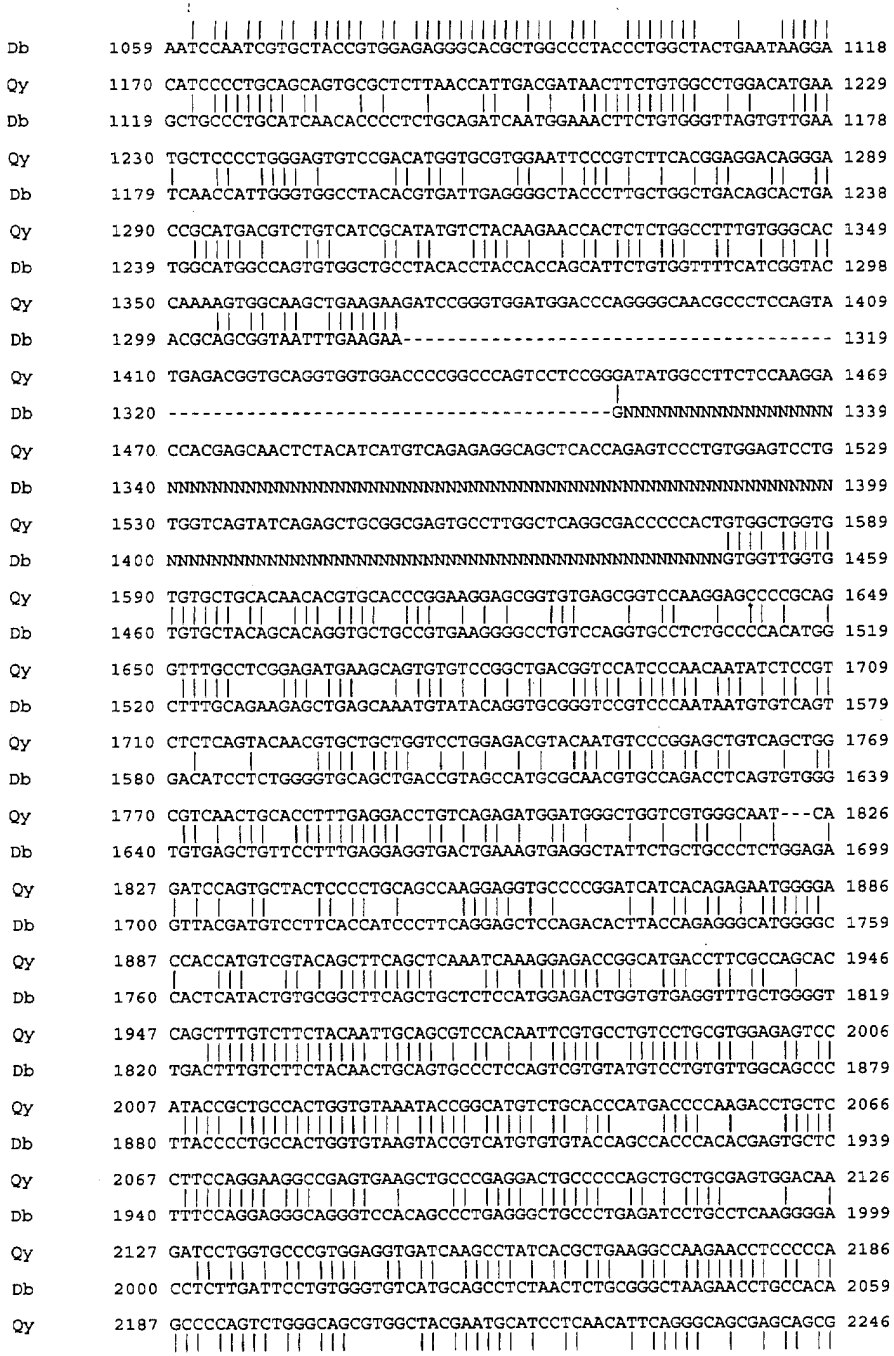

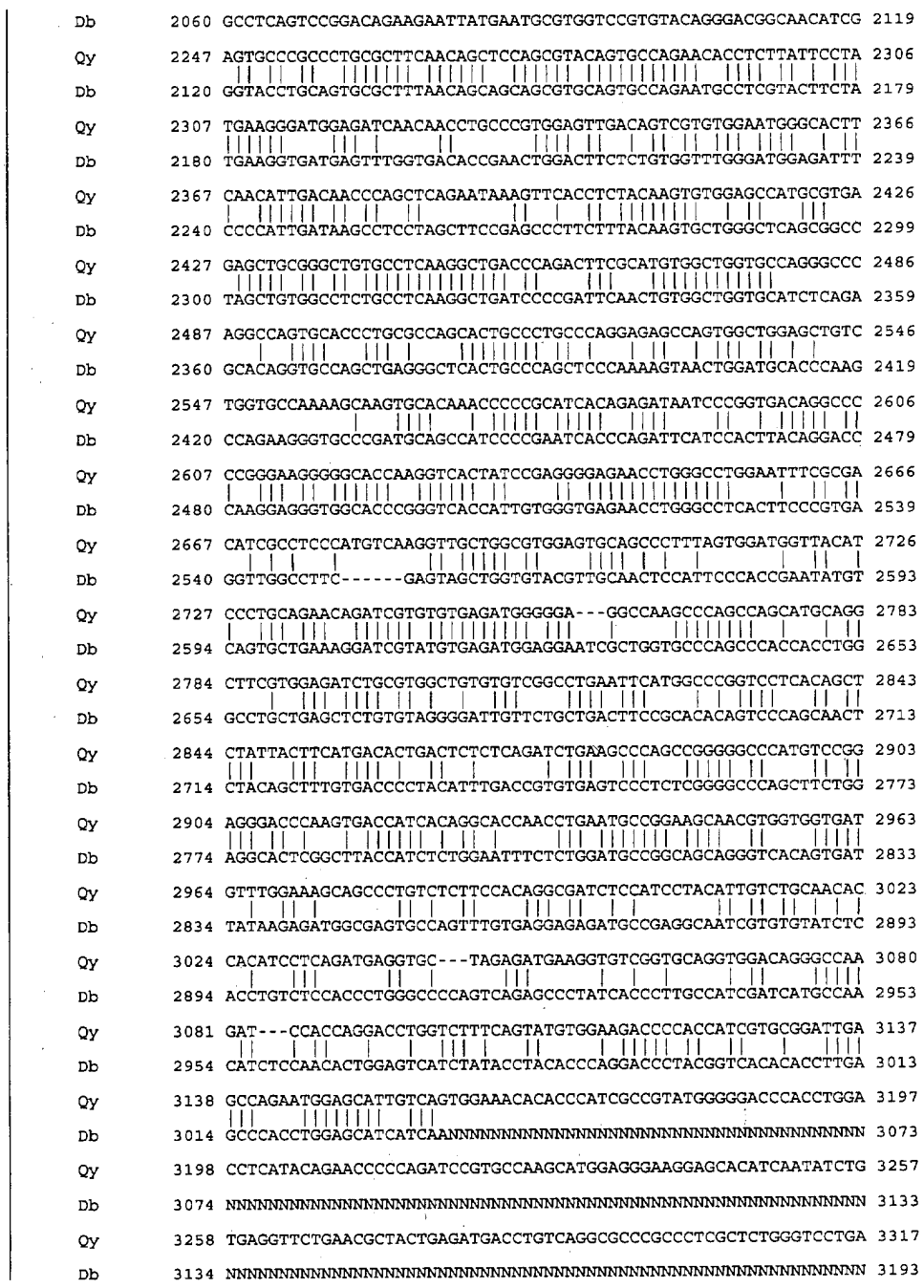

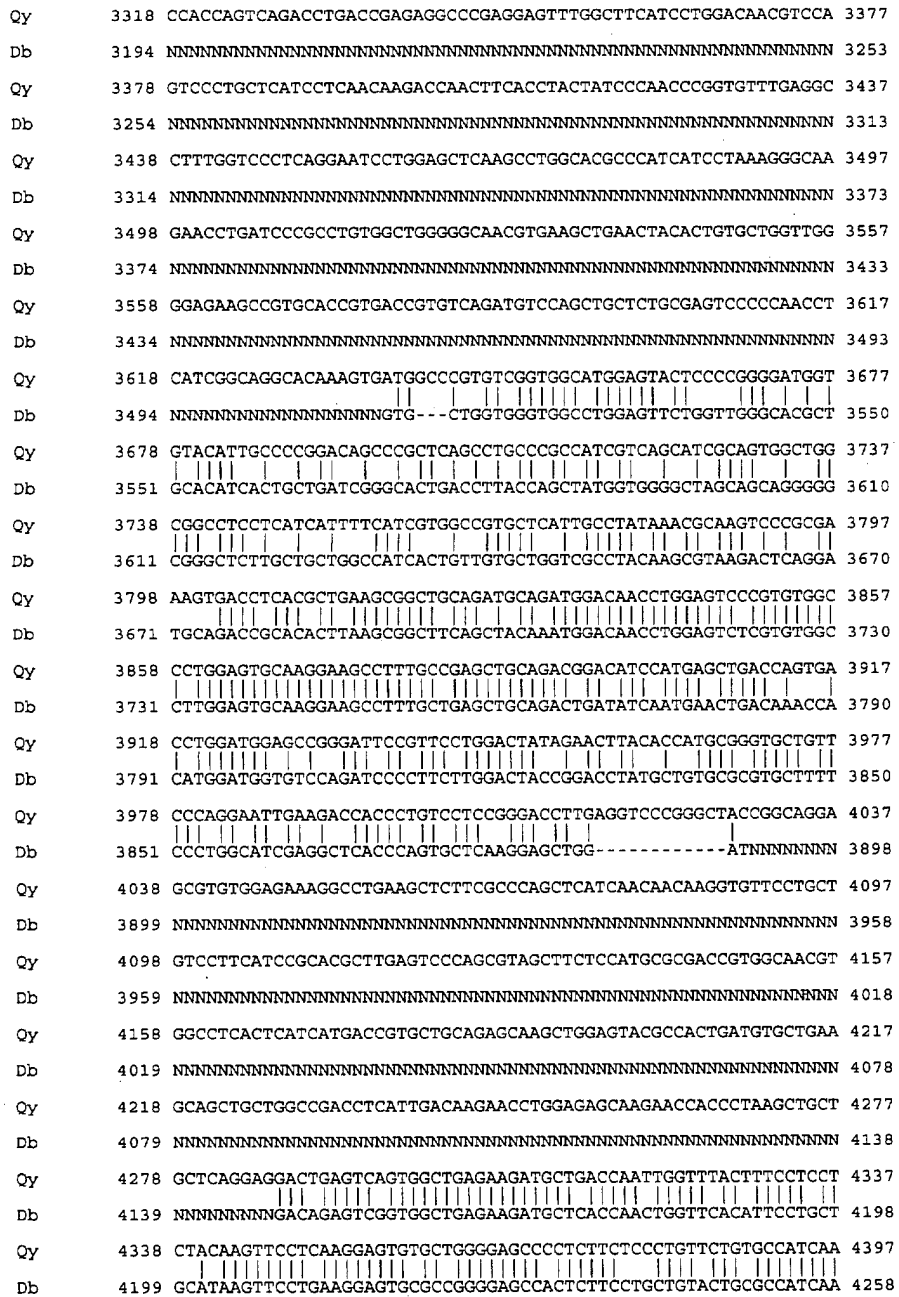

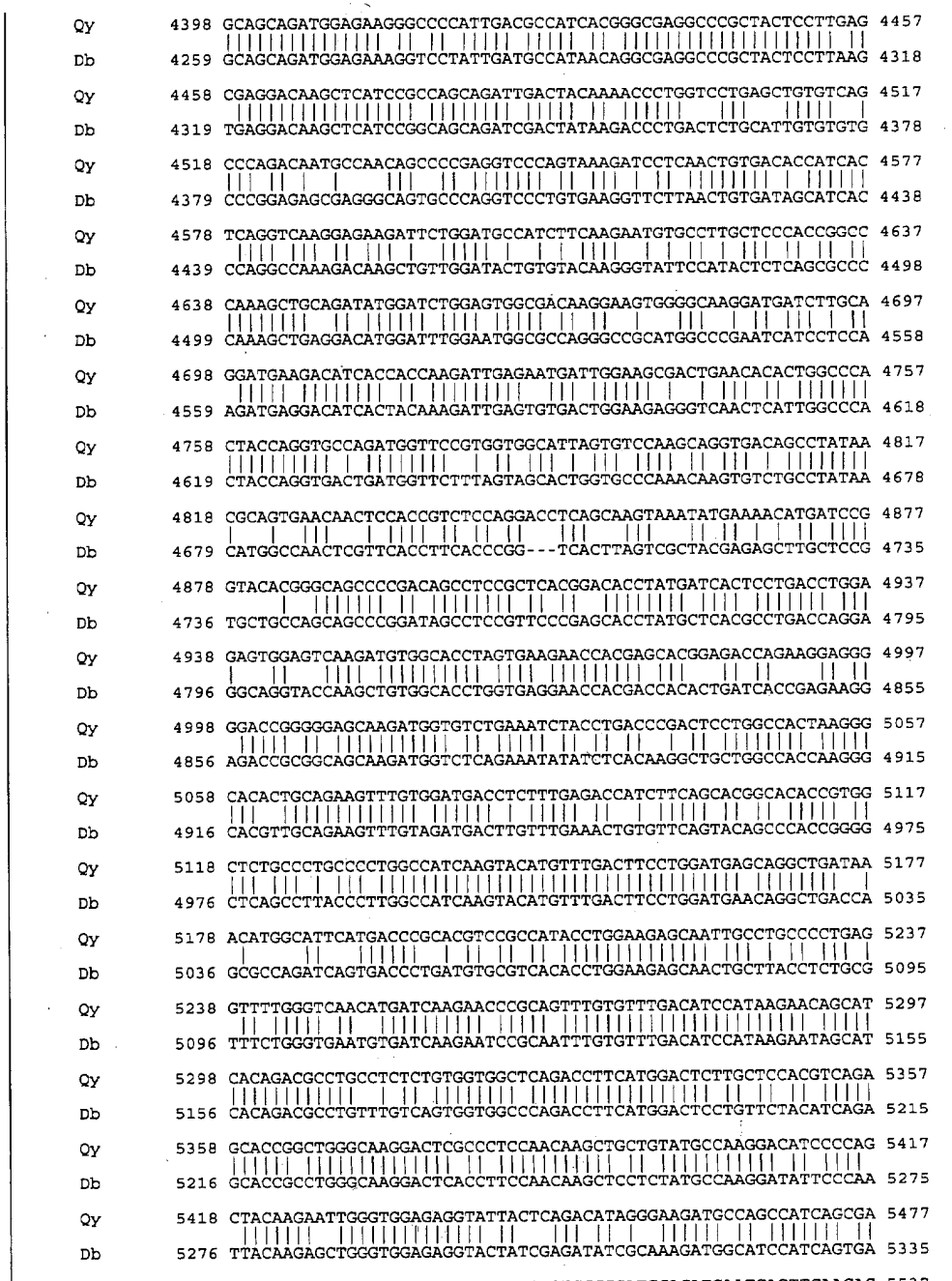

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VERSION     AY420667.1  GI:39776624
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REFERENCE   1  (bases 1 to 5520)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
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            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
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REFERENCE   2  (bases 1 to 5520)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
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  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence as made by sequencing genomic exons and ordering them
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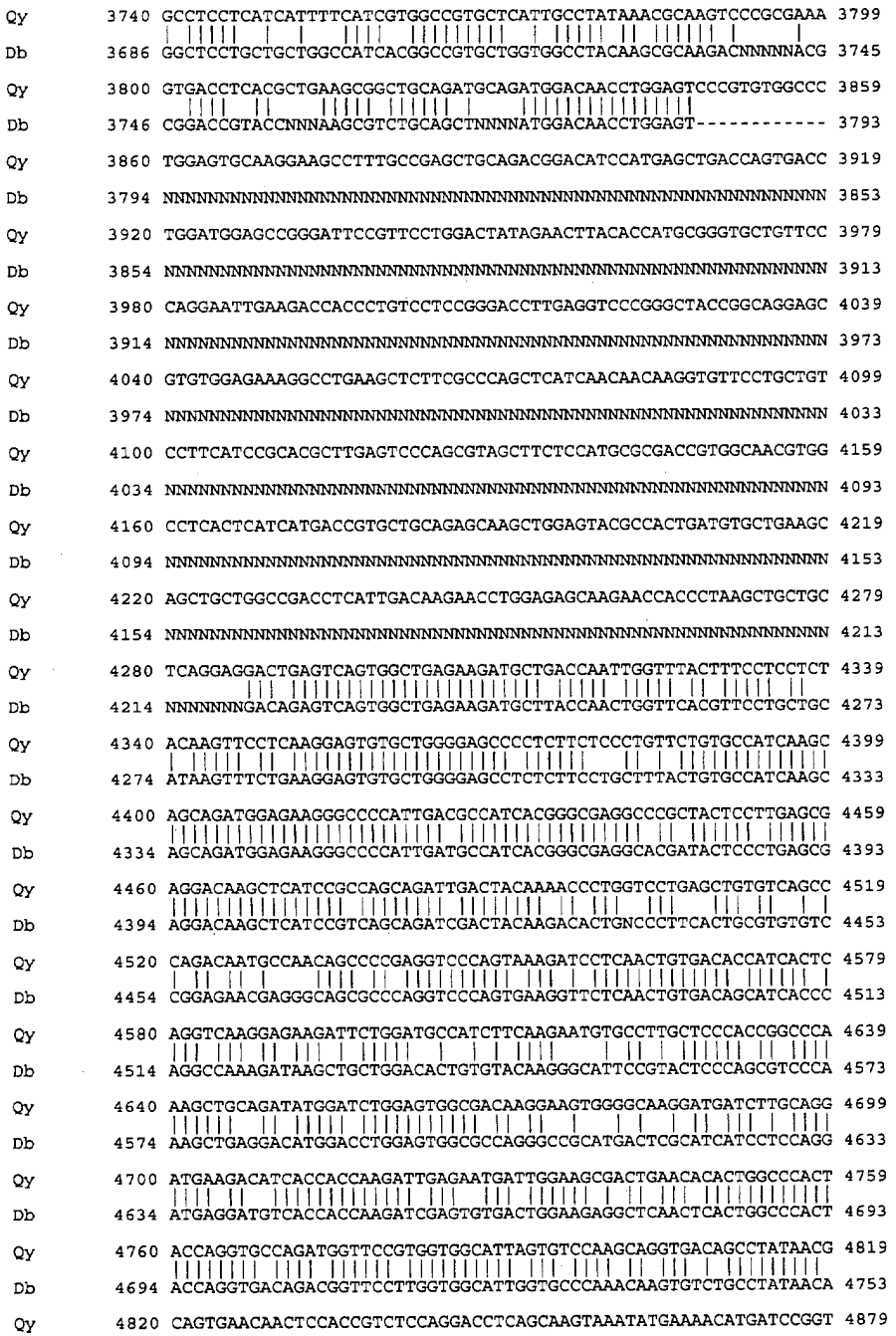

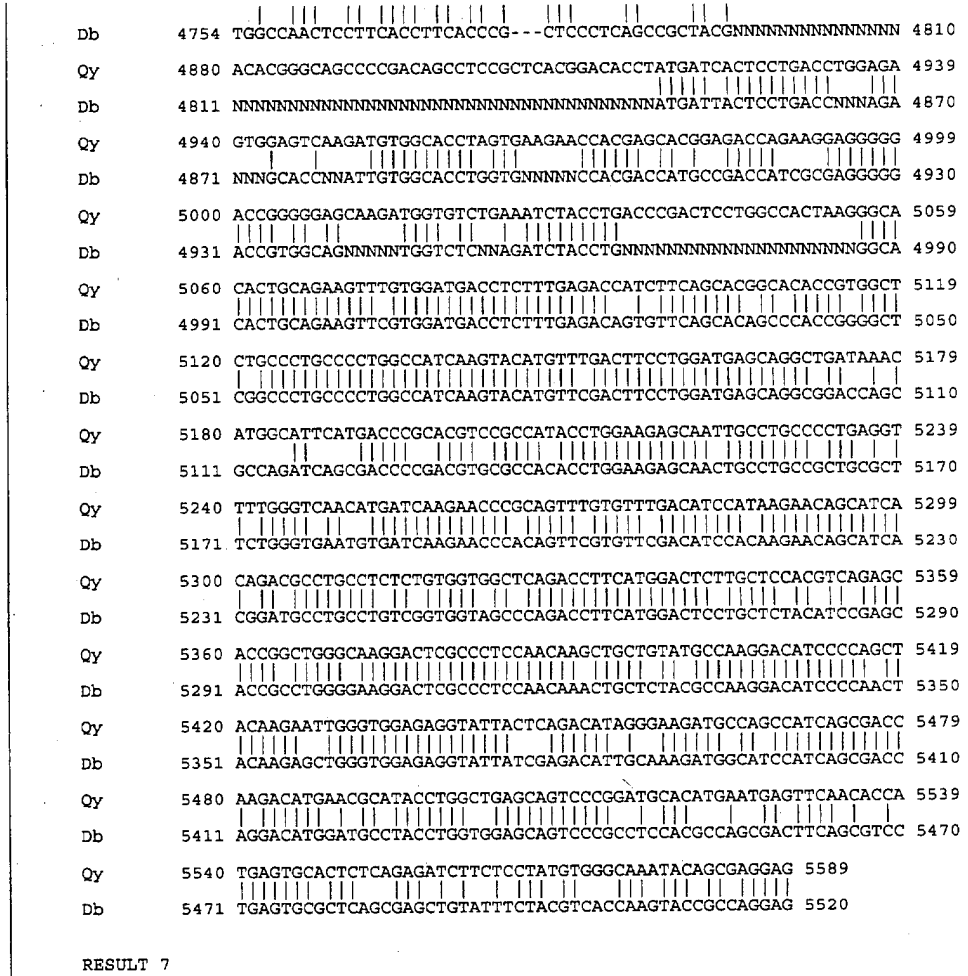

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AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302

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REFERENCE   2  (bases 1 to 5341)
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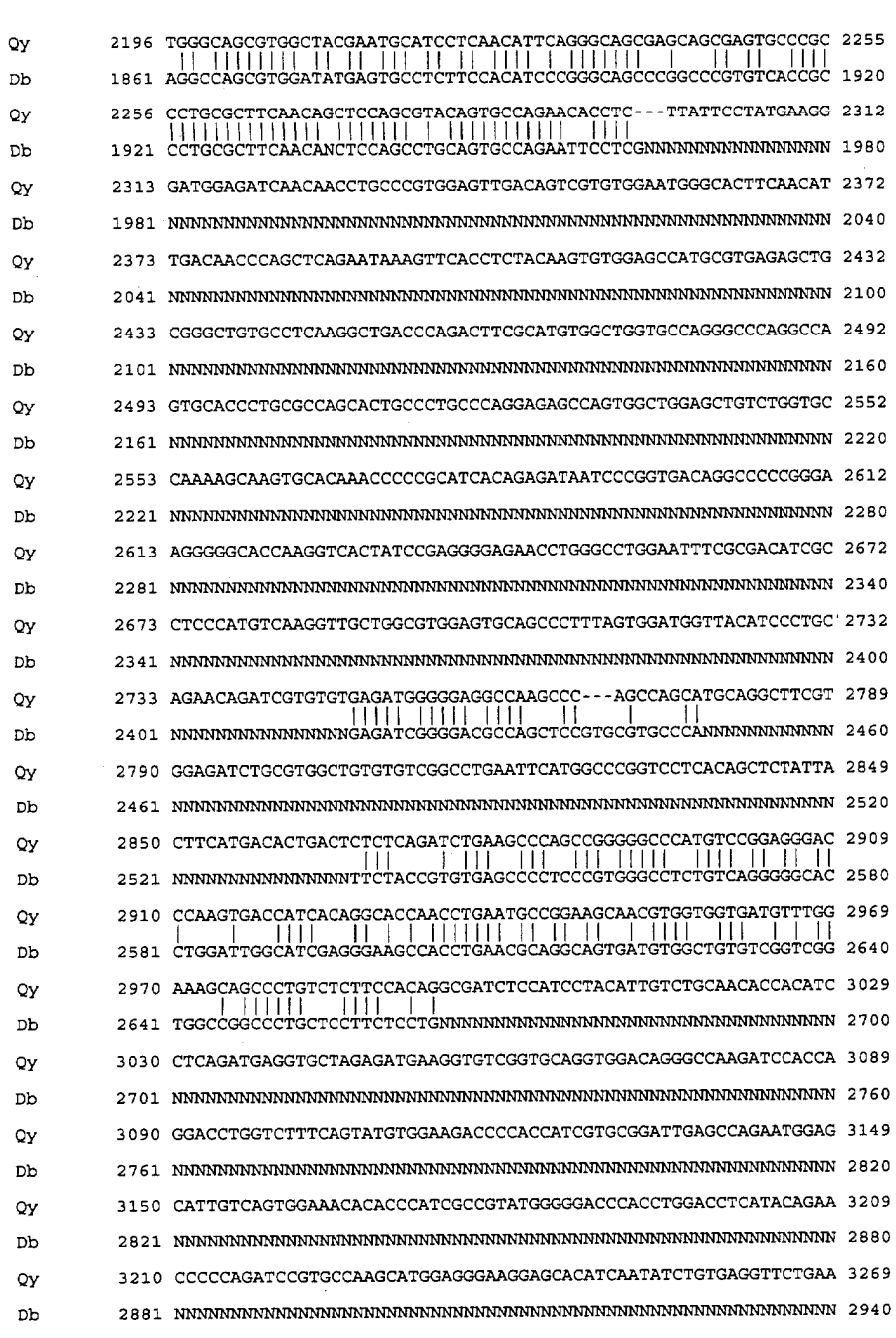

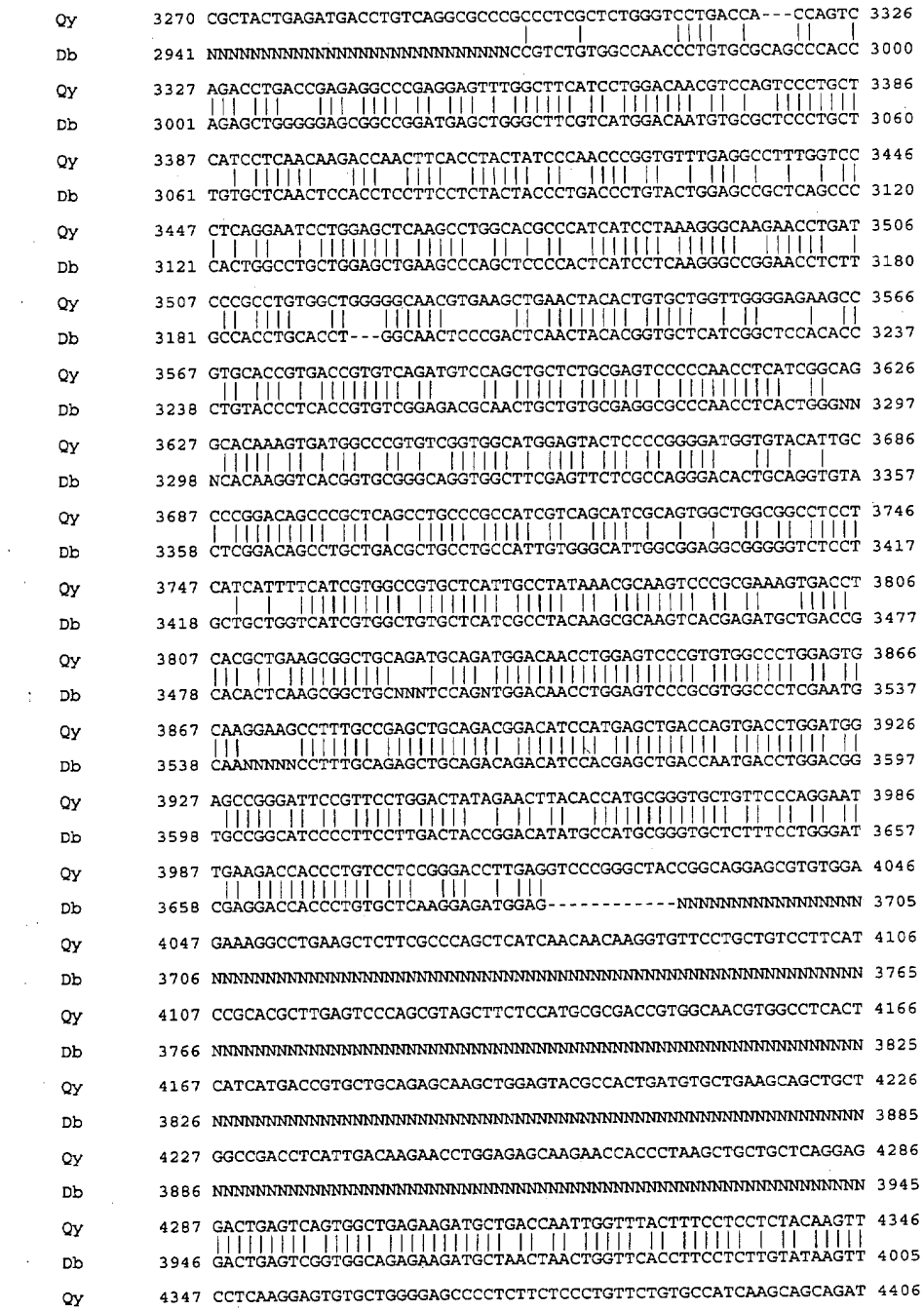

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Qy       5667 CATGAGCTTAGACAGCTGA 5685
Db       5323 GATGGCCCTGAGCAGCTGA 5341
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RESULT 8
AK049319
LOCUS AK049319 3355 bp mRNA linear HTC 20-SEP-2003
DEFINITION Mus musculus ES cells cDNA, RIKEN full-length enriched library, clone:C330023B09 product:PLEXIN 3 homolog [Mus musculus], full insert sequence.
ACCESSION AK049319
VERSION AK049319.1 GI:26340035
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 3355)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,

```
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
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            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.go.jp/
            URL:http://fantom.gsc.riken.go.jp/.
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                      /db_xref="MGI:2416574"
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                      /clone="C330023B09"
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ORIGIN

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Qy       3458 TGGAGCTCAAGCCTGGCACGCCCATCATCCTAAAGGGCAAGAACCTGATCCCGCCTGTGG 3517
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Db             1 TAGATGTCAAACCTGGTTCACATGTTGTATTGAAGGGCAAGAACCTGATCCCTGCTGCAG 60

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Qy       3758 TCGTGGCCGTGCTCATTGCCTATAAACGCAAGTCCCGCGAAAGTGACCTCACGCTGAAGC 3817
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Qy       3878 TTGCCGAGCTGCAGACGGACATCCATGAGCTGACCAGTGACCTGGATGGAGCCGGGATTC 3937
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Qy      4838 TCTCCAGGACCTCAGCAAGTAAATATGAAAACATGATCCGGTACACGGGCAGCCCCGACA 4897

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Db      2083 TCTACTTCTATGTCACCAAGTACCGTCAGGAGATCCTCACCTCGCTGGACCGAGATGCCT 2142

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Qy      5678 ACAGCTGA 5685

Db      2203 GCAGCTGA 2210
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RESULT 9
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DEFINITION  AGENCOURT_14542448 NIA Human H1 Embryonic Stem Cell cDNA Library
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ACCESSION   CD653539
VERSION     CD653539.1  GI:31892045
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 838)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Irene Ginis and Mahendra Rao, NIA
             cDNA Library Preparation: Yulan Piao and Minoru Ko
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC c            lone distribution information
            can be found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
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FEATURES             Location/Qualifiers
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                     cell line .  Undifferentiated human ES cell line WA01/H1
                     was obtained from WiCell Research Institute, Inc.,
                     Madison, Wi, cultured according to their instructions, on
                     MEF feeders. They formed round colonies with defined edges
                     and were positive for alkaline phosphatase, SSEA-4, OCT3,
                     OCT4, REX1, UTF, TERT, SOX2, CX43 and CX45.  They are
                     negative for GATA2, GATA4, PDX1, NCAM, MSX1, FLT3, SSEA-1,
                     TUBB3, NES, GFAP, and EOMES. When confluent (18-10 days
                     after plating), the ES cells from 4 X 6cm dishes were
                     treated with 1 mg/ml collagenase, type IV
                     (Invitrogen/GIBCO) for 5-10 min and gently scraped off
                     with 5 ml pipette.  RNA was purified with TRIzol Reagent
                     from Invitrogen. Protocol ref:  Genome Res. 11: 1553-1558
                     (2001). [PMID:11544199]) Double-stranded cDNAs were
                     synthesized with an Oligo(dT) primer [Invitrogen:
                     5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTTT-3'] from
                     3.4g of total RNA, treated with T4 DNA polymerase, and
                     purified by ethanol-precipitation. The cDNAs were ligated
                     to Lone-linker LL-Sal4, purified by phenol/chloroform
                     extraction, and separated from free linkers by
                     Centricon-100 column.  Then, the cDNAs were amplified by
                     long-range high fidelity PCR using Ex Taq polymerase
                     (Takara) with a primer Sal4-S for 25 cycles.  The products
                     were purified by phenol/chloroform extraction and
                     Centricon-100 column. The cDNAs were digested with SalI
                     and NotI enzymes and cloned into SalI/NotI site of
                     pCMV-SPORT6 plasmid vector. The average insert size is
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about 3.6kb."
ORIGIN

Query Match 13.1%; Score 743.8; DB 14; Length 838;
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Matches 770; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

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Qy       3999 TGTCCTCCGGGACCTTGAGGTCCCGGGCTACCGGCAGGAGCGTGTGGAGAAAGGCCTGAA 4058
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Db        252 TGTCCTCCGGGACCTTGAGGTCCCGGGCTACCGGCAGGAGCGTGTGGAGAAAGGCCTGAA 311

Qy       4059 GCTCTTCGCCCAGCTCATCAACAACAAGGTGTTCCTGCTGTCCTTCATCCGCACGCTTGA 4118
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 GCTCTTCGCCCAGCTCATCAACAACAAGGTGTTCCTGCTGTCCTTCATCCGCACGCTTGA 371

Qy       4119 GTCCCAGCGTAGCTTCTCCATGCGCGACCGTGGCAACGTGGCCTCACTCATCATGACCGT 4178
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        372 GTCCCAGCGTAGCTTCTCCATGCGCGACCGTGGCAACGTGGCCTCACTCATCATGACCGT 431

Qy       4179 GCTGCAGAGCAAGCTGGAGTACGCCACTGATGTGCTGAAGCAGCTGCTGGCCGACCTCAT 4238
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        432 GCTGCAGAGCAAGCTGGAGTACGCCACTGATGTGCTGAAGCAGCTGCTGGCCGACCTCAT 491

Qy       4239 TGACAAGAACCTGGAGAGCAAGAACCACCCTAAGCTGCTGCTCAGGAGGACTGAGTCAGT 4298
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        492 TGACAAGAACCTGGAGAGCAAGAACCACCCTAAGCTGCTGCTCAGGAGGACTGAGTCAGT 551

Qy       4299 GGCTGAGAAGATGCTGACCAATTGGTTTACTTTCCTCCTCTACAAGTTCCTCAAGGAGTG 4358
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        552 GGCTGAGAAGATGCTGACCAATTGGTTTACTTTCCTCCTCTACAAGTTCCTCAAGGAGTG 611

Qy       4359 TGCTGGGGAGCCCCTCTTCTCCCTGTTCTGTGCCATCAAGCAGCAGATGGAGAAGGGCCC 4418
             |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        612 TGCTGGGGAGCCCCTCTTCTCCCTGTTCTGTGCCATCNAGCAGCAGATGGAGAAGGGCCC 671

Qy       4419 CATTGACGCCATCACGGGCGAGGCCCGCTACTCCTTGAGCGAGGACAAGCTCATCCGCCA 4478
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        672 CATTGACGCCATCACGGGCGAAGCCCGCTACTCCTTGAGCGANNGACAGCTCATCCGCCA 731

Qy       4479 GCAGATTGACTACAAAACCCTGGTCCTGAGCTGTGTCAGCCCAGACAATGCCAACAGCCC 4538
             |||||||       |||||||||  |||||||||||||||||||||||    |  |    ||
Db        732 GCAGATTTGACTACAAACCCTGGGTCTGAGCTGTGTCAGCCCAGACATGCCACA---GCC 788

Qy       4539 CGAGGTCCCAGTAAAGATC 4557
             ||||||||  ||||  |   ||
Db        789 CGAGGTCCNAGTAGATCTC 807
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RESULT 10
BM547417
LOCUS BM547417 1059 bp mRNA linear EST 20-FEB-2002
DEFINITION AGENCOURT_6507625 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5724374 5', mRNA sequence.
ACCESSION BM547417
VERSION BM547417.1 GI:18781167
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1059)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM12713 row: i column: 15
High quality sequence stop: 713.
FEATURES Location/Qualifiers
source 1. .1059
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5724374"
/lab_host="DH10B"
/clone_lib="NIH_MGC_125"
/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6; Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."
ORIGIN

Query Match 11.6%; Score 658.8; DB 12; Length 1059;
Best Local Similarity 81.4%; Pred. No. 5.2e-128;
Matches 788; Conservative 0; Mismatches 177; Indels 3; Gaps 2;

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Qy       3762 GGCCGTGCTCATTGCCTATAAACGCAAGTCCCGCGAAAGTGACCTCACGCTGAAGCGGCT 3821
             ||  || |||||||||| || |||||||| || ||| ||||||||| || ||||||||
Db         11 GGATGTCCTCATTGCCTACAAGCGCAAGTCTCGAGAAAATGACCTCACTCTCAAGCGGCT 70

Qy       3822 GCAGATGCAGATGGACAACCTGGAGTCCCGTGTGGCCCTGGAGTGCAAGGAAGCCTTTGC 3881
             ||| |||||||||||||| |||||||||||||||||| ||||||||||||||| |||||
Db         71 GCAAATGCAGATGGACAATCTGGAGTCCCGTGTGGCCTTGGAGTGCAAGGAAGCTTTTGC 130

Qy       3882 CGAGCTGCAGACGGACATCCATGAGCTGACCAGTGACCTGGATGGAGCCGGGATTCCGTT 3941
              |||||  |||||||| ||| |||||  |||||||||||||||||  |  | || || || |
Db        131 TGAGCTCCAGACGGATATCAATGAGTTGACCAGTGACCTGGACCGCTCAGGAATCCCTTA 190

Qy       3942 CCTGGACTATAGAACTTACACCATGCGGGTGCTGTTCCCAGGAATTGAAGACCACCCTGT 4001
             |||||||||| | || ||| | ||||| || |||||||| || || || |||||||| ||
Db        191 CCTGGACTATCGTACCTACGCTATGCGAGTCCTGTTCCCGGGCATCGAGGACCACCCCGT 250

Qy       4002 CCTCCGGGACCTTGAGGTCCCGGGCTACCGGCAGGAGCGTGTGGAGAAAGGCCTGAAGCT 4061
             ||| ||||| || ||||| |  ||  || |||||  ||| |||||||| | |||||||||
Db        251 CCTGCGGGAGCTGGAGGTACAAGGAAACGGGCAGCAGCACGTGGAGAAGGCCCTGAAGCT 310

Qy       4062 CTTCGCCCAGCTCATCAACAACAAGGTGTTCCTGCTGTCCTTCATCCGCACGCTTGAGTC 4121
             ||| |||||||||||||||||||||||||||||||||||||||||||||| |||
Db        311 CTTTGCCCAGCTCATCAACAACAAGGTGTTCCTGCTGACCTTCATCCGCACCCTGGAGCT 370

Qy       4122 CCAGCGTAGCTTCTCCATGCGCGACCGTGGCAACGTGGCCTCACTCATCATGACCGTGCT 4181
             |||||  || |||||||||||||||| |||||||||| || ||||||||||||  ||
Db        371 GCAGCGCAGTTTCTCCATGCGCGACCGGGGCAACGTGGCTTCGCTCATCATGACCGGCCT 430

Qy       4182 GCAGAGCAAGCTGGAGTACGCCACTGATGTGCTGAAGCAGCTGCTGGCCGACCTCATTGA 4241
             ||||  ||   ||||| || |||||||||| || |||||||||  | |||||||| ||
Db        431 GCAGGGCCGCCTGGAATATGCCACTGATGTCCTCAAGCAGCTGCTCTCTGACCTCATCGA 490
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Qy       4242 CAAGAACCTGGAGAGCAAGAACCACCCTAAGCTGCTGCTCAGGAGGACTGAGTCAGTGGC 4301
Db        491 TAAGAACCTGGAGAACAAGAACCACCCCAAGCTGCTACTCCGGAGGACAGAGTCTGTGGC 550

Qy       4302 TGAGAAGATGCTGACCAATTGGTTTACTTTCCTCCTCTACAAGTTCCTCAAGGAGTGTGC 4361
Db        551 TGAAAAGATGCTGACCAATTGGTTCGCCTTCCTCCTGCACAAGTTCCTAAAGGAGTGCGC 610

Qy       4362 TGGGGAGCCCCTCTTCTCCCTGTTCTGTGCCATCAAGCAGCAGATGGAGAAGGGCCCCAT 4421
Db        611 AGGGGAGCCACTCTTCATGCTATACTGTGCCATCAAGCAGCAGATGGAGAAGGGCCCCAT 670

Qy       4422 TGACGCCATCACGGGCGAGGCCCGCTACTCCTTGAGCGAGGACAAGCTCATCCGCCAGCA 4481
Db        671 TGATGCCATCACGGGCGAGGCCCGCTACTCCCTGAGCGAGGACAAGCTCATCCGGCAGCA 730

Qy       4482 GATTGACTACAAAACCCTGGTCCTGAGCTGTGTCAGCCCAGACAATGCCAACAGCCCCGA 4541
Db        731 GATCGAGTACAAGACCCTGATCCTGAACTGCGTCAACCCTGACAACGAGAACAGTCCAGA 790

Qy       4542 GGTCCCAGTAAAGATCCTCAACTGTGACACCATCACTCAGGTCAAGGAGAAGATTCTGGA 4601
Db        791 GATCCCCAGTGAAGTGTTAAACTGTGACACCATCCCCCAGGTCAAGGAGAAGATTCTTGA 850

Qy       4602 TGCCATCTTCAAGAATGT-GCCTTGCTCCCACCGGCCCAAAGCTGCAGATATGGATCTGG 4660
Db        851 TGCCGGGGATAAGAATGTGGCCCTATTCCCAGCGGCCGAGGGCAGTGGACATGGACTTGG 910

Qy       4661 AGTGGCGACAAGG--AAGTGGGGCAAGGATGATCTTGCAGGATGAAGACATCACCACCAA 4718
Db        911 GATGGCGGCAAGGCCCGGATCGCCCGGGTCCGGGCTTGCAGATGAGGACATCCCCCCCCA 970

Qy       4719 GATTGAGA 4726
Db        971 GATTGAGA 978
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RESULT 11
AL529477
LOCUS       AL529477               1201 bp    mRNA    linear   EST 23-MAY-2003
DEFINITION  AL529477 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
            cDNA clone CS0DD006YE12 5-PRIME, mRNA sequence.
ACCESSION   AL529477
VERSION     AL529477.2  GI:31067320
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 13, 2001 this sequence version replaced gi:12792970.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            792.r For more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DD006BC06QP1&cluster=792.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DD006BC06QP1.
FEATURES             Location/Qualifiers
     source          1..1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DD006YE12"
                     /tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
                     /clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
```

```
  Query Match             11.4%;  Score 650.6;  DB 9;  Length 1201;
  Best Local Similarity   82.5%;  Pred. No. 3e-126;
  Matches  780;  Conservative    1;  Mismatches  160;  Indels    4;  Gaps    3;

Qy       3773 TTGCCTATAAACGCAAGTCCCGCGAAAGTGACCTCACGCTGAAGCGGCTGCAGATGCAGA 3832
Db         63 TTGCCTACAAGCGCAAGTCTCGAGAAAATGACCTCACTCTCAAGCGGCTGCAAATGCAGA 122

Qy       3833 TGGACAACCTGGAGTCCCGTGTGGCCCTGGAGTGCAAGGAAGCCTTTGCCGAGCTGCAGA 3892
Db        123 TGGACAATCTGGAGTCCCGTGTGGCCTTGGAGTGCAAGGAAGCTTTTGCTGAGCTCCAGA 182

Qy       3893 CGGACATCCATGAGCTGACCAGTGACCTGGATGGAGCCGGGATTCCGTTCCTGGACTATA 3952
Db        183 CGGATATCAATGAGTTGACCAGTGACCTGGACCGCTCAGGAATCCCTTACCTGGACTATC 242

Qy       3953 GAACTTACACCATGCGGGTGCTGTTCCCAGGAATTGAAGACCACCCTGTCCTCCGGGACC 4012
Db        243 GTACCTACGCTATGCGAGTCCTGTTCCCGGGCATCGAGGACCACCCCGTCCTGCGGGAGC 302

Qy       4013 TTGAGGTCCCGGGCTACCGGCAGGAGCGTGTGGAGAAAGGCCTGAAGCTCTTCGCCCAGC 4072
Db        303 TGGAGGTACAAGGAAACGGGCAGCAGCACGTGGAGAAGGCCCTGAAGCTCTTTGCCCAGC 362

Qy       4073 TCATCAACAACAAGGTGTTCCTGCTGTCCTTCATCCGCACGCTTGAGTCCCAGCGTAGCT 4132
Db        363 TCATCAACAACAAGGTGTTCCTGCTGACCTTCATCCGCACCCTGGAGCTGCAGCGCAGTT 422

Qy       4133 TCTCCATGCGCGACCGTGGCAACGTGGCCTCACTCATCATGACCGTGCTGCAGAGCAAGC 4192
Db        423 TCTCCATGCGCGACCGGGGCAACGTGGCTTCGCTCATCATGACCGGCCTGCAGGGC-SCC 481

Qy       4193 TGGAGTACGCCACTGATGTGCTGAAGCAGCTGCTGGCCGACCTCATTGACAAGAACCTGG 4252
Db        482 TGGAATATGCCACTGATGTCCTCAAGCAGCTGCTCTCTGACCTCATCGATAAGAACCTGG 541

Qy       4253 AGAGCAAGAACCACCCTAAGCTGCTGCTCAGGAGGACTGAGTCAGTGGCTGAGAAGATGC 4312
Db        542 AGAACAAGAACCACCCCAAGCTGCTACTCCGGAGGACAGAGTCTGTGGCTGAAAAGATGC 601

Qy       4313 TGACCAATTGGTTTACTTTCCTCCTCTACAAGTTCCTCAAGGAGTGTGCTGGGGAGCCCC 4372
Db        602 TGACCAATTGGTTCGCCTTCCTCCTGCACAAGTTCCTAAAGGAGTGCGCAGGGGAGCCAC 661

Qy       4373 TCTTCTCCCTGTTCTGTGCCATCAAGCAGCAGATGGAGAAGGGCCCCCATTGACGCCATCA 4432
Db        662 TCTTCATGCTATACTGTGCCATCAAGCAGCAGATGGAGAAGGGCCCCCATTGATGCCATCA 721

Qy       4433 CGGGCGAGGCCCGCTACTCCTTGAGCGAGGACAAGCTCATCCGCCAGCAGATTGACTACA 4492
Db        722 CGGGCGAGG-CCGCTACTCCCTGAGCGAGGACAAGCTCATCCGGCAGCAGATCGAGTACA 780

Qy       4493 AAACCCTGGTCCTGAGCTGTGTCAGCCCAGACAATGCCAACAGCCCCGAGGTCCCAGTAA 4552
Db        781 AGACCCTGATCCTGAACTGCGTCAACCCTGACAACGAGAACAGTCCAGAGATCCCAGTGA 840

Qy       4553 AGATCCTCAACTGTGACACCATCACTCAGGTCAAGGAGAAGATTCTGGATGCCATCTTCA 4612
Db        841 AGGTGTTAAACTGTGACACCATCACACAGGTCAAGGAGAAGATTCTTGATGCCGTGTATA 900

Qy       4613 AGAATGTGCCTTGCTCCCACCGGCCCAAAGCTGCAGATATGGATCTGGAGTGGCGACAAG 4672
Db        901 AGAATGTGCCCTATTCCCAGCGGCCGAGGGCAGTGGACATGGACTTGGAGTGGCGCAAGG 960

Qy       4673 GAAGTGGGGCAAGGATGATCTTGCAGGATGAAGACATCACCACCA 4717
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Db        961 CCGGATCGCCCGGGTCGTGCT--GCARATGAGGACATCACCACAA 1003


RESULT 12
CA316867
LOCUS       CA316867                745 bp    mRNA    linear   EST 09-JUL-2003
DEFINITION  UI-M-FW0-cbk-j-22-0-UI.r1 NIH_BMAP_FW0 Mus musculus cDNA clone
            IMAGE:6810839 5', mRNA sequence.
ACCESSION   CA316867
VERSION     CA316867.1  GI:24534991
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 745)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jim Lin, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
             This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
            Seq primer: pYX-5.
FEATURES             Location/Qualifiers
     source          1. .745
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6810839"
                     /tissue_type="whole brain"
                     /dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
                     /lab_host="DH10B (T1 phage resistant)"
                     /clone_lib="NIH_BMAP_FW0"
                     /note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
                     Site_2: Not I; The library was constructed according
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. Denatured RNA was size fractionated on a 1% agarose
                     gel. First strand cDNA synthesis was primed with oligo-dT
                     primer containing a Not I site. Double strand cDNA was
                     size selected according to mRNA size fraction, ligated
                     with EcoR I adaptor, digested with NotI and then cloned
                     directionally into pYX-Asc vector. The library tag
                     sequence located between the Not I site and the polyA tail
                     is AGCGAGACAG. This library was created for the University
                     Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
                     Developing Mouse Nervous System', supported by National
                     Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                     program coordinator."
ORIGIN

  Query Match           11.2%;  Score 638.4;  DB 14;  Length 745;
  Best Local Similarity   91.0%;  Pred. No. 8.7e-124;
  Matches  678;  Conservative    0;  Mismatches   67;  Indels    0;  Gaps    0;

Qy       3867 CAAGGAAGCCTTTGCCGAGCTGCAGACGGACATCCATGAGCTGACCAGTGACCTGGATGG 3926
              ||||||||| |||||||||||||||| || |||||||||| ||||||||||||||||||
Db          1 CAAGGAAGCTTTTGCCGAGCTGCAGACAGATATCCATGAGCTTACCAGTGACCTGGATGG 60

Qy       3927 AGCCGGGATTCCGTTCCTGGACTATAGAACTTACACCATGCGGGTGCTGTTCCCAGGAAT 3986
              ||| |||||||| || |||||||| ||||| || ||||||||||||||||||||| ||
Db         61 AGCTGGGATTCCCTTTCTGGACTACAGAACCTATACCATGCGGGTGCTGTTCCCAGGGAT 120

Qy       3987 TGAAGACCACCCTGTCCTCCGGGACCTTGAGGTCCCGGGCTACCGGCAGGAGCGTGTGGA 4046
              |||||||||||||||| || || |||||||||||||| ||||||||||||||||||||

Db        121 TGAAGACCACCCTGTGCTACGAGACCTTGAGGTCCCAGGCTACCGGCAGGAGCGTGTGGA 180

Qy       4047 GAAAGGCCTGAAGCTCTTCGCCCAGCTCATCAACAACAAGGTGTTCCTGCTGTCCTTCAT 4106
              |||||| || |||||||||||||||||||||||||||||||||||||||||| || |||||
Db        181 GAAAGGACTCAAGCTCTTCGCCCAGCTCATCAACAACAAGGTGTTCCTGCTCTCTTTCAT 240

Qy       4107 CCGCACGCTTGAGTCCCAGCGTAGCTTCTCCATGCGCGACCGTGGCAACGTGGCCTCACT 4166
              |||||| || ||||| ||||| || || |||||||||||||| || |||||||||||| ||
Db        241 CCGCACTCTGGAGTCTCAGCGCAGTTTTTCCATGCGCGACCGAGGTAACGTGGCCTCCCT 300

Qy       4167 CATCATGACCGTGCTGCAGAGCAAGCTGGAGTACGCCACTGATGTGCTGAAGCAGCTGCT 4226
              ||||||||| || || |||||||||||| ||||| |||||||| |||||||||||||| ||
Db        301 CATCATGACGGTACTTCAGAGCAAGCTAGAGTATGCCACTGACGTGCTGAAGCAGCTACT 360

Qy       4227 GGCCGACCTCATTGACAAGAACCTGGAGAGCAAGAACCACCCTAAGCTGCTGCTCAGGAG 4286
              ||| |||||||||| ||||||||||||||||||||||||||| ||||||||||||||||||
Db        361 GGCTGACCTCATTGATAAGAACCTGGAGAGCAAGAACCACCCCAAGCTGCTGCTCAGGAG 420

Qy       4287 GACTGAGTCAGTGGCTGAGAAGATGCTGACCAATTGGTTTACTTTCCTCCTCTACAAGTT 4346
              ||| ||||| ||||| ||||||||| |||| |||||||| ||||||||||||||||||||
Db        421 GACGGAGTCGGTGGCCGAGAAGATGTTGACTAATTGGTTCACTTTCCTCCTCTACAAGTT 480

Qy       4347 CCTCAAGGAGTGTGCTGGGGAGCCCCTCTTCTCCCTGTTCTGTGCCATCAAGCAGCAGAT 4406
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCTCAAGGAGTGTGCTGGGGAGCCACTCTTCTCCCTGTTCTGTGCCATCAAGCAGCAGAT 540

Qy       4407 GGAGAAGGGCCCCCATTGACGCCATCACGGGCGAGGCCCGCTACTCCTTGAGCGAGGACAA 4466
              |||||||||||||||||| |||||||| || |||||||||||||| | || ||||||||
Db        541 GGAGAAGGGCCCCATTGATGCCATCACCGGAGAGGCCCGCTACTCGCTAAGTGAGGACAA 600

Qy       4467 GCTCATCCGCCAGCAGATTGACTACAAAACCCTGGTCCTGAGCTGTGTCAGCCCAGACAA 4526
              |||||||| |||||||||| || |||||| |||||||||||||||||| |||||| ||
Db        601 ACTCATCCGACAGCAGATTGAATATAAAACCTTGGTCCTGAGCTGTGTCAGTCCAGATAA 660

Qy       4527 TGCCAACAGCCCCCGAGGTCCCAGTAAAGATCCTCAACTGTGACACCATCACTCAGGTCAA 4586
              ||  |||||||| |||||||||| ||||||||||||||||||||||||||||||||||||
Db        661 TGTTAACAGCCCAGAGGTCCCAGTGAAGATCCTCAACTGTGACACCATCACTCAGGTCAN 720

Qy       4587 GGAGAAGATTCTGGATGCCATCTTC 4611
              |||||||| || ||||||||||||
Db        721 AGAGAAGATCCTAGATGCCATCTTC 745


RESULT 13
BX470595
LOCUS       BX470595                618 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  DKFZp686G07110_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
            DKFZp686G07110 5', mRNA sequence.
ACCESSION   BX470595
VERSION     BX470595.1  GI:31664922
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 618)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
            Fobo,G., Han,M. and Wiemann,S.
  TITLE     EST (Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., et al.)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by BMFZ (Biomedical Research Center at the Heinrich-
            Heine-University, Duesseldorf/Germany) within the cDNA sequencing
            consortium of the German Genome Project. No s1 sequence available.
            This clone (DKFZp686G07110) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
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     source          1. .618
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp686G07110"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="686 (synonym: hlcc3)"
                     /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
                     cDNA-collection"
ORIGIN

  Query Match            10.8%;  Score 613;  DB 13;  Length 618;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-118;
  Matches  613;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2683 AAGGTTGCTGGCGTGGAGTGCAGCCCTTTAGTGGATGGTTACATCCCTGCAGAACAGATC 2742
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db             6 AAGGTTGCTGGCGTGGAGTGCAGCCCTTTAGTGGATGGTTACATCCCTGCAGAACAGATC 65

Qy       2743 GTGTGTGAGATGGGGGAGGCCAAGCCCAGCCAGCATGCAGGCTTCGTGGAGATCTGCGTG 2802
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            66 GTGTGTGAGATGGGGGAGGCCAAGCCCAGCCAGCATGCAGGCTTCGTGGAGATCTGCGTG 125

Qy       2803 GCTGTGTGTCGGCCTGAATTCATGGCCCGGTCCTCACAGCTCTATTACTTCATGACACTG 2862
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           126 GCTGTGTGTCGGCCTGAATTCATGGCCCGGTCCTCACAGCTCTATTACTTCATGACACTG 185

Qy       2863 ACTCTCTCAGATCTGAAGCCCAGCCGGGGGCCCATGTCCGGAGGGACCCAAGTGACCATC 2922
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Db           186 ACTCTCTCAGATCTGAAGCCCAGCCGGGGGCCCATGTCCGGAGGGACCCAAGTGACCATC 245

Qy       2923 ACAGGCACCAACCTGAATGCCGGAAGCAACGTGGTGGTGATGTTTGGAAAGCAGCCCTGT 2982
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           246 ACAGGCACCAACCTGAATGCCGGAAGCAACGTGGTGGTGATGTTTGGAAAGCAGCCCTGT 305

Qy       2983 CTCTTCCACAGGCGATCTCCATCCTACATTGTCTGCAACACCACATCCTCAGATGAGGTG 3042
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Db           306 CTCTTCCACAGGCGATCTCCATCCTACATTGTCTGCAACACCACATCCTCAGATGAGGTG 365

Qy       3043 CTAGAGATGAAGGTGTCGGTGCAGGTGGACAGGGCCAAGATCCACCAGGACCTGGTCTTT 3102
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Db           366 CTAGAGATGAAGGTGTCGGTGCAGGTGGACAGGGCCAAGATCCACCAGGACCTGGTCTTT 425

Qy       3103 CAGTATGTGGAAGACCCCACCATCGTGCGGATTGAGCCAGAATGGAGCATTGTCAGTGGA 3162
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Db           426 CAGTATGTGGAAGACCCCACCATCGTGCGGATTGAGCCAGAATGGAGCATTGTCAGTGGA 485

Qy       3163 AACACACCCATCGCCGTATGGGGGACCCACCTGGACCTCATACAGAACCCCCAGATCCGT 3222
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Db           486 AACACACCCATCGCCGTATGGGGGACCCACCTGGACCTCATACAGAACCCCCAGATCCGT 545

Qy       3223 GCCAAGCATGGAGGGAAGGAGCACATCAATATCTGTGAGGTTCTGAACGCTACTGAGATG 3282
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Db           546 GCCAAGCATGGAGGGAAGGAGCACATCAATATCTGTGAGGTTCTGAACGCTACTGAGATG 605

Qy       3283 ACCTGTCAGGCGC 3295
             |||||||||||||
Db           606 ACCTGTCAGGCGC 618


RESULT 14
BM544169
LOCUS       BM544169               1027 bp    mRNA    linear   EST 20-FEB-2002
DEFINITION  AGENCOURT_6490555 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5587657
            5', mRNA sequence.
ACCESSION   BM544169
VERSION     BM544169.1  GI:18775199
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1027)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Invitrogen
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12357  row: i  column: 02
            High quality sequence stop: 676.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:5587657"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_125"
                     /note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
                     Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool
                     of three ovaries, from females ranging in age from 38 to
                     49 yo. Library is oligo-dT primed and directionally cloned
                     (EcoRV site is destroyed upon cloning). Average insert
                     size 2.1 kb, insert size range 1-3.5 kb. Library is
                     normalized and enriched for full-length clones and was
                     constructed by C. Gruber (Invitrogen). Research Genetics
                     tracking code 036."
ORIGIN

  Query Match            10.5%;  Score 599.2;  DB 12;  Length 1027;
  Best Local Similarity  78.9%;  Pred. No. 2e-115;
  Matches  764;  Conservative    0;  Mismatches  198;  Indels    6;  Gaps    4;

Qy       4280 TCAGGAGGACTGAGTCAGTGGCTGAGAAGATGCTGACCAATTGGTTTACTTTCCTCCTCT 4339
             ||  | |  |||||||| ||||| |||||||||||| || || ||||| || |||||| | |
Db             12 TCCTGGGATCTGAGTCGGTGGCAGAGAAGATGCTAACTAACTGGTTCACCTTCCTCTTGT 71

Qy       4340 ACAAGTTCCTCAAGGAGTGTGCTGGGGAGCCCCTCTTCTCCCTGTTCTGTGCCATCAAGC 4399
             | |||||||||||||||||| |||||||||| || |||   |||| ||| ||||||||||
Db             72 ATAAGTTCCTCAAGGAGTGCGCTGGGGAGCCGCTGTTCATGCTGTACTGCGCCATCAAGC 131

Qy       4400 AGCAGATGGAGAAGGGCCCCATTGACGCCATCACGGGCGAGGCCCGCTACTCCTTGAGCG 4459
             |||||||||||||||||||||||||||||||||||||||||||| ||||| |||||||| |||| |
Db             132 AGCAGATGGAGAAGGGCCCCATTGACGCCATCACGGGTGAGGCACGCTACTCCCTGAGTG 191

Qy       4460 AGGACAAGCTCATCCGCCAGCAGATTGACTACAAAACCCTGGTCCTGAGCTGTGTCAGCC 4519
             |||||||||||||||| |||||||||||||||| || |||  |||| |||||| | ||
Db             192 AGGACAAGCTCATCCGGCAGCAGATTGACTACAAGACACTGACCCTGAACTGTGTGAACC 251

Qy       4520 CAGACAATGCCAACAGCCCCGAGGTCCCAGTAAAGATCCTCAACTGTGACACCATCACTC 4579
             | || ||||  ||    || ||||| || || |||   ||  |||||||||  |||| |
Db             252 CTGAGAATGAGAATGCACCTGAGGTGCCGGTGAAGGGGCTGGACTGTGACACGGTCACCC 311

Qy       4580 AGGTCAAGGAGAAGATTCTGGATGCCATCTTCAAGAATGTGCCTTGCTCCCACCGGCCCA 4639
             ||| |||||||||| | ||||| ||  || ||||   |||||  | ||||||  |||||||
Db             312 AGGCCAAGGAGAAGCTGCTGGACGCTGCCTACAAGGGCGTGCCCTACTCCCAGCGGCCCA 371

Qy       4640 AAGCTGCAGATATGGATCTGGAGTGGCGACAAGGAAGTGGGGCAAGGATGATCTTGCAGG 4699
             | || || || ||||| |||||||||||| || ||  |   |||  | || ||| ||||||
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Qy       4700 ATGAAGACATCACCACCAAGATTGAGAATGATTGGAAGCGACTGAACACACTGGCCCACT 4759
             | ||| ||| |||||||||||||| || |||||||||  | ||||||||||||| ||||
Db             432 ACGAGGACGTCACCACCAAGATTGACAACGATTGGAAGAGGCTGAACACACTGGCTCACT 491

Qy       4760 ACCAGGTGCCAGATGGTTCCGTGGTGGCATTAGTGTCCAAGCAGGTGACAGCCTATAACG 4819
             |||||||| |||| || ||| |||||||| | ||| ||||||||  | | ||||| |||
Db             492 ACCAGGTGACAGACGGGTCCTCGGTGGCACTGGTGCCCAAGCAGACGTCCGCCTACAACA 551
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Qy       4820 CAGTGAACAACTCCACCGTCTCCAGGACCTCAGCAAGTAAATATGAAAACATGATCCGGT 4879
Db        552 TCTCCAACTCCTCCACCTTCACCAAG---TCCCTCAGCAGATACGAGAGCATGCTGCGCA 608

Qy       4880 ACACGGGCAGCCCCGACAGCCTCCGCTCACGGACACCTATGATCACTCCTGACCTGGAGA 4939
Db        609 CGGCCAGCAGCCCCGACAGCCTGCGCTCGCGCACGCCCATGATCACGCCCGACCTGGAGA 668

Qy       4940 GTGGAGTCAAGATGTGGCACCTAGTGAAGAACCACGAGCACGGAGACCAGAAGGAGGGGG 4999
Db        669 GCGGCACCAAGCTGTGGCACCTGGTGAAGAA-CACGACCACCTGGACCAGCGTGAGGGTG 727

Qy       5000 ACCGGGGGAGCAAGATGGTGTCTGAAATCTACCTGACCCGACTCCTGGCCACTAAGGGCA 5059
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Qy       5060 CACTGCAGAAGTTTGTGGATGACCTCTTTGAGACCATCTTCAGCACGGCACACC-GTGGC 5118
Db        788 CACTGCAGAAGTTTGTGGACGACCTGTTTGAGAACATCTTCAGCACGGCACACCGGGGGC 847

Qy       5119 TCTGCCCTGCCCCTGGCCATCAAGTACATGTTTGACTT-CCTGGATGAGCAGGCTGATAA 5177
Db        848 TCAGCCCTGCCGCTGCCCATCAAGTACATGTTCGACTTCCCTGGATGAGCAGGCCGACAA 907

Qy       5178 ACATGGCATTCATGACCCGCACGTCCGCCATACCTGGAAGAGCAATTGCCTGCCCCTGAG 5237
Db        908 GCACCAGATCCACCATGCTGACGTGCGCCACACCTGGAAGAGCAACTGCCTGGCCCTGGG 967

Qy       5238 GTTTTGGG 5245
Db        968 CCTTCTGG 975
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RESULT 15
BU149880
LOCUS BU149880 882 bp mRNA linear EST 03-SEP-2002
DEFINITION AGENCOURT_8095739 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6088019 5', mRNA sequence.
ACCESSION BU149880
VERSION BU149880.1 GI:22663412
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 882)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2325 row: i column: 12
High quality sequence stop: 631.

FEATURES Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6088019"
/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_112"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned

GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 10.2%; Score 578; DB 13; Length 882;
Best Local Similarity 78.5%; Pred. No. 5.6e-111;
Matches 692; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

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Qy       4363 GGGGAGCCCCCTCTTCTCCCTGTTCTGTGCCATCAAGCAGCAGATGGAGAAGGGCCCCATT 4422
Db          1 GGGGAGCCACTCTTCATGCTATACTGTGCCATCAAGCAGCAGATGGAGAAGGGCCCCATT 60

Qy       4423 GACGCCATCACGGGCGAGGCCCGCTACTCCTTGAGCGAGGACAAGCTCATCCGCCAGCAG 4482
Db          61 GATGCCATCACGGGCGAGGCCCGCTACTCCCTGAGCGAGGACAAGCTCATCCGGCAGCAG 120

Qy       4483 ATTGACTACAAAACCCTGGTCCTGAGCTGTGTCAGCCCAGACAATGCCAACAGCCCCGAG 4542
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Qy       4543 GTCCCAGTAAAGATCCTCAACTGTGACACCATCACTCAGGTCAAGGAGAAGATTCTGGAT 4602
Db         181 ATCCCAGTGAAGGTGTTAAACTGTGACACCATCACACAGGTCAAGGAGAAGATTCTTGAT 240

Qy       4603 GCCATCTTCAAGAATGTGCCTTGCTCCCACCGGCCCAAAGCTGCAGATATGGATCTGGAG 4662
Db         241 GCCGTGTATAAGAATGTGCCCTATTCCCAGCGGCCGAGGGCAGTGGACATGGACTTGGAG 300

Qy       4663 TGGCGACAAGGAAGTGGGGCAAGGATGATCTTGCAGGATGAAGACATCACCACCAAGATT 4722
Db         301 TGGCGCCAAGGCCGGATCGCCCGGGTCGTGCTGCAAGATGAGGACATCACCACCAAGATT 360

Qy       4723 GAGAATGATTGGAAGCGACTGAACACACTGGCCCACTACCAGGTGCCAGATGGTTCCGTG 4782
Db         361 GAGGGTGACTGGAAGCGGCTCAACACACTGATGCATTATCAGGTGTCAGACAGGTCGGTG 420

Qy       4783 GTGGCATTAGTGTCCAAGCAGGTGACAGCCTATAACGCAGTGAACAACTCCACCGTCTCC 4842
Db         421 GTGGCTCTGGTCCCCAAACAGACCTCCTCCTACAACATCCCTGCCTCTGCCAGCATCTCC 480

Qy       4843 AGGACCTCAGCAAGTAAATATGAAAACATGATCCGGTACACGGGCAGCCCCGACAGCCTC 4902
Db         481 CGGACGTCCATCAGCAGATATGACTCCTCCTTCAGGTATACGGGCAGCCCCGACAGCCTG 540

Qy       4903 CGCTCACGGACACCTATGATCACTCCTGACCTGGAGAGTGGAGTCAAGATGTGGCACCTA 4962
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Qy       4963 GTGAAGAACCACGAGCACGGAGACCAGAAGGAGGGGGACCGGGGGAGCAAGATGGTGTCT 5022
Db         601 GTGAAGAACCATGACCACGGTGACCAGAAGGAGGGTGACCGGGGCAGCAAGATGGTGTCC 660

Qy       5023 GAAATCTACCTGACCCGACTCCTGGCCACTAAGGGCACACTGCAGAAGTTTGTGGATGAC 5082
Db         661 GAGATCTACCTGACCCGGCTACTGGCCACCAAGGGCACCCTGCAGAAGTTTGTGGACGAC 720

Qy       5083 CTCTTTGAGACCATCTTCAGCACGGCACACCGTGGCTCTGCCCTGCCCCTGGCCATCAAG 5142
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Qy       5143 TACATGTTTGACTTCCTGGATGAGCAGGCTGATAAACATGGCATTCATGACCCGCACGTC 5202
Db         781 TACATGTTTGATTTCCTAGATGAGCAGGCAGACAGGCACAGCATCCATGACACAGATGTG 840

Qy       5203 CGCCATACCTGGAAGAGCAATTGCCTGCCCCTGAGGTTTTGG 5244
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Search completed: February 19, 2004, 23:13:56

Job time : 8756 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 19, 2004, 23:18:35 ; Search time 14115 Seconds
(without alignments)
17475.395 Million cell updates/sec

Title: US-09-964-956-12
Perfect score: 5691
Sequence: 1 atgaaagccatgccctggaa.....gcttagacagctgaaataaa 5691

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
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6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
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13: gb_un:*
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25: em_pl:*
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27: em_sts:*
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30: em_htg_hum:*
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32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5691	100.0	5691	6	AX503782	AX503782 Sequence
2	5532	97.2	6367	6	AX492982	AX492982 Sequence
3	2237	39.3	5986	9	AB046770	AB046770 Homo sapi
4	1371	24.1	2015	9	BC028744	BC028744 Homo sapi
5	1371	24.1	3310	9	AK123428	AK123428 Homo sapi
c 6	1188	20.9	179145	9	AC009785	AC009785 Homo sapi
7	1108	19.5	3666	6	AX833678	AX833678 Sequence
8	1108	19.5	3666	9	AK095606	AK095606 Homo sapi
c 9	1106	19.4	188090	9	AC011625	AC011625 Homo sapi
c 10	1068	18.8	179592	2	AC009723	AC009723 Homo sapi
11	878	15.4	3556	9	HSM805617	AL834504 Homo sapi
12	793	13.9	2597	6	AX574564	AX574564 Sequence
13	793	13.9	2597	9	AY358850	AY358850 Homo sapi
14	706	12.4	1029	9	HSM802037	AL137352 Homo sapi
c 15	509	8.9	74655	2	AC025595	AC025595 Homo sapi
16	491	8.6	601	6	AX088116	AX088116 Sequence
17	479	8.4	3560	6	AX747045	AX747045 Sequence
18	479	8.4	3560	9	AK091538	AK091538 Homo sapi
c 19	272	4.8	198470	9	AC018643	AC018643 Human Chr
c 20	241	4.2	171557	2	AC147276	AC147276 Pan trogl
c 21	216	3.8	185272	9	AC105443	AC105443 Homo sapi
c 22	134	2.4	151153	9	AC009364	AC009364 Homo sapi
23	134	2.4	183538	2	AC147272	AC147272 Pan trogl
24	123	2.2	171557	2	AC147276	AC147276 Pan trogl
25	74	1.3	74655	2	AC025595	AC025595 Homo sapi
26	61	1.1	247656	2	AC112331	AC112331 Rattus no
27	61	1.1	274459	2	AC093959	AC093959 Rattus no
28	61	1.1	284400	2	AC096840	AC096840 Rattus no
29	53	0.9	7022	10	AB073228	AB073228 Mus muscu
30	53	0.9	172060	2	AC102171	AC102171 Mus muscu
31	49	0.9	6039	9	HSSEXGENE	X87852 H.sapiens m
c 32	48	0.8	144560	2	BX664737	BX664737 Homo sapi
c 33	48	0.8	160656	2	AL592072	AL592072 Homo sapi
34	48	0.8	219447	9	HUMFLNG6PD	L44140 Homo sapien
35	47	0.8	4445	9	AK126101	AK126101 Homo sapi
36	47	0.8	5263	9	HSNOVPROT	X87832 Homo sapien
37	47	0.8	5895	6	AX686475	AX686475 Sequence
38	47	0.8	6147	6	AX704766	AX704766 Sequence
39	47	0.8	6693	6	BD183298	BD183298 Novel gen
40	47	0.8	91240	9	AC130566	AC130566 Homo sapi
c 41	47	0.8	152135	9	AC011199	AC011199 Homo sapi
42	47	0.8	221370	2	AC126205	AC126205 Rattus no
c 43	47	0.8	228898	2	AC131554	AC131554 Rattus no
44	45	0.8	465	11	HSC67G05	AL158469 H.sapiens
c 45	44	0.8	172060	2	AC102171	AC102171 Mus muscu
c 46	44	0.8	238662	2	AC102156	AC102156 Mus muscu
47	39	0.7	1817	9	BC006193	BC006193 Homo sapi
48	39	0.7	2875	9	BC009343	BC009343 Homo sapi
49	39	0.7	3985	9	HSOCTPROT	X87831 Homo sapien
50	39	0.7	6263	9	AB007932	AB007932 Homo sapi
51	39	0.7	6387	6	AX405895	AX405895 Sequence
52	39	0.7	118429	2	AL158017	AL158017 Homo sapi
c 53	39	0.7	198906	9	AL356275	AL356275 Human DNA
54	38	0.7	776	4	AF176418	AF176418 Bos tauru
55	38	0.7	6466	10	D86948	D86948 Mus musculu
56	38	0.7	211217	2	AC122387	AC122387 Mus muscu
c 57	35	0.6	218548	2	AC132672	AC132672 Rattus no
c 58	35	0.6	224751	2	BX649286	BX649286 Danio rer
59	35	0.6	229922	2	AC102141	AC102141 Mus muscu
60	35	0.6	230199	5	BX537358	BX537358 Zebrafish
61	35	0.6	251269	2	AC145193	AC145193 Gallus ga
c 62	35	0.6	260656	2	BX640582	BX640582 Danio rer
63	34	0.6	5982	10	D86950	D86950 Mus musculu
c 64	34	0.6	188873	2	AC073658	AC073658 Mus muscu
65	34	0.6	198653	2	AC091474	AC091474 Mus muscu

	66	34	0.6	200322	2	AL808145 AL808145 Mus muscu
	67	34	0.6	203189	10	AL807376 AL807376 Mouse DNA
	68	34	0.6	214505	2	AC025784 AC025784 Mus muscu
c	69	34	0.6	220228	2	AC094668 AC094668 Rattus no
	70	33	0.6	146405	10	AC122795 AC122795 Mus muscu
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	73	32	0.6	4320	10	AK129133 AK129133 Mus muscu
	74	32	0.6	8466	10	AB072381 AB072381 Mus muscu
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c	76	31	0.5	208593	2	AC140383 AC140383 Mus muscu
	77	31	0.5	229392	2	AC112372 AC112372 Rattus no
	78	31	0.5	238662	2	AC102156 AC102156 Mus muscu
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	80	29	0.5	582	5	AB055678 AB055678 Danio rer
	81	29	0.5	768	6	AX865902 AX865902 Sequence
	82	29	0.5	768	6	BD145964 BD145964 Primer fo
	83	29	0.5	1012	9	BC032125 BC032125 Homo sapi
	84	29	0.5	1767	6	AX878694 AX878694 Sequence
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	86	29	0.5	1767	9	AK021813 AK021813 Homo sapi
	87	29	0.5	2294	9	AK094367 AK094367 Homo sapi
	88	29	0.5	4196	9	AK128612 AK128612 Homo sapi
	89	26	0.5	26	6	AX503877 AX503877 Sequence
	90	26	0.5	6163	5	XELPLEX D38175 Xenopus lae
	91	26	0.5	75429	2	AC101416 AC101416 Mus muscu
	92	25	0.4	2284	10	BC056475 BC056475 Mus muscu
	93	25	0.4	6730	6	AX305728 AX305728 Sequence
	94	25	0.4	6730	10	D86949 D86949 Mus musculu
	95	25	0.4	6893	10	AK122289 AK122289 Mus muscu
c	96	25	0.4	212744	2	AC106326 AC106326 Rattus no
c	97	25	0.4	216192	10	AC111280 AC111280 Rattus no
	98	25	0.4	228202	5	BX284664 BX284664 Zebrafish
	99	24	0.4	1486	4	OCHEMOPEX X16429 Oryctolagus
	100	23	0.4	190	6	AX904782 AX904782 Sequence
	101	23	0.4	190	6	BD040315 BD040315 Sequence
	102	23	0.4	1758	9	HSM802538 AL162013 Homo sapi
	103	23	0.4	147686	10	AL845480 AL845480 Mouse DNA
	104	23	0.4	157250	2	AC027264 AC027264 Homo sapi
c	105	23	0.4	164057	9	AL590138 AL590138 Human DNA
	106	23	0.4	169305	9	AC021036 AC021036 Homo sapi
c	107	23	0.4	183353	10	AL935278 AL935278 Mouse DNA
	108	23	0.4	190748	9	AC010969 AC010969 Homo sapi
c	109	23	0.4	217392	2	AC107414 AC107414 Rattus no
c	110	23	0.4	218448	2	BX324190 BX324190 Danio rer
c	111	23	0.4	229132	2	AC112047 AC112047 Rattus no
	112	23	0.4	253343	10	AC102566 AC102566 Mus muscu
	113	22	0.4	22	6	AX503876 AX503876 Sequence
	114	22	0.4	6178	10	AK129175 AK129175 Mus muscu
c	115	22	0.4	143406	10	AC092857 AC092857 Rattus no
c	116	22	0.4	174928	10	AC121975 AC121975 Mus muscu
c	117	22	0.4	182452	9	AL161731 AL161731 Human DNA
c	118	22	0.4	190125	2	AC142099 AC142099 Mus muscu
c	119	22	0.4	197333	2	AC120001 AC120001 Mus muscu
c	120	22	0.4	202391	10	AC110040 AC110040 Mus muscu
c	121	22	0.4	205587	2	AC139761 AC139761 Mus muscu
c	122	22	0.4	207228	2	AC109215 AC109215 Mus muscu
c	123	22	0.4	228678	2	AC110740 AC110740 Mus muscu
	124	22	0.4	230329	2	AC142070 AC142070 Rattus no
c	125	22	0.4	232691	10	AC116772 AC116772 Mus muscu
c	126	22	0.4	234882	2	AC127871 AC127871 Rattus no
c	127	22	0.4	237777	2	AC096165 AC096165 Rattus no
c	128	22	0.4	244795	2	AC131632 AC131632 Rattus no
c	129	22	0.4	246196	2	AC105641 AC105641 Rattus no
	130	22	0.4	254380	2	AC105841 AC105841 Rattus no
	131	22	0.4	273225	2	AC129440 AC129440 Rattus no
c	132	22	0.4	349841	1	BX572606 BX572606 Rhodopseu
c	133	21	0.4	21	6	AX503878 AX503878 Sequence
	134	21	0.4	261	10	AF540386 AF540386 Mus muscu
	135	21	0.4	1874	10	RATGABAAF L08494 Rattus norv
	136	21	0.4	2134	10	BC013663 BC013663 Mus muscu
	137	21	0.4	2591	10	RNGABAA5 X51992 R.norvegicu
	138	21	0.4	2689	10	BC062112 BC062112 Mus muscu
	139	21	0.4	2815	10	BC011069 BC011069 Mus muscu
	140	21	0.4	3078	10	MMPCTAI1A X69025 M.musculus
	141	21	0.4	3111	10	RRU36444 U36444 Rattus norv
	142	21	0.4	5249	10	AK122467 AK122467 Mus muscu
c	143	21	0.4	46794	2	AC114683 AC114683 Homo sapi
c	144	21	0.4	60111	2	AC117617 AC117617 Mus muscu
c	145	21	0.4	65513	2	AC103748 AC103748 Homo sapi
	146	21	0.4	66118	9	AL162259 AL162259 Human DNA
c	147	21	0.4	73947	9	AL445248 AL445248 Human DNA
	148	21	0.4	83559	9	AC044786 AC044786 Homo sapi
c	149	21	0.4	98861	9	AL136961 AL136961 Human DNA
c	150	21	0.4	99512	9	AC004606 AC004606 Homo sapi
c	151	21	0.4	101458	2	AP000680 AP000680 Homo sapi
c	152	21	0.4	109602	2	AC131780 AC131780 Mus muscu
	153	21	0.4	109610	10	AC135241 AC135241 Mus muscu
	154	21	0.4	109624	10	AC144935 AC144935 Mus muscu
	155	21	0.4	110000	2	AC109940_0 AC109940 Rattus no
	156	21	0.4	115145	10	AL807240 AL807240 Mouse DNA
	157	21	0.4	129414	2	AC143614 AC143614 Macaca mu
c	158	21	0.4	134506	9	HS357I16 AL021921 Human DNA
c	159	21	0.4	135638	1	AF484556 AF484556 Streptomy
c	160	21	0.4	137908	10	AL607024 AL607024 Mouse DNA
c	161	21	0.4	142696	2	AC143051 AC143051 Macaca mu
	162	21	0.4	147138	10	AL672094 AL672094 Mouse DNA
	163	21	0.4	151174	2	AC016189 AC016189 Homo sapi
	164	21	0.4	154896	2	AC110481 AC110481 Rattus no
	165	21	0.4	158170	8	AC093180 AC093180 Oryza sat
	166	21	0.4	158538	2	AC118677 AC118677 Mus muscu
c	167	21	0.4	160989	8	OSJN00089 AL606683 Oryza sat
c	168	21	0.4	165776	2	AC109157 AC109157 Mus muscu
c	169	21	0.4	166804	8	OSJN00077 AL606638 Oryza sat
c	170	21	0.4	168639	2	AC121229 AC121229 Rattus no
	171	21	0.4	171368	9	HSU95738 U95738 Human chrom
c	172	21	0.4	172029	9	AC104416 AC104416 Homo sapi
	173	21	0.4	172506	2	AC105743 AC105743 Oryza sat
	174	21	0.4	175745	2	BX530060 BX530060 Danio rer
c	175	21	0.4	175849	9	AL512366 AL512366 Human DNA
c	176	21	0.4	175965	2	AC131778 AC131778 Mus muscu
	177	21	0.4	176329	2	AC119047 AC119047 Rattus no
c	178	21	0.4	178525	9	AC018612 AC018612 Homo sapi
c	179	21	0.4	178739	2	AC024688 AC024688 Homo sapi
c	180	21	0.4	183133	10	AC101851 AC101851 Mus muscu
c	181	21	0.4	185973	2	AC128212 AC128212 Rattus no
c	182	21	0.4	187960	9	AP000866 AP000866 Homo sapi
	183	21	0.4	189268	2	AC024021 AC024021 Homo sapi
	184	21	0.4	190104	2	AC122985 AC122985 Rattus no
	185	21	0.4	192729	2	AC147396 AC147396 Bos tauru
c	186	21	0.4	195961	10	AC124709 AC124709 Mus muscu
c	187	21	0.4	196204	9	AC073957 AC073957 Homo sapi
	188	21	0.4	198197	2	BX322641 BX322641 Mus muscu
	189	21	0.4	198197	10	AC125035 AC125035 Mus muscu
	190	21	0.4	199577	2	AC125873 AC125873 Rattus no
	191	21	0.4	204426	2	AC108778 AC108778 Mus muscu
c	192	21	0.4	208094	2	AC023305 AC023305 Mus muscu
c	193	21	0.4	209968	2	AC125872 AC125872 Rattus no
c	194	21	0.4	211550	9	AC073912 AC073912 Homo sapi
	195	21	0.4	211789	2	BX649475 BX649475 Mus muscu
	196	21	0.4	218961	2	AC117329 AC117329 Rattus no
c	197	21	0.4	219804	2	AC129723 AC129723 Rattus no
	198	21	0.4	224915	2	AC096902 AC096902 Rattus no
	199	21	0.4	227164	2	AC103418 AC103418 Rattus no
c	200	21	0.4	229045	2	AC126138 AC126138 Rattus no
	201	21	0.4	230760	10	AF133093 AF133093 Mus muscu
c	202	21	0.4	231435	2	AC113813 AC113813 Rattus no
	203	21	0.4	233465	2	AC131137 AC131137 Rattus no
	204	21	0.4	233615	2	AP000933 AP000933 Homo sapi
c	205	21	0.4	234885	2	AC097033 AC097033 Rattus no
	206	21	0.4	234972	2	AC096372 AC096372 Rattus no
	207	21	0.4	235460	2	AC107798 AC107798 Mus muscu
c	208	21	0.4	238934	2	AC096011 AC096011 Rattus no
c	209	21	0.4	241404	2	AC099365 AC099365 Rattus no
c	210	21	0.4	241730	2	AC103283 AC103283 Rattus no
c	211	21	0.4	241949	2	AC094309 AC094309 Rattus no

	212	21	0.4	244343	2	AC106516 AC106516 Rattus no
c	213	21	0.4	245892	2	AC096984 AC096984 Rattus no
c	214	21	0.4	247645	2	AC118405 AC118405 Rattus no
	215	21	0.4	250415	2	AC097418 AC097418 Rattus no
c	216	21	0.4	250627	2	AC097031 AC097031 Rattus no
	217	21	0.4	254288	2	AC126112 AC126112 Rattus no
	218	21	0.4	254708	2	AC111761 AC111761 Rattus no
	219	21	0.4	260600	2	AC115307 AC115307 Rattus no
c	220	21	0.4	262886	2	AC121209 AC121209 Rattus no
c	221	21	0.4	265567	2	AC096335 AC096335 Rattus no
c	222	21	0.4	271040	2	AC121473 AC121473 Rattus no
c	223	21	0.4	276800	1	SCO939115 AL939115 Streptomy
	224	21	0.4	279593	2	AC114015 AC114015 Rattus no
c	225	21	0.4	280025	2	AC108655 AC108655 Rattus no
	226	21	0.4	283782	2	AC096338 AC096338 Rattus no
	227	21	0.4	294396	2	AC105485 AC105485 Rattus no
c	228	21	0.4	316005	2	AC111792 AC111792 Rattus no
c	229	21	0.4	346542	2	AC120727 AC120727 Rattus no
c	230	21	0.4	347368	2	AC096620 AC096620 Rattus no
c	231	20	0.4	207	9	HS62A1R Z62020 H.sapiens C
	232	20	0.4	242	9	HS63MRNAG X87197 H.sapiens m
c	233	20	0.4	272	9	HS179E11F Z54966 H.sapiens C
c	234	20	0.4	311	6	AR251662 AR251662 Sequence
c	235	20	0.4	318	6	BD204150 BD204150 5'EST and
c	236	20	0.4	324	6	AX408405 AX408405 Sequence
c	237	20	0.4	328	6	AX260802 AX260802 Sequence
	238	20	0.4	332	10	AF029886 AF029886 Rattus no
	239	20	0.4	381	9	HSA430739 AJ430739 Homo sapi
c	240	20	0.4	382	6	AX895484 AX895484 Sequence
c	241	20	0.4	382	6	BD031017 BD031017 Sequence
c	242	20	0.4	412	6	AX895483 AX895483 Sequence
c	243	20	0.4	412	6	BD031016 BD031016 Sequence
	244	20	0.4	419	6	AX396560 AX396560 Sequence
c	245	20	0.4	456	6	AX895482 AX895482 Sequence
c	246	20	0.4	456	6	BD031015 BD031015 Sequence
c	247	20	0.4	462	6	BD265166 BD265166 Compounds
c	248	20	0.4	462	6	AR401152 AR401152 Sequence
c	249	20	0.4	462	6	AX192598 AX192598 Sequence
c	250	20	0.4	486	6	AX895485 AX895485 Sequence
c	251	20	0.4	486	6	BD031018 BD031018 Sequence
	252	20	0.4	506	6	AX804284 AX804284 Sequence
c	253	20	0.4	615	6	AX884867 AX884867 Sequence
c	254	20	0.4	615	6	BD024477 BD024477 Sequence
c	255	20	0.4	616	6	BD229563 BD229563 Human gen
c	256	20	0.4	635	8	AF362041 AF362041 Dendrobiu
c	257	20	0.4	670	6	AX899105 AX899105 Sequence
c	258	20	0.4	670	6	BD034638 BD034638 Sequence
c	259	20	0.4	689	6	AX899102 AX899102 Sequence
c	260	20	0.4	689	6	BD034635 BD034635 Sequence
c	261	20	0.4	700	6	AX410652 AX410652 Sequence
c	262	20	0.4	700	9	BC006791 BC006791 Homo sapi
c	263	20	0.4	700	9	HSU12404 U12404 Human Csa-1
c	264	20	0.4	709	9	BC011366 BC011366 Homo sapi
c	265	20	0.4	741	6	BD189960 BD189960 Tumor ant
c	266	20	0.4	741	9	AB082926 AB082926 Homo sapi
c	267	20	0.4	744	6	AX899094 AX899094 Sequence
c	268	20	0.4	744	6	BD034627 BD034627 Sequence
c	269	20	0.4	750	6	BD220723 BD220723 Human gen
c	270	20	0.4	824	6	AX867417 AX867417 Sequence
c	271	20	0.4	824	6	BD147479 BD147479 Primer fo
	272	20	0.4	1396	9	S76730 S76730 MM1=clone M
	273	20	0.4	1403	10	BC024509 BC024509 Mus muscu
	274	20	0.4	1413	9	BT006887 BT006887 Homo sapi
	275	20	0.4	1413	12	BT007594 BT007594 Synthetic
	276	20	0.4	1618	10	MMU58887 U58887 Mus musculu
	277	20	0.4	1636	6	AR175265 AR175265 Sequence
	278	20	0.4	1662	10	BC027096 BC027096 Mus muscu
c	279	20	0.4	1782	10	AF077338 AF077338 Rat norve
c	280	20	0.4	1860	10	BC061993 BC061993 Rattus no
c	281	20	0.4	1876	9	HSM800181 AL050280 Homo sapi
	282	20	0.4	1946	9	AK025415 AK025415 Homo sapi
c	283	20	0.4	2060	6	AX879531 AX879531 Sequence
c	284	20	0.4	2060	6	BD157886 BD157886 Primer fo
c	285	20	0.4	2060	9	AK022651 AK022651 Homo sapi
	286	20	0.4	2166	9	BC004542 BC004542 Homo sapi
c	287	20	0.4	2291	9	BC011892 BC011892 Homo sapi
c	288	20	0.4	2389	9	AF464935 AF464935 Homo sapi
c	289	20	0.4	2444	6	E36720 E36720 Novel trans
c	290	20	0.4	2522	6	AR339211 AR339211 Sequence
c	291	20	0.4	2533	10	BC004762 BC004762 Mus muscu
c	292	20	0.4	2564	6	AX746754 AX746754 Sequence
c	293	20	0.4	2564	9	AK091056 AK091056 Homo sapi
c	294	20	0.4	2775	10	AB041607 AB041607 Mus muscu
	295	20	0.4	2935	10	BC003293 BC003293 Mus muscu
	296	20	0.4	2971	6	BD127371 BD127371 Primer fo
	297	20	0.4	2971	9	AK074932 AK074932 Homo sapi
	298	20	0.4	3038	9	AK126394 AK126394 Homo sapi
	299	20	0.4	3184	10	BC051045 BC051045 Mus muscu
	300	20	0.4	3504	9	AK056543 AK056543 Homo sapi
	301	20	0.4	3726	9	AK025701 AK025701 Homo sapi
c	302	20	0.4	3849	6	AX058889 AX058889 Sequence
	303	20	0.4	4125	8	CRE427966 AJ427966 Chlamydom
	304	20	0.4	4355	10	BC054788 BC054788 Mus muscu
	305	20	0.4	4378	10	BC053092 BC053092 Mus muscu
	306	20	0.4	4725	10	AF190578 AF190578 Mus muscu
	307	20	0.4	5310	10	BC007481 BC007481 Mus muscu
	308	20	0.4	6252	6	AX088110 AX088110 Sequence
	309	20	0.4	6252	6	AX210612 AX210612 Sequence
	310	20	0.4	6252	6	AX335107 AX335107 Sequence
	311	20	0.4	6252	9	AB002313 AB002313 Human mRN
c	312	20	0.4	8560	1	AF173226 AF173226 Stenotrop
c	313	20	0.4	11158	1	AE004552 AE004552 Pseudomon
c	314	20	0.4	12744	1	AF204401 AF204401 Streptomy
c	315	20	0.4	13714	1	AE003997 AE003997 Xylella f
c	316	20	0.4	13842	6	BD217185 BD217185 DNA encod
	317	20	0.4	18979	10	BX842567 BX842567 Mouse DNA
c	318	20	0.4	23518	9	AL589739 AL589739 Human DNA
c	319	20	0.4	27950	9	BX649592 BX649592 Human DNA
c	320	20	0.4	29074	3	LMFL5213T AL352992 Leishmani
c	321	20	0.4	32539	9	HSL1C2 Z49154 Human DNA s
c	322	20	0.4	37948	1	AF079138 AF079138 Streptomy
c	323	20	0.4	37948	6	BD217173 BD217173 DNA encod
c	324	20	0.4	38506	6	BD232534 BD232534 Recombina
c	325	20	0.4	38506	6	AR271680 AR271680 Sequence
c	326	20	0.4	38506	6	AR277664 AR277664 Sequence
c	327	20	0.4	40548	8	AB011480 AB011480 Arabidops
	328	20	0.4	48662	3	AC024755 AC024755 Caenorhab
	329	20	0.4	52573	2	AC136259 AC136259 Rattus no
c	330	20	0.4	59657	9	AC074013 AC074013 Homo sapi
c	331	20	0.4	62297	10	AY115107 AY115107 Mus muscu
c	332	20	0.4	67173	9	AL359962 AL359962 Human DNA
c	333	20	0.4	70282	9	AP001505 AP001505 Homo sapi
	334	20	0.4	74194	9	AL596449 AL596449 Human DNA
	335	20	0.4	74595	9	AC130276 AC130276 Homo sapi
	336	20	0.4	77758	8	AB016885 AB016885 Arabidops
c	337	20	0.4	79340	8	AP003956 AP003956 Oryza sat
c	338	20	0.4	79884	9	AC109440 AC109440 Homo sapi
c	339	20	0.4	85440	2	AC034264 AC034264 Mus muscu
c	340	20	0.4	88421	6	AX417445 AX417445 Sequence
c	341	20	0.4	88588	9	AC010453 AC010453 Homo sapi
	342	20	0.4	89743	10	AC003062 AC003062 Mouse Chr
	343	20	0.4	91419	9	AL591480 AL591480 Human DNA
c	344	20	0.4	92580	2	AC016302 AC016302 Homo sapi
c	345	20	0.4	95593	10	BX470092 BX470092 Mouse DNA
	346	20	0.4	98522	2	AC110929_7 Continuation (8 of
c	347	20	0.4	99108	9	AC008666 AC008666 Homo sapi
c	348	20	0.4	99202	10	AL928807 AL928807 Mouse DNA
c	349	20	0.4	100719	9	BX255925 BX255925 Human DNA
c	350	20	0.4	101305	10	AL663025 AL663025 Mouse DNA
	351	20	0.4	106323	9	AL513477 AL513477 Human DNA
	352	20	0.4	108015	10	AL645744 AL645744 Mouse DNA
	353	20	0.4	108795	9	AC114483 AC114483 Homo sapi
	354	20	0.4	110000	2	AC013623_0 AC013623 Mus muscu
	355	20	0.4	110000	2	AC107201_2 Continuation (3 of
c	356	20	0.4	110000	2	AC110950_3 Continuation (4 of
c	357	20	0.4	110000	2	AC142490_1 Continuation (2 of

	358	20	0.4	110000	2	LMFLCHR36_23 Continuation (24 o
c	359	20	0.4	112339	9	HS110F11 AL033526 Human DNA
	360	20	0.4	112714	2	AC144689 AC144689 Ornithorh
	361	20	0.4	112846	9	AC004991 AC004991 Homo sapi
	362	20	0.4	114774	2	AL603748 AL603748 Homo sapi
c	363	20	0.4	115292	9	AC108742 AC108742 Homo sapi
	364	20	0.4	115295	9	AL136967 AL136967 Human DNA
c	365	20	0.4	117000	9	AC117475 AC117475 Homo sapi
c	366	20	0.4	118299	10	AL929069 AL929069 Mouse DNA
	367	20	0.4	120323	2	BX539322 BX539322 Danio rer
c	368	20	0.4	126982	2	BX649443 BX649443 Homo sapi
c	369	20	0.4	128720	2	AC124970 AC124970 Medicago
	370	20	0.4	129519	10	AL645951 AL645951 Mouse DNA
c	371	20	0.4	130110	9	AL731777 AL731777 Human DNA
	372	20	0.4	133915	9	AC108740 AC108740 Homo sapi
	373	20	0.4	134666	2	AC140091 AC140091 Bos tauru
c	374	20	0.4	135692	9	AC021134 AC021134 Homo sapi
	375	20	0.4	136687	10	AC005816 AC005816 Mus muscu
	376	20	0.4	137506	9	AC004824 AC004824 Homo sapi
c	377	20	0.4	140113	2	AC116824 AC116824 Mus muscu
	378	20	0.4	140630	9	AL357514 AL357514 Human DNA
	379	20	0.4	140894	2	AC144754 AC144754 Ornithorh
	380	20	0.4	141854	2	AC021595 AC021595 Homo sapi
	381	20	0.4	142727	2	AP005723 AP005723 Oryza sat
c	382	20	0.4	148651	2	AC060778 AC060778 Homo sapi
c	383	20	0.4	150240	9	AC146458 AC146458 Pan trogl
	384	20	0.4	150724	10	AP003150 AP003150 Mus muscu
	385	20	0.4	152337	8	AY325816 AY325816 Zea mays
c	386	20	0.4	152395	9	AC123022 AC123022 Homo sapi
	387	20	0.4	152449	2	AC080175 AC080175 Homo sapi
c	388	20	0.4	152992	2	AC023804 AC023804 Mus muscu
c	389	20	0.4	153736	2	AC141187 AC141187 Rattus no
c	390	20	0.4	154412	9	HS144F13 AL035404 Human DNA
	391	20	0.4	154741	10	AC124694 AC124694 Mus muscu
c	392	20	0.4	155349	2	AL162257 AL162257 Homo sapi
c	393	20	0.4	155818	9	AL954253 AL954253 Pan trogl
	394	20	0.4	156124	10	AC125325 AC125325 Mus muscu
c	395	20	0.4	156393	2	AC116177 AC116177 Homo sapi
c	396	20	0.4	157088	10	AC127292 AC127292 Mus muscu
	397	20	0.4	157168	10	AL772232 AL772232 Mouse DNA
c	398	20	0.4	157790	9	AL133413 AL133413 Human DNA
	399	20	0.4	158037	2	AC010131 AC010131 Homo sapi
	400	20	0.4	158573	2	AC078823 AC078823 Homo sapi
	401	20	0.4	159499	2	AC146456 AC146456 Pan trogl
c	402	20	0.4	160178	9	AL162584 AL162584 Human DNA
c	403	20	0.4	162701	2	AC073317 AC073317 Homo sapi
c	404	20	0.4	162956	2	AC068168 AC068168 Homo sapi
c	405	20	0.4	162996	2	AC051655 AC051655 Homo sapi
c	406	20	0.4	164632	2	AC025624 AC025624 Homo sapi
	407	20	0.4	165353	2	AC140690 AC140690 Rattus no
c	408	20	0.4	165890	2	BX649446 BX649446 Danio rer
	409	20	0.4	167561	2	AC119710 AC119710 Rattus no
	410	20	0.4	167710	2	AC109891 AC109891 Rattus no
c	411	20	0.4	167825	2	AC142899 AC142899 Macaca mu
c	412	20	0.4	167962	2	AC073484 AC073484 Homo sapi
	413	20	0.4	168813	9	AP000555 AP000555 Homo sapi
c	414	20	0.4	168981	10	AL591469 AL591469 Mouse DNA
c	415	20	0.4	169649	2	AC046163 AC046163 Homo sapi
	416	20	0.4	169741	9	AC097468 AC097468 Homo sapi
	417	20	0.4	170245	9	HS109F14 AL022721 Human DNA
c	418	20	0.4	170525	2	AC101804 AC101804 Mus muscu
c	419	20	0.4	170652	2	AC092934 AC092934 Homo sapi
c	420	20	0.4	171052	2	AC025802 AC025802 Homo sapi
	421	20	0.4	173164	8	OSJN00025 AL606594 Oryza sat
c	422	20	0.4	173389	9	CNS05TCM AL355103 Human chr
	423	20	0.4	173700	9	AC096919 AC096919 Homo sapi
	424	20	0.4	173837	10	AC124681 AC124681 Mus muscu
c	425	20	0.4	173956	9	AC105383 AC105383 Homo sapi
c	426	20	0.4	175066	9	AC005900 AC005900 Homo sapi
	427	20	0.4	176027	2	AL732575 AL732575 Mus muscu
	428	20	0.4	176144	2	AC012408 AC012408 Homo sapi
	429	20	0.4	176629	9	AC008641 AC008641 Homo sapi
	430	20	0.4	179276	2	AC067884 AC067884 Homo sapi
c	431	20	0.4	179591	2	AC112970 AC112970 Mus muscu
c	432	20	0.4	179756	2	AC074039 AC074039 Mus muscu
	433	20	0.4	180239	10	AL671190 AL671190 Mouse DNA
	434	20	0.4	180690	10	AC121922 AC121922 Mus muscu
c	435	20	0.4	181388	2	AC130062 AC130062 Rattus no
c	436	20	0.4	181808	9	AL356267 AL356267 Human DNA
	437	20	0.4	183440	2	AC069295 AC069295 Homo sapi
	438	20	0.4	183462	10	AC126675 AC126675 Mus muscu
	439	20	0.4	184467	2	AC073241 AC073241 Homo sapi
c	440	20	0.4	184590	9	AL390059 AL390059 Human DNA
	441	20	0.4	184686	2	AC136893 AC136893 Gallus ga
	442	20	0.4	184758	2	AC122546 AC122546 Mus muscu
	443	20	0.4	185399	2	AC026940 AC026940 Homo sapi
	444	20	0.4	185666	2	AC101747 AC101747 Mus muscu
c	445	20	0.4	185788	2	AC136510 AC136510 Pan trogl
c	446	20	0.4	185879	2	AC135705 AC135705 Rattus no
	447	20	0.4	186285	2	AC140098 AC140098 Sus scrof
c	448	20	0.4	186795	2	AC090492 AC090492 Mus muscu
c	449	20	0.4	187117	9	AC016749 AC016749 Homo sapi
c	450	20	0.4	188417	9	AC025205 AC025205 Homo sapi
	451	20	0.4	188873	2	AC073658 AC073658 Mus muscu
c	452	20	0.4	189118	2	AC133935 AC133935 Mus muscu
	453	20	0.4	189846	2	AC140443 AC140443 Mus muscu
c	454	20	0.4	189939	2	AC109273 AC109273 Mus muscu
	455	20	0.4	190909	2	AC147151 AC147151 Pan trogl
c	456	20	0.4	190997	2	BX649409 BX649409 Danio rer
c	457	20	0.4	191603	2	AC110561 AC110561 Mus muscu
c	458	20	0.4	191701	2	AC080189 AC080189 Homo sapi
c	459	20	0.4	193289	2	AC113069 AC113069 Mus muscu
	460	20	0.4	193311	2	AC134403 AC134403 Mus muscu
c	461	20	0.4	193577	8	AP004365 AP004365 Oryza sat
c	462	20	0.4	193709	2	AC074205 AC074205 Mus muscu
	463	20	0.4	194305	2	AC117694 AC117694 Mus muscu
	464	20	0.4	195313	2	AC133328 AC133328 Rattus no
c	465	20	0.4	196146	2	AC023609 AC023609 Mus muscu
c	466	20	0.4	197201	2	AC119091 AC119091 Rattus no
	467	20	0.4	199103	2	AC080076 AC080076 Homo sapi
c	468	20	0.4	200348	9	AC005516 AC005516 Homo sapi
c	469	20	0.4	200512	2	AC135358 AC135358 Mus muscu
c	470	20	0.4	201239	2	AC135866 AC135866 Rattus no
c	471	20	0.4	203071	2	AC120394 AC120394 Mus muscu
	472	20	0.4	203106	10	AC021667 AC021667 Mus muscu
	473	20	0.4	203560	2	AC026298 AC026298 Homo sapi
	474	20	0.4	205053	9	AC011749 AC011749 Homo sapi
	475	20	0.4	205819	2	AC106805 AC106805 Homo sapi
c	476	20	0.4	206470	2	AC135811 AC135811 Rattus no
c	477	20	0.4	206592	10	AC122471 AC122471 Mus muscu
	478	20	0.4	207256	10	AL669950 AL669950 Mouse DNA
c	479	20	0.4	207265	2	AC122227 AC122227 Mus muscu
	480	20	0.4	208207	10	AC145450 AC145450 Mus muscu
	481	20	0.4	208404	10	AC102364 AC102364 Mus muscu
c	482	20	0.4	209247	2	AC106113 AC106113 Rattus no
	483	20	0.4	209448	2	AC137314 AC137314 Rattus no
c	484	20	0.4	210844	2	AC129214 AC129214 Mus muscu
	485	20	0.4	212814	2	AC078978 AC078978 Homo sapi
	486	20	0.4	213056	2	AC117723 AC117723 Mus muscu
	487	20	0.4	214042	10	AC127556 AC127556 Mus muscu
c	488	20	0.4	215795	2	BX649437 BX649437 Danio rer
	489	20	0.4	215826	10	AC129078 AC129078 Mus muscu
	490	20	0.4	215895	2	AC097998 AC097998 Rattus no
	491	20	0.4	215967	2	AC120425 AC120425 Mus muscu
	492	20	0.4	216314	2	AC110164 AC110164 Mus muscu
	493	20	0.4	216896	2	AC111973 AC111973 Rattus no
c	494	20	0.4	218018	2	AC123866 AC123866 Mus muscu
c	495	20	0.4	218242	2	AC105680 AC105680 Rattus no
c	496	20	0.4	219036	2	AC105588 AC105588 Rattus no
c	497	20	0.4	219443	2	AC023320 AC023320 Homo sapi
	498	20	0.4	219649	2	AC133222 AC133222 Rattus no
	499	20	0.4	220524	2	AC103065 AC103065 Rattus no
c	500	20	0.4	220887	10	AC124741 AC124741 Mus muscu
	501	20	0.4	220930	2	AC135137 AC135137 Rattus no
	502	20	0.4	221753	2	AC114835 AC114835 Rattus no
	503	20	0.4	221859	10	AL732309 AL732309 Mouse DNA

c	504	20	0.4	222182	2	AC123412 AC123412 Rattus no
	505	20	0.4	222589	10	AC113264 AC113264 Mus muscu
	506	20	0.4	222639	2	AC130083 AC130083 Rattus no
	507	20	0.4	223911	2	AC136740 AC136740 Mus muscu
c	508	20	0.4	224138	10	AC133573 AC133573 Mus muscu
	509	20	0.4	224764	2	AC122263 AC122263 Mus muscu
c	510	20	0.4	224859	2	AC073800 AC073800 Mus muscu
	511	20	0.4	225012	2	AC113462 AC113462 Mus muscu
c	512	20	0.4	225403	2	AC140451 AC140451 Mus muscu
c	513	20	0.4	225509	2	AC073782 AC073782 Mus muscu
c	514	20	0.4	225541	2	AC126700 AC126700 Rattus no
	515	20	0.4	225782	2	AC109529 AC109529 Rattus no
c	516	20	0.4	227848	2	AC123606 AC123606 Mus muscu
c	517	20	0.4	228051	2	AC097434 AC097434 Rattus no
	518	20	0.4	228178	2	AC111655 AC111655 Rattus no
	519	20	0.4	228413	2	AC132453 AC132453 Mus muscu
c	520	20	0.4	228852	2	AC131526 AC131526 Rattus no
c	521	20	0.4	229909	2	AC111310 AC111310 Rattus no
	522	20	0.4	230188	2	AC091604 AC091604 Mus muscu
	523	20	0.4	233160	2	AC134155 AC134155 Rattus no
	524	20	0.4	233510	2	AC136569 AC136569 Rattus no
	525	20	0.4	233718	2	AC094024 AC094024 Rattus no
	526	20	0.4	234053	2	AC128262 AC128262 Rattus no
c	527	20	0.4	234300	2	AC118431 AC118431 Rattus no
c	528	20	0.4	235050	2	AC096077 AC096077 Rattus no
	529	20	0.4	235427	2	AC140082 AC140082 Rattus no
c	530	20	0.4	236159	2	AC130109 AC130109 Rattus no
c	531	20	0.4	237304	2	AC096114 AC096114 Rattus no
c	532	20	0.4	238007	10	AC097745 AC097745 Rattus no
	533	20	0.4	239628	2	AC128574 AC128574 Rattus no
c	534	20	0.4	240203	2	AC126562 AC126562 Rattus no
c	535	20	0.4	240362	2	AC132623 Mus muscu
c	536	20	0.4	241781	2	AC122087 AC122087 Rattus no
	537	20	0.4	242000	2	AC127751 AC127751 Rattus no
c	538	20	0.4	242482	2	AC115149 AC115149 Rattus no
	539	20	0.4	242531	10	AC108805 AC108805 Mus muscu
c	540	20	0.4	242662	2	AC080020 AC080020 Mus muscu
c	541	20	0.4	243047	2	AC126579 Rattus no
c	542	20	0.4	243269	2	AC117152 AC117152 Rattus no
	543	20	0.4	243378	10	AC122324 AC122324 Mus muscu
	544	20	0.4	243770	2	AC120763 AC120763 Rattus no
	545	20	0.4	244814	2	AC098223 AC098223 Rattus no
c	546	20	0.4	245790	2	AC130142 AC130142 Rattus no
	547	20	0.4	246238	2	AC120998 AC120998 Rattus no
	548	20	0.4	246951	2	AC107248 AC107248 Rattus no
c	549	20	0.4	247108	2	AC123333 AC123333 Rattus no
c	550	20	0.4	248417	2	AC130165 AC130165 Rattus no
	551	20	0.4	248938	2	AC095006 AC095006 Rattus no
c	552	20	0.4	249245	2	AC110695 AC110695 Rattus no
	553	20	0.4	250335	2	AC114441 AC114441 Rattus no
c	554	20	0.4	251813	2	AC123454 AC123454 Rattus no
c	555	20	0.4	252110	2	AC094353 AC094353 Rattus no
c	556	20	0.4	252404	2	AC097117 AC097117 Rattus no
c	557	20	0.4	252411	2	AC094615 AC094615 Rattus no
c	558	20	0.4	252839	2	AC095096 AC095096 Rattus no
c	559	20	0.4	253874	2	AC131560 AC131560 Rattus no
	560	20	0.4	254483	2	AC095874 AC095874 Rattus no
c	561	20	0.4	257210	2	AC098622 AC098622 Rattus no
c	562	20	0.4	257398	2	AC131885 AC131885 Rattus no
c	563	20	0.4	259807	2	AC131539 AC131539 Rattus no
	564	20	0.4	261065	2	AC128913 AC128913 Rattus no
	565	20	0.4	261224	10	AL645527 AL645527 Mouse DNA
c	566	20	0.4	263259	2	AC121737 AC121737 Rattus no
c	567	20	0.4	263297	2	AC134030 AC134030 Rattus no
	568	20	0.4	263776	2	AC087335 AC087335 Mus muscu
c	569	20	0.4	265136	2	AC094847 AC094847 Rattus no
c	570	20	0.4	267462	2	AC131806 AC131806 Rattus no
c	571	20	0.4	268050	1	AL627266 AL627266 Salmonell
c	572	20	0.4	270105	2	AC099650 AC099650 Homo sapi
	573	20	0.4	270668	2	AC096354 AC096354 Rattus no
c	574	20	0.4	272677	2	AC097289 AC097289 Rattus no
c	575	20	0.4	274703	2	AC110414 AC110414 Rattus no
c	576	20	0.4	275507	2	AC099381 AC099381 Rattus no
c	577	20	0.4	275900	2	AC123150 AC123150 Rattus no
c	578	20	0.4	281085	2	AC123455 AC123455 Rattus no
c	579	20	0.4	284347	2	AC135290 AC135290 Mus muscu
c	580	20	0.4	285152	2	AC116112 AC116112 Mus muscu
	581	20	0.4	286451	2	AC115130 AC115130 Rattus no
	582	20	0.4	289103	2	AC126288 AC126288 Rattus no
c	583	20	0.4	290753	2	AC123256 AC123256 Rattus no
c	584	20	0.4	292100	1	SCO939121 AL939121 Streptomy
	585	20	0.4	300029	1	AE016842 AE016842 Salmonell
	586	20	0.4	303688	10	AE016754 AE016754 Mus muscu
	587	20	0.4	312626	2	AC109713 AC109713 Rattus no
	588	20	0.4	325265	2	AC118802 AC118802 Rattus no
c	589	20	0.4	325265	2	AC118802 AC118802 Rattus no
c	590	20	0.4	340000	9	HS21C101 AL163301 Homo sapi
	591	20	0.4	348764	1	BX569689 BX569689 Synechoco
c	592	19	0.3	258	4	BTL29486 L29486 Bos taurus
c	593	19	0.3	382	11	AY254001 AY254001 Sus scrof
	594	19	0.3	426	9	HSA240590 AJ240590 Homo sapi
	595	19	0.3	429	10	F257137S07 AF257143 Mus muscu
	596	19	0.3	503	5	AB062427 AB062427 Anguilla
	597	19	0.3	503	6	BD012143 BD012143 Novel pep
	598	19	0.3	529	11	G58051 G58051 SHGC-103874
c	599	19	0.3	539	11	G97698 G97698 S208P6575FF
	600	19	0.3	545	4	AF381310 AF381310 Ornithorh
	601	19	0.3	553	1	AF448095 AF448095 Synechoco
	602	19	0.3	560	1	AF245157 AF245157 Synechoco
	603	19	0.3	560	1	AF245158 AF245158 Synechoco
	604	19	0.3	561	1	AF448096 AF448096 Synechoco
	605	19	0.3	565	1	AF245125 AF245125 Synechoco
	606	19	0.3	567	1	AF245154 AF245154 Synechoco
c	607	19	0.3	570	11	HSC01A04 AL158551 H.sapiens
	608	19	0.3	572	1	AF245155 AF245155 Synechoco
c	609	19	0.3	588	6	AR093091 AR093091 Sequence
c	610	19	0.3	588	6	BD009915 BD009915 BH3 inter
	611	19	0.3	612	1	SSU52342 U52342 Synechococc
	612	19	0.3	612	1	SSU52343 U52343 Synechococc
c	613	19	0.3	648	14	AF367124 AF367124 Foot-and-
c	614	19	0.3	658	9	AY449016 AY449016 Autos aza
c	615	19	0.3	658	9	AY449075 AY449075 Autos aza
c	616	19	0.3	658	9	AY449165 AY449165 Ateles fu
	617	19	0.3	739	6	BD125041 BD125041 Primer fo
	618	19	0.3	739	6	BD126697 BD126697 Primer fo
c	619	19	0.3	759	11	BV044442 BV044442 S212P6045
c	620	19	0.3	779	11	BV063339 BV063339 S212P6040
c	621	19	0.3	791	6	AR271766 AR271766 Sequence
c	622	19	0.3	791	10	MMU75506 U75506 Mus musculu
	623	19	0.3	796	9	HSA340034 AJ340034 Homo sapi
	624	19	0.3	867	1	AB014978 AB014978 Pseudomon
	625	19	0.3	900	6	I41261 I41261 Sequence 1
	626	19	0.3	900	6	I61439 I61439 Sequence 1
	627	19	0.3	900	6	I72547 I72547 Sequence 1
	628	19	0.3	1100	10	AB056724 AB056724 Rattus no
	629	19	0.3	1157	8	EIN318591 AJ318591 Eleusine
	630	19	0.3	1170	8	CDA279036 AJ279036 Cynodon d
	631	19	0.3	1188	8	ETE318590 AJ318590 Eragrosti
	632	19	0.3	1188	8	MRE318585 AJ318585 Melinis r
	633	19	0.3	1188	8	PGE318584 AJ318584 Paspalidi
	634	19	0.3	1188	8	PMA318586 AJ318586 Panicum m
c	635	19	0.3	1236	6	AR320776 AR320776 Sequence
	636	19	0.3	1296	6	AX489396 AX489396 Sequence
	637	19	0.3	1340	8	AK121530 AK121530 Oryza sat
c	638	19	0.3	1370	3	AK115471 AK115471 Ciona int
	639	19	0.3	1413	10	AF182168 AF182168 Rattus no
	640	19	0.3	1467	6	AX698013 AX698013 Sequence
c	641	19	0.3	1477	1	EIN9981 AJ009981 Enterobac
	642	19	0.3	1515	4	SSIGFBPII2 U21118 Sus scrofa
	643	19	0.3	1562	10	BC025092 BC025092 Mus muscu
	644	19	0.3	1617	10	BC018162 BC018162 Mus muscu
	645	19	0.3	1689	10	BC034240 BC034240 Mus muscu
	646	19	0.3	1749	5	AB045224 AB045224 Gallus ga
	647	19	0.3	1763	10	MMU277454 AJ277454 Mus Muscu
c	648	19	0.3	1886	9	AF131827 AF131827 Homo sapi
c	649	19	0.3	1906	10	BC002031 BC002031 Mus muscu

c	650	19	0.3	1955	9	HSU04209 U04209 Human assoc
	651	19	0.3	1963	3	SGNAAL1 X55439 S. gregaria
c	652	19	0.3	1966	9	BC023557 BC023557 Homo sapi
c	653	19	0.3	1992	4	RABTCBCA1 M14577 Rabbit T-ce
	654	19	0.3	2000	6	AX656080 AX656080 Sequence
	655	19	0.3	2002	10	BC033315 BC033315 Mus muscu
c	656	19	0.3	2052	9	BC050742 BC050742 Homo sapi
	657	19	0.3	2072	3	AF145606 AF145606 Drosophil
	658	19	0.3	2170	10	AB100266 AB100266 Mus muscu
c	659	19	0.3	2238	4	RABNANUCOT M84020 Oryctolagus
c	660	19	0.3	2238	6	I11726 I11726 Sequence 1
	661	19	0.3	2304	10	RAT3AHSD M64393 Rat 3-alpha
	662	19	0.3	2345	10	AF077765 AF077765 Mus muscu
	663	19	0.3	2350	9	HUMPTHL1 M24348 Human parat
	664	19	0.3	2404	9	AK025131 AK025131 Homo sapi
	665	19	0.3	2414	6	BD127385 BD127385 Primer fo
	666	19	0.3	2414	9	AK074960 AK074960 Homo sapi
c	667	19	0.3	2444	6	AX713537 AX713537 Sequence
c	668	19	0.3	2444	9	AK055075 AK055075 Homo sapi
	669	19	0.3	2466	10	RATS3AD D17310 Rattus norv
	670	19	0.3	2477	6	AR410736 AR410736 Sequence
	671	19	0.3	2477	6	AX464198 AX464198 Sequence
	672	19	0.3	2477	6	AX697578 AX697578 Sequence
	673	19	0.3	2477	6	BD075507 BD075507 Secretory
	674	19	0.3	2477	6	BD172367 BD172367 Secreted
	675	19	0.3	2477	6	BD172686 BD172686 Secreted
	676	19	0.3	2477	6	BD173005 BD173005 Secreted
	677	19	0.3	2477	6	BD173324 BD173324 Secreted
	678	19	0.3	2477	6	BD175358 BD175358 Secretory
	679	19	0.3	2477	9	AY358496 AY358496 Homo sapi
c	680	19	0.3	2530	9	AK127587 AK127587 Homo sapi
c	681	19	0.3	2764	6	AX713968 AX713968 Sequence
c	682	19	0.3	2764	9	AK055937 AK055937 Homo sapi
	683	19	0.3	2886	8	AY251482 AY251482 Echinochl
	684	19	0.3	2942	6	AX833475 AX833475 Sequence
	685	19	0.3	2942	9	AK095247 AK095247 Homo sapi
	686	19	0.3	2997	6	AX713389 AX713389 Sequence
	687	19	0.3	2997	9	AK054713 AK054713 Homo sapi
	688	19	0.3	3458	6	AX714243 AX714243 Sequence
	689	19	0.3	3458	9	AK056454 AK056454 Homo sapi
	690	19	0.3	3671	6	AX074078 AX074078 Sequence
	691	19	0.3	3734	9	HSM807851 BX647705 Homo sapi
	692	19	0.3	3761	9	AB094095 AB094095 Homo sapi
	693	19	0.3	3844	10	MMNADPTRH Z49204 M.musculus
	694	19	0.3	4121	10	AK129006 AK129006 Mus muscu
	695	19	0.3	4142	10	BC008518 BC008518 Mus muscu
	696	19	0.3	4474	6	I58526 I58526 Sequence 9
	697	19	0.3	4474	6	I87001 I87001 Sequence 9
	698	19	0.3	4474	6	AX036110 AX036110 Sequence
	699	19	0.3	4784	10	AF249295 AF249295 Mus muscu
	700	19	0.3	4809	5	AF254792 AF254792 Danio rer
	701	19	0.3	5050	9	HUMCD43 M61827 Human leuko
	702	19	0.3	5295	10	BC060277 BC060277 Mus muscu
	703	19	0.3	5528	10	AK122377 AK122377 Mus muscu
	704	19	0.3	5693	10	BC036727 BC036727 Mus muscu
	705	19	0.3	5810	10	AB011534 AB011534 Rattus no
	706	19	0.3	5939	9	HSM806877 BX640787 Homo sapi
	707	19	0.3	6503	9	HSSIAL X52075 Human gene
	708	19	0.3	6647	9	HSM808937 BX648786 Homo sapi
	709	19	0.3	7161	9	AB011168 AB011168 Homo sapi
	710	19	0.3	7174	9	HSM804580 AL833267 Homo sapi
c	711	19	0.3	8388	9	HS17CTNS1 AF112441 Homo sapi
	712	19	0.3	9942	10	AF329470 AF329470 Rattus no
	713	19	0.3	10029	1	AE010387 AE010387 Methanopy
	714	19	0.3	10029	1	AE014485 AE014485 Brucella
c	715	19	0.3	10707	1	AE000099 AE000099 Rhizobium
	716	19	0.3	10708	10	RNITPR2R X61677 Rat ITPR2 g
c	717	19	0.3	11614	1	AE009582 AE009582 Brucella
c	718	19	0.3	11688	1	AE009454 AE009454 Brucella
c	719	19	0.3	12081	10	AL772229 AL772229 Mouse DNA
	720	19	0.3	12631	1	AE014357 AE014357 Brucella
	721	19	0.3	12938	1	AE012470 AE012470 Xanthomon
	722	19	0.3	14207	10	AF463762 AF463762 Mus muscu
c	723	19	0.3	14735	10	AF317901 AF317901 Mus muscu
	724	19	0.3	17042	1	AE006932 AE006932 Mycobacte
	725	19	0.3	18510	9	U72787 U72787 Homo sapien
c	726	19	0.3	20300	6	AX451337 AX451337 Sequence
c	727	19	0.3	22996	9	AC087175 AC087175 Homo sapi
c	728	19	0.3	26919	9	AP000335 AP000335 Homo sapi
c	729	19	0.3	27555	2	AC012903 AC012903 Drosophil
	730	19	0.3	28235	2	AC014089 AC014089 Drosophil
c	731	19	0.3	30310	6	AR271852 AR271852 Sequence
c	732	19	0.3	34010	1	RSPNGR234 Z68203 Rhizobium s
c	733	19	0.3	38192	9	BX530088 BX530088 Human DNA
	734	19	0.3	39730	1	MTCY8D5 Z92669 Mycobacteri
c	735	19	0.3	40806	1	MSGY140 AD000006 Mycobacte
	736	19	0.3	43385	9	BX537148 BX537148 Human DNA
	737	19	0.3	43557	2	AC147080 AC147080 Homo sapi
c	738	19	0.3	43567	2	AC102848 AC102848 Mus muscu
	739	19	0.3	45276	9	AL512654 AL512654 Human DNA
	740	19	0.3	46651	9	AC000404 AC000404 Genomic s
	741	19	0.3	47782	2	AC068445 AC068445 Homo sapi
	742	19	0.3	49850	2	AC139554 AC139554 Homo sapi
	743	19	0.3	51705	6	AX695614 AX695614 Sequence
c	744	19	0.3	53242	9	AL365494 AL365494 Human DNA
	745	19	0.3	55818	9	AC112228 AC112228 Homo sapi
c	746	19	0.3	58198	9	AC073524 AC073524 Homo sapi
c	747	19	0.3	60190	8	AP004786 AP004786 Oryza sat
	748	19	0.3	60196	6	AX697977 AX697977 Sequence
	749	19	0.3	62370	2	AL451008 AL451008 Homo sapi
c	750	19	0.3	62377	2	AL360009 AL360009 Homo sapi
c	751	19	0.3	62980	10	AL928702 AL928702 Mouse DNA
	752	19	0.3	63229	2	AC111184 AC111184 Homo sapi
c	753	19	0.3	63525	9	AC108463 AC108463 Homo sapi
c	754	19	0.3	63898	2	OSIG00045 AL732350 Oryza sat
	755	19	0.3	64513	2	AC101466 AC101466 Mus muscu
c	756	19	0.3	64513	2	AC101466 AC101466 Mus muscu
c	757	19	0.3	64824	2	AC067782 AC067782 Homo sapi
c	758	19	0.3	65796	2	AC124642 AC124642 Mus muscu
	759	19	0.3	67211	2	AC133284 AC133284 Mus muscu
c	760	19	0.3	67211	2	AC133284 AC133284 Mus muscu
	761	19	0.3	67718	2	AC135349 AC135349 Homo sapi
	762	19	0.3	68010	2	AC101197 AC101197 Mus muscu
c	763	19	0.3	68052	2	AC100691 AC100691 Mus muscu
	764	19	0.3	68417	2	AC040891 AC040891 Homo sapi
	765	19	0.3	69333	9	AC109778 AC109778 Homo sapi
c	766	19	0.3	69586	2	AC115076 AC115076 Mus muscu
c	767	19	0.3	70089	2	AC027491 AC027491 Homo sapi
c	768	19	0.3	70574	2	AC136312 AC136312 Homo sapi
	769	19	0.3	71517	9	AC073862 AC073862 Homo sapi
	770	19	0.3	74098	9	BS000067 BS000067 Pan trogl
	771	19	0.3	74530	2	AC108375 AC108375 Pan trogl
c	772	19	0.3	74687	10	AL683882 AL683882 Mouse DNA
c	773	19	0.3	77155	9	AC117478 AC117478 Homo sapi
	774	19	0.3	80627	2	AC027381 AC027381 Mus muscu
	775	19	0.3	80656	9	AC110616 AC110616 Homo sapi
c	776	19	0.3	81105	2	AC109046 AC109046 Rattus no
c	777	19	0.3	82179	2	AC100650 AC100650 Mus muscu
	778	19	0.3	82414	2	AC129265 AC129265 Rattus no
c	779	19	0.3	83433	2	AC137046 AC137046 Rattus no
	780	19	0.3	83989	9	AL603713 AL603713 Human DNA
c	781	19	0.3	84364	9	HS522J7 Z98885 Human DNA s
	782	19	0.3	85795	8	AP006090 AP006090 Lotus cor
c	783	19	0.3	86451	2	AC107037 AC107037 Pan trogl
	784	19	0.3	88499	9	AP001136 AP001136 Homo sapi
	785	19	0.3	88712	2	AC097315 AC097315 Mus muscu
	786	19	0.3	88823	9	AL713965 AL713965 Human DNA
	787	19	0.3	90100	2	AC104180 AC104180 Leishmani
	788	19	0.3	92799	2	AC135817 AC135817 Rattus no
	789	19	0.3	92956	2	AC138707 AC138707 Homo sapi
c	790	19	0.3	92956	2	AC138707 AC138707 Homo sapi
c	791	19	0.3	93280	9	AL159174 AL159174 Human DNA
	792	19	0.3	93393	4	AC104483 AC104483 Sus scrof
c	793	19	0.3	95108	2	AC127818 AC127818 Rattus no
c	794	19	0.3	95347	9	HSDJ81L22 AL109934 Human DNA
	795	19	0.3	95546	9	AC022816 AC022816 Homo sapi

c	796	19	0.3	96009	2	BX545853 BX545853 Mus muscu
c	797	19	0.3	99342	9	HS201D17 AL020990 Human DNA
c	798	19	0.3	100000	9	AP000215 AP000215 Homo sapi
	799	19	0.3	104309	9	AL391358 AL391358 Human DNA
	800	19	0.3	104663	10	AL732560 AL732560 Mouse DNA
c	801	19	0.3	105616	10	AL935134 AL935134 Mouse DNA
	802	19	0.3	107226	9	AC010618 AC010618 Homo sapi
	803	19	0.3	107413	4	AL773560 AL773560 Pig DNA s
c	804	19	0.3	107611	9	AC019221 AC019221 Homo sapi
c	805	19	0.3	108000	9	AP001180 AP001180 Homo sapi
c	806	19	0.3	109347	9	AL137157 AL137157 Human DNA
c	807	19	0.3	110000	2	AC009579_1 Continuation (2 of
c	808	19	0.3	110000	2	AC079517_1 Continuation (2 of
c	809	19	0.3	110000	2	AC096007_2 Continuation (3 of
	810	19	0.3	110000	2	AC096315_5 Continuation (6 of
c	811	19	0.3	110000	2	AC109940_0 AC109940 Rattus no
c	812	19	0.3	110000	2	AC111011_1 Continuation (2 of
c	813	19	0.3	110000	2	AC114711_1 Continuation (2 of
c	814	19	0.3	110000	2	AC116152_0 AC116152 Mus muscu
c	815	19	0.3	110000	2	AC117962_5 Continuation (6 of
	816	19	0.3	110000	2	AC119867_0 AC119867 Mus muscu
	817	19	0.3	110000	2	AC130075_1 Continuation (2 of
	818	19	0.3	110000	2	AC145312_2 Continuation (3 of
c	819	19	0.3	110000	2	AL354832_0 AL354832 Homo sapi
c	820	19	0.3	110000	2	AL954350_0 AL954350 Homo sapi
	821	19	0.3	110000	2	AL954350_3 Continuation (4 of
	822	19	0.3	111106	5	BX663531 BX663531 Chicken D
	823	19	0.3	113891	9	AC004797 AC004797 Homo sapi
c	824	19	0.3	115888	9	AC002468 AC002468 Human Chr
	825	19	0.3	116022	2	AL355533 AL355533 Homo sapi
	826	19	0.3	116311	9	AL360181 AL360181 Human DNA
	827	19	0.3	118495	9	AL590556 AL590556 Human DNA
	828	19	0.3	118593	9	HS288L1 Z82196 Human DNA s
	829	19	0.3	119066	2	AC026377 AC026377 Mus muscu
	830	19	0.3	119295	2	AC127427 AC127427 Magnaport
	831	19	0.3	120311	10	AC006945 AC006945 Mus muscu
c	832	19	0.3	120613	2	AC111401 AC111401 Rattus no
	833	19	0.3	123022	9	AC090717 AC090717 Homo sapi
	834	19	0.3	123159	2	HSAC000384 AC000384 Homo sapi
	835	19	0.3	123489	9	HSBA27F12 AL109914 Human DNA
	836	19	0.3	124289	9	AC010285 AC010285 Homo sapi
c	837	19	0.3	124392	9	AL136451 AL136451 Human DNA
c	838	19	0.3	126753	2	AF252826 AF252826 Homo sapi
	839	19	0.3	126894	9	AL157875 AL157875 Human DNA
	840	19	0.3	127431	9	AC027796 AC027796 Homo sapi
c	841	19	0.3	127544	9	CNS01RG4 AL157756 Human chr
c	842	19	0.3	127677	9	AC102945 AC102945 Homo sapi
c	843	19	0.3	127698	9	AC138028 AC138028 Homo sapi
c	844	19	0.3	128090	2	AC108372 AC108372 Pan trogl
	845	19	0.3	128608	10	AL928638 AL928638 Mouse DNA
c	846	19	0.3	129492	9	AC138466 AC138466 Homo sapi
	847	19	0.3	129506	2	AC136100 AC136100 Rattus no
c	848	19	0.3	130023	2	AC011843 AC011843 Homo sapi
c	849	19	0.3	131189	2	AC101756 AC101756 Mus muscu
c	850	19	0.3	131353	9	HS508I15 AL021707 Human DNA
	851	19	0.3	131888	9	HSJ1057D4 AL121777 Human DNA
	852	19	0.3	132150	9	AC005586 AC005586 Homo sapi
c	853	19	0.3	132336	2	AF215842 AF215842 Homo sapi
	854	19	0.3	132703	8	CNS08CBT AL928756 Oryza sat
	855	19	0.3	133455	2	AC145489 AC145489 Homo sapi
c	856	19	0.3	133898	2	AC143858 AC143858 Macaca mu
	857	19	0.3	134089	9	AC112917 AC112917 Homo sapi
	858	19	0.3	135039	9	AC006060 AC006060 Homo sapi
c	859	19	0.3	135554	2	AC116945 AC116945 Tetraodon
c	860	19	0.3	136579	9	HS998G20 AL035246 Human DNA
c	861	19	0.3	136778	2	AC108376 AC108376 Pan trogl
	862	19	0.3	136956	2	AC137338 AC137338 Rattus no
c	863	19	0.3	138242	10	AC122519 AC122519 Mus muscu
	864	19	0.3	138824	8	AC051633 AC051633 Oryza sat
	865	19	0.3	139376	9	AC020659 AC020659 Homo sapi
	866	19	0.3	139918	2	AC135564 AC135564 Oryza sat
c	867	19	0.3	141017	10	AC126444 AC126444 Mus muscu
	868	19	0.3	141079	9	HSA218C14 AL121894 Human DNA
	869	19	0.3	142114	8	AC073166 AC073166 Oryza sat
	870	19	0.3	142560	2	AC021906 AC021906 Homo sapi
	871	19	0.3	142777	10	AC006404 AC006404 Mus muscu
	872	19	0.3	142781	2	AC141934 AC141934 Rattus no
c	873	19	0.3	143165	2	AL591114 AL591114 Homo sapi
c	874	19	0.3	143278	5	AC140945 AC140945 Gallus ga
c	875	19	0.3	143805	9	HSDJ335E1 AL109920 Human DNA
c	876	19	0.3	144500	2	AC010231 AC010231 Homo sapi
c	877	19	0.3	144794	2	AP001182 AP001182 Homo sapi
c	878	19	0.3	145879	10	AL928915 AL928915 Mouse DNA
	879	19	0.3	145918	9	AC012307 AC012307 Homo sapi
	880	19	0.3	146153	3	AC007452 AC007452 Drosophil
	881	19	0.3	147555	2	AC142206 AC142206 Homo sapi
	882	19	0.3	147727	2	AC011950 AC011950 Homo sapi
c	883	19	0.3	147829	2	AC068806 AC068806 Mus muscu
c	884	19	0.3	149030	9	AC005375 AC005375 Homo sapi
c	885	19	0.3	149087	9	AL157826 AL157826 Human DNA
	886	19	0.3	149320	2	AC126357 AC126357 Homo sapi
	887	19	0.3	150206	8	OSJN00083 AL606668 Oryza sat
	888	19	0.3	151163	9	HSA305P22 AL121673 Human DNA
c	889	19	0.3	151839	2	AC102905 AC102905 Mus muscu
	890	19	0.3	151903	2	AC024349 AC024349 Homo sapi
c	891	19	0.3	152058	4	AC091756 AC091756 Sus scrof
c	892	19	0.3	152209	2	AL591023 AL591023 Homo sapi
	893	19	0.3	152246	9	AC023473 AC023473 Homo sapi
c	894	19	0.3	152464	2	AC109229 AC109229 Mus muscu
c	895	19	0.3	152827	2	AC143347 AC143347 Homo sapi
c	896	19	0.3	153021	10	AL663042 AL663042 Mouse DNA
	897	19	0.3	153154	2	AC117770 AC117770 Mus muscu
	898	19	0.3	153588	2	AC145282 AC145282 Silurana
c	899	19	0.3	153723	9	AC074101 AC074101 Homo sapi
c	900	19	0.3	154262	2	AC127629 AC127629 Rattus no
	901	19	0.3	154379	2	BX255900 BX255900 Danio rer
	902	19	0.3	154983	9	AC018866 AC018866 Homo sapi
	903	19	0.3	154997	2	AC143903 AC143903 Macaca mu
	904	19	0.3	155021	9	AC007159 AC007159 Homo sapi
c	905	19	0.3	155278	9	HSDJ655C4 AL080286 Human DNA
	906	19	0.3	155345	9	AC137627 AC137627 Homo sapi
c	907	19	0.3	155382	9	AC127520 AC127520 Homo sapi
	908	19	0.3	155663	9	AC092048 AC092048 Homo sapi
c	909	19	0.3	155670	3	AC012097 AC012097 Drosophil
c	910	19	0.3	155680	9	AL390205 AL390205 Human DNA
	911	19	0.3	155824	2	AC087296 AC087296 Homo sapi
c	912	19	0.3	156122	2	AC127546 AC127546 Mus muscu
c	913	19	0.3	156264	9	AC103921 AC103921 Homo sapi
	914	19	0.3	156339	2	AC132073 AC132073 Bos tauru
c	915	19	0.3	157063	10	AL928950 AL928950 Mouse DNA
	916	19	0.3	157340	2	AC015652 AC015652 Homo sapi
c	917	19	0.3	157519	5	AL929204 AL929204 Zebrafish
	918	19	0.3	157530	9	AC146347 AC146347 Pan trogl
	919	19	0.3	157631	2	AC130421 AC130421 Homo sapi
	920	19	0.3	157654	2	AC091791 AC091791 Sus scrof
	921	19	0.3	157964	2	AC134625 AC134625 Rattus no
	922	19	0.3	158041	2	AC140688 AC140688 Rattus no
c	923	19	0.3	158156	2	AL357393 AL357393 Homo sapi
c	924	19	0.3	158274	2	AC013592 AC013592 Homo sapi
c	925	19	0.3	158307	10	AL592112 AL592112 Mouse DNA
c	926	19	0.3	158338	2	AC024720 AC024720 Homo sapi
	927	19	0.3	158449	2	AC115869 AC115869 Mus muscu
	928	19	0.3	158510	9	AC079090 AC079090 Homo sapi
	929	19	0.3	158920	2	AC135955 AC135955 Canis fam
	930	19	0.3	158976	2	AC117771 AC117771 Mus muscu
	931	19	0.3	159065	3	AC091634 AC091634 Drosophil
c	932	19	0.3	159266	2	AC026097 AC026097 Homo sapi
	933	19	0.3	159397	2	AC027040 AC027040 Homo sapi
c	934	19	0.3	159599	2	AC142212 AC142212 Mus muscu
	935	19	0.3	159720	9	AC068716 AC068716 Homo sapi
c	936	19	0.3	159902	9	AC025571 AC025571 Homo sapi
c	937	19	0.3	159983	2	AC013713 AC013713 Homo sapi
c	938	19	0.3	160074	9	AC105361 AC105361 Homo sapi
c	939	19	0.3	160109	9	AL161727 AL161727 Human DNA
c	940	19	0.3	160396	9	AC107421 AC107421 Homo sapi
	941	19	0.3	160429	2	AC136950 AC136950 Homo sapi

c 942	19	0.3	160452	9	AC110607	AC110607 Homo sapi
c 943	19	0.3	160677	2	AC125266	AC125266 Mus muscu
944	19	0.3	160785	10	AC009287	AC009287 Mus muscu
c 945	19	0.3	161025	2	AC101976	AC101976 Mus muscu
946	19	0.3	161181	2	AC116868	AC116868 Mus muscu
947	19	0.3	161218	9	AC011501	AC011501 Homo sapi
c 948	19	0.3	161223	2	AC124011	AC124011 Mus muscu
c 949	19	0.3	161251	2	AC147284	AC147284 Pan trogl
c 950	19	0.3	161309	9	AC100839	AC100839 Homo sapi
c 951	19	0.3	161508	2	AC092088	AC092088 Canis fam
952	19	0.3	161826	2	AC026157	AC026157 Homo sapi
953	19	0.3	162172	8	AC140026	AC140026 Medicago
c 954	19	0.3	162213	2	AC061981	AC061981 Homo sapi
955	19	0.3	162377	2	AC142205	AC142205 Homo sapi
956	19	0.3	162471	9	AC067945	AC067945 Homo sapi
957	19	0.3	162573	10	AC125121	AC125121 Mus muscu
958	19	0.3	162877	9	AC018509	AC018509 Homo sapi
c 959	19	0.3	163073	2	AC118746	AC118746 Mus muscu
960	19	0.3	163108	8	AC137921	AC137921 Oryza sat
c 961	19	0.3	163283	9	AL355606	AL355606 Human DNA
962	19	0.3	163377	9	AC087714	AC087714 Homo sapi
963	19	0.3	164014	10	AC138116	AC138116 Mus muscu
964	19	0.3	164123	9	AL360078	AL360078 Human DNA
965	19	0.3	164224	2	AC122791	AC122791 Mus muscu
c 966	19	0.3	164515	2	AC120298	AC120298 Rattus no
967	19	0.3	164692	10	AC127586	AC127586 Mus muscu
968	19	0.3	164831	9	AL590406	AL590406 Human DNA
969	19	0.3	165018	9	AC079173	AC079173 Homo sapi
c 970	19	0.3	165329	9	AL583850	AL583850 Human DNA
c 971	19	0.3	165447	9	AC027575	AC027575 Homo sapi
c 972	19	0.3	166019	2	AC015648	AC015648 Homo sapi
c 973	19	0.3	166296	2	AC102929	AC102929 Mus muscu
974	19	0.3	166326	2	AC101741	AC101741 Mus muscu
c 975	19	0.3	166335	2	AC010313	AC010313 Homo sapi
c 976	19	0.3	166338	9	AC026165	AC026165 Homo sapi
977	19	0.3	166847	9	AC008393	AC008393 Homo sapi
978	19	0.3	166973	9	AL451049	AL451049 Human DNA
979	19	0.3	167205	2	AC023871	AC023871 Homo sapi
c 980	19	0.3	167273	10	AC083894	AC083894 Mus muscu
981	19	0.3	167794	2	AC146591	AC146591 Callithri
c 982	19	0.3	167852	9	AC072061	AC072061 Homo sapi
983	19	0.3	168030	2	AC091462	AC091462 Mus muscu
c 984	19	0.3	168133	2	AC140997	AC140997 Rattus no
c 985	19	0.3	168413	2	AC009877	AC009877 Homo sapi
986	19	0.3	168432	10	AC133574	AC133574 Mus muscu
c 987	19	0.3	168558	2	BX322549	BX322549 Danio rer
988	19	0.3	168712	10	AC126929	AC126929 Mus muscu
c 989	19	0.3	168857	2	AC021591	AC021591 Homo sapi
990	19	0.3	169010	10	AL672260	AL672260 Mouse DNA
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c 992	19	0.3	169184	9	AC022398	AC022398 Homo sapi
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ALIGNMENTS

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AX503782
LOCUS AX503782 5691 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 12 from Patent WO0226826.
ACCESSION AX503782
VERSION AX503782.1 GI:23385966
KEYWORDS .
SOURCE Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gerlach,V.L., Macdougall,J.R., Smithson,G., Millet,I., Stone,D., Gunther,E., Ellerman,K., Grosse,W.M., Alsobrook,J.P., Lepley,D.M., Burgess,C.E., Padigaru,M., Kekuda,R., Spytek,K.A., Leach,M.D. and Shimkets,R.A.
TITLE Proteins and nucleic acids encoding same
JOURNAL Patent: WO 0226826-A 12 04-APR-2002;
Curagen Corporation (US)
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ORIGIN

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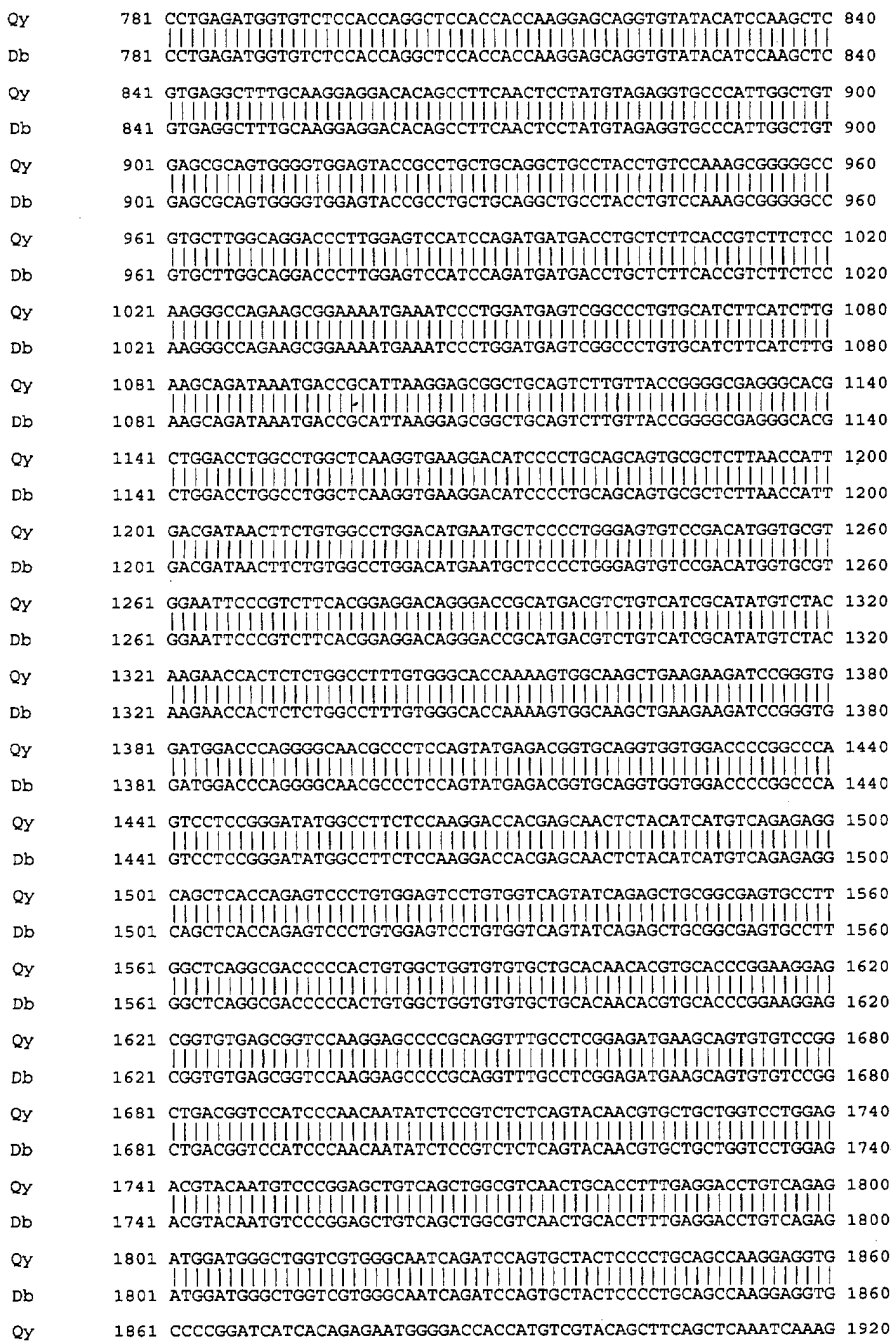
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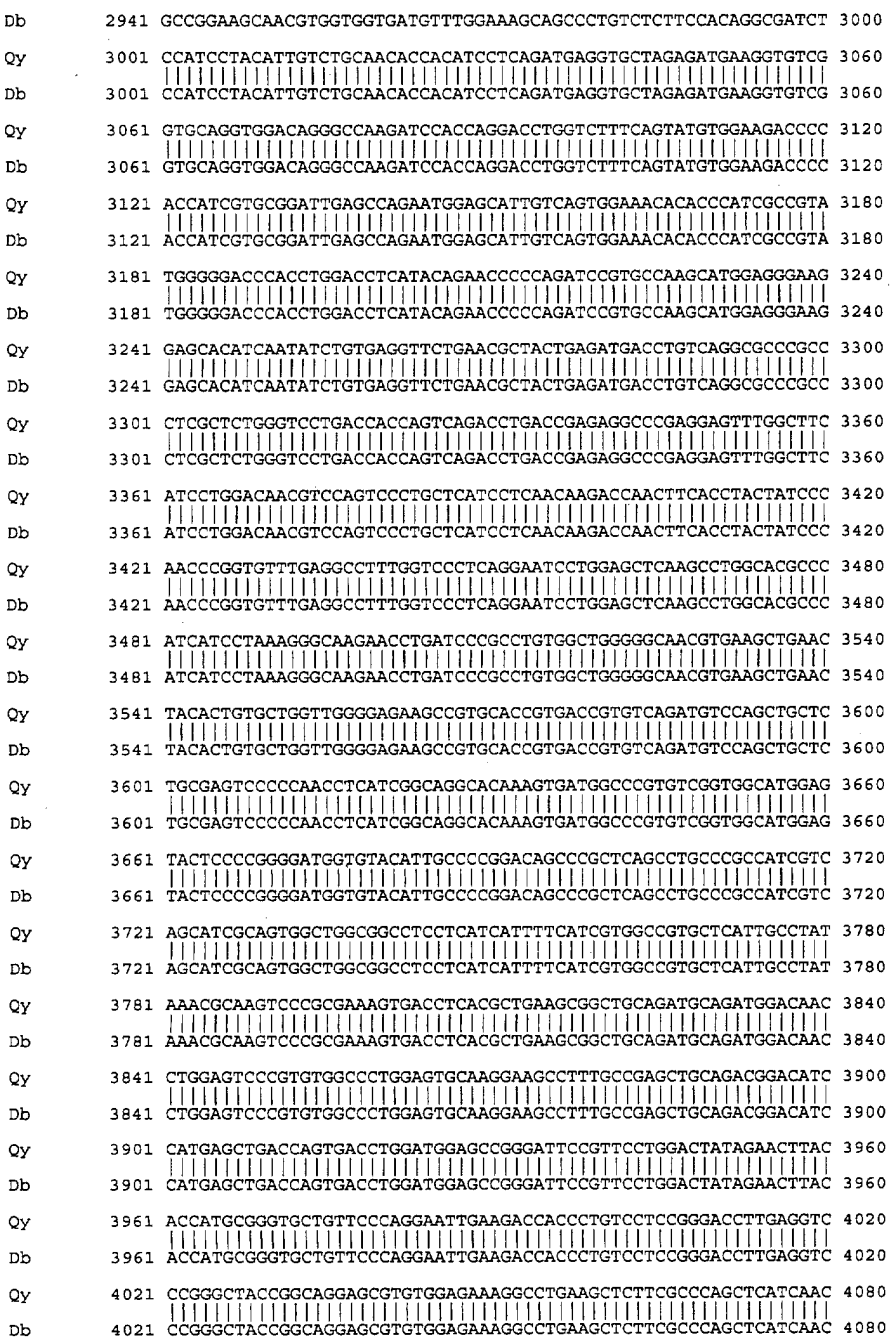
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ACCESSION AX492982
VERSION AX492982.1 GI:23338637
KEYWORDS .
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1
AUTHORS Kallick,D.A., Lee,S., Xu,Y., Yao,M.G., Yue,H., Bandman,O.B.,
Burford,N., Gandhi,A.R., Graul,R.C., Lal,P.G., Lu,D.A., Lu,Y.,
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Ramkumar,J., Walia,N.K. and Warren,B.A.
TITLE Cell adhesion proteins
JOURNAL Patent: WO 02059312-A 19 01-AUG-2002;
INCYTE GENOMICS INC (US)
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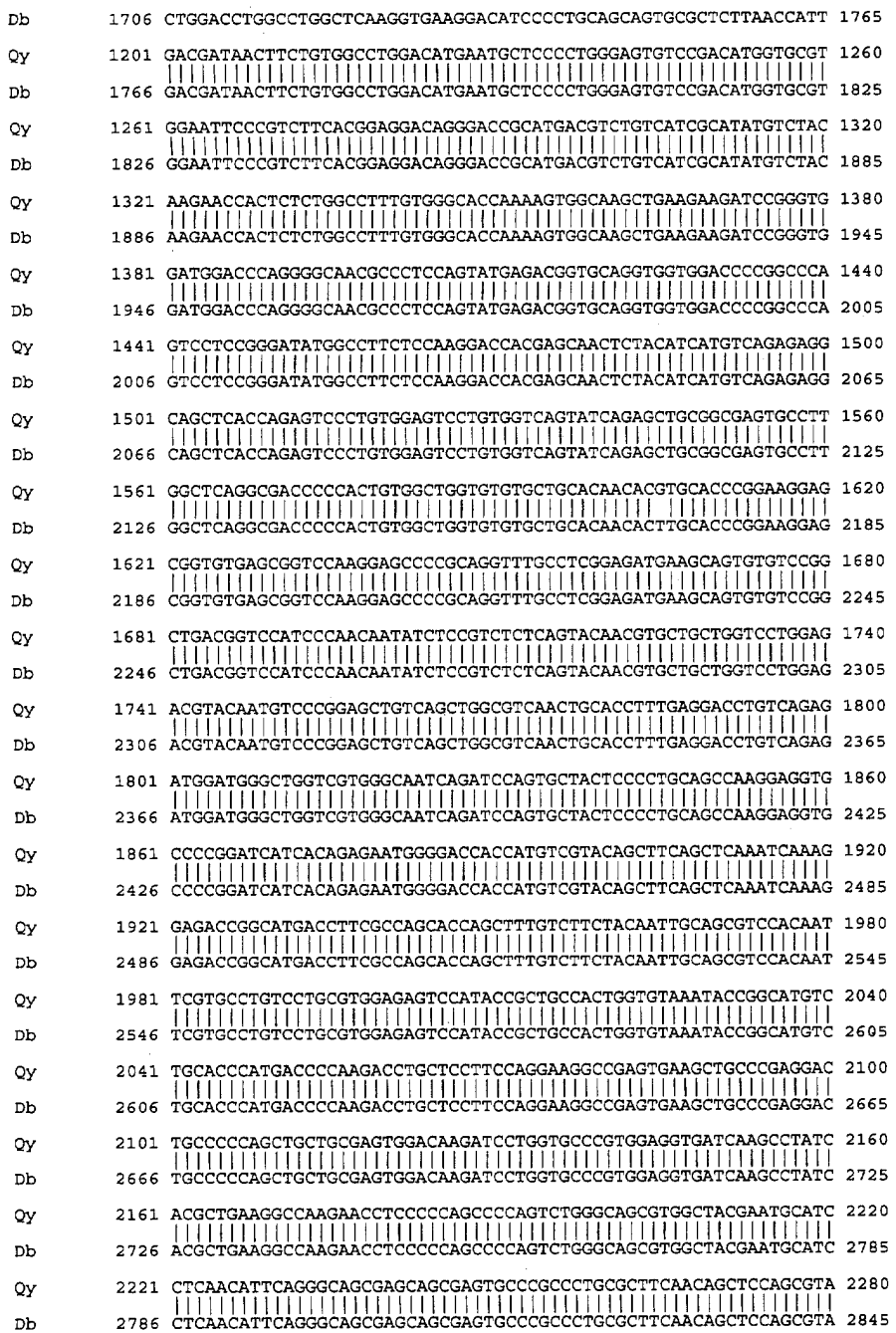
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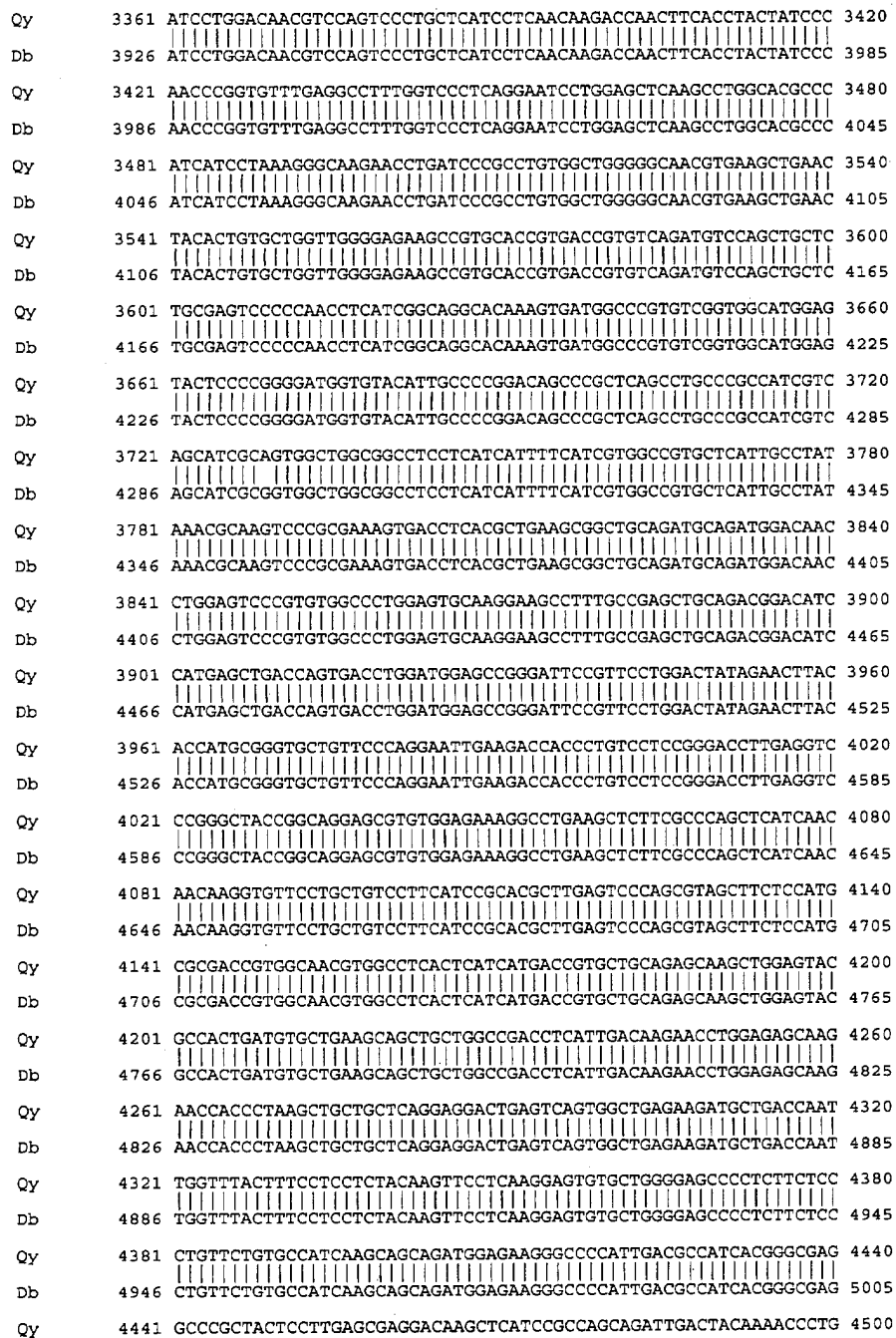
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Qy       5641 TACAAACTAGAACAAGTCATAACCCTCATGAGCTTAGACAGCTGA 5685
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RESULT 3
AB046770
LOCUS       AB046770                5986 bp    mRNA    linear   PRI 10-MAY-2002
DEFINITION  Homo sapiens mRNA for KIAA1550 protein, partial cds.
ACCESSION   AB046770
VERSION     AB046770.2  GI:20521937
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Nagase,T., Kikuno,R., Nakayama,M., Hirosawa,M. and Ohara,O.
  TITLE     Prediction of the coding sequences of unidentified human genes.
            XVIII. The complete sequences of 100 new cDNA clones from brain
            which code for large proteins in vitro
  JOURNAL   DNA Res. 7 (4), 273-281 (2000)
  MEDLINE   20450683
   PUBMED   10997877
REFERENCE   2  (bases 1 to 5986)
  AUTHORS   Ohara,O., Nagase,T. and Kikuno,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-AUG-2000) Osamu Ohara, Kazusa DNA Research Institute,
            Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba
            292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
            URL:http://www.kazusa.or.jp/huge, Tel:81-438-52-3913,
            Fax:81-438-52-3914)
COMMENT     On May 9, 2002 this sequence version replaced gi:10047164.
FEATURES             Location/Qualifiers
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                     /note="This sequence was obtained by subcloning of the DNA
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                     PVAGGNVKLNYTVLVGEKPCTVTVSDVQLLCESPNLIGRHKVMARVGGMEYSPGMVYI
                     APDSPLSLPAIVSIAVAGGLLIIFIVAVLIAYKRKSRESDLTLKRLQMQMDNLESRVA
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ORIGIN

  Query Match           39.3%;  Score 2237;  DB 9;  Length 5986;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2237;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 GGAGCCCCGCAGGTTTGCCTCGGAGATGAAGCAGTGTGTCCGGCTGACGGTCCATCCCAA 60

Qy       1698 CAATATCTCCGTCTCTCAGTACAACGTGCTGCTGGTCCTGGAGACGTACAATGTCCCGGA 1757
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Db         61 CAATATCTCCGTCTCTCAGTACAACGTGCTGCTGGTCCTGGAGACGTACAATGTCCCGGA 120

Qy       1758 GCTGTCAGCTGGCGTCAACTGCACCTTTGAGGACCTGTCAGAGATGGATGGGCTGGTCGT 1817
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Qy       1878 GAATGGGGACCACCATGTCGTACAGCTTCAGCTCAAATCAAAGGAGACCGGCATGACCTT 1937
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Qy       1998 GGAGAGTCCATACCGCTGCCACTGGTGTAAATACCGGCATGTCTGCACCCATGACCCCAA 2057
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Qy       2058 GACCTGCTCCTTCCAGGAAGGCCGAGTGAAGCTGCCCGAGGACTGCCCCCAGCTGCTGCG 2117
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Qy       2118 AGTGGACAAGATCCTGGTGCCCGTGGAGGTGATCAAGCCTATCACGCTGAAGGCCAAGAA 2177
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Db        481 AGTGGACAAGATCCTGGTGCCCGTGGAGGTGATCAAGCCTATCACGCTGAAGGCCAAGAA 540

Qy       2178 CCTCCCCCAGCCCCAGTCTGGGCAGCGTGGCTACGAATGCATCCTCAACATTCAGGGCAG 2237
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Db        541 CCTCCCCCAGCCCCAGTCTGGGCAGCGTGGCTACGAATGCATCCTCAACATTCAGGGCAG 600

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Qy       2358 TGGGCACTTCAACATTGACAACCCAGCTCAGAATAAAGTTCACCTCTACAAGTGTGGAGC 2417
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Db        721 TGGGCACTTCAACATTGACAACCCAGCTCAGAATAAAGTTCACCTCTACAAGTGTGGAGC 780

Qy       2418 CATGCGTGAGAGCTGCGGGCTGTGCCTCAAGGCTGACCCAGACTTCGCATGTGGCTGGTG 2477
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Db        781 CATGCGTGAGAGCTGCGGGCTGTGCCTCAAGGCTGACCCAGACTTCGCATGTGGCTGGTG 840

Qy       2478 CCAGGGCCCAGGCCAGTGCACCCTGCGCCAGCACTGCCCTGCCCAGGAGAGCCAGTGGCT 2537
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCAGGGCCCAGGCCAGTGCACCCTGCGCCAGCACTGCCCTGCCCAGGAGAGCCAGTGGCT 900

Qy       2538 GGAGCTGTCTGGTGCCAAAAGCAAGTGCACAAACCCCCGCATCACAGAGATAATCCCGGT 2597
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Qy       2598 GACAGGCCCCCGGGAAGGGGGCACCAAGGTCACTATCCGAGGGGAGAACCTGGGCCTGGA 2657
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Db        961 GACAGGCCCCCGGGAAGGGGGCACCAAGGTCACTATCCGAGGGGAGAACCTGGGCCTGGA 1020

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Qy       2718 TGGTTACATCCCTGCAGAACAGATCGTGTGTGAGATGGGGGAGGCCAAGCCCAGCCAGCA 2777

Db       1081 TGGTTACATCCCTGCAGAACAGATCGTGTGTGAGATGGGGGAGGCCAAGCCCAGCCAGCA 1140

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Qy       3618 CATCGGCAGGCACAAAGTGATGGCCCGTGTCGGTGGCATGGAGTACTCCCCGGGGATGGT 3677

Db       1981 CATCGGCAGGCACAAAGTGATGGCCCGTGTCGGTGGCATGGAGTACTCCCCGGGGATGGT 2040

Qy       3678 GTACATTGCCCCGGACAGCCCGCTCAGCCTGCCCGCCATCGTCAGCATCGCAGTGGCTGG 3737

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Qy       3738 CGGCCTCCTCATCATTTTCATCGTGGCCGTGCTCATTGCCTATAAACGCAAGTCCCGCGA 3797

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Qy       3798 AAGTGACCTCACGCTGAAGCGGCTGCAGATGCAGATGGACAACCTGGAGTCCCGTGTGGC 3857

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Db       2221 CCTGGAGTGCAAGGAAG 2237
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RESULT 4
BC028744

LOCUS	BC028744 2015 bp mRNA linear PRI 08-OCT-2003
DEFINITION	Homo sapiens hypothetical protein DKFZp434G0625, mRNA (cDNA clone MGC:34033 IMAGE:4828816), complete cds.
ACCESSION	BC028744
VERSION	BC028744.2 GI:34190713
KEYWORDS	MGC.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 2015)
AUTHORS	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE	22388257
PUBMED	12477932
REFERENCE	2 (bases 1 to 2015)
AUTHORS	Strausberg,R.
TITLE	Direct Submission
JOURNAL	Submitted (29-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	On Aug 25, 2003 this sequence version replaced gi:22382104. Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN) cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org contact: amadan@systemsbiology.org Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting Clone distribution: MGC clone distribution information can be found

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          through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
          Series: IRAK Plate: 47 Row: b Column: 11.
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ORIGIN

  Query Match             24.1%;  Score 1371;  DB 9;  Length 2015;
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  Matches 1371;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAAAGCCATGCCCTGGAACTGGACCTGCCTTCTCTCCCACCTCCTCATGGTGGGCATG 60
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Db        378 ATGAAAGCCATGCCCTGGAACTGGACCTGCCTTCTCTCCCACCTCCTCATGGTGGGCATG 437

Qy         61 GGCTCCTCCACTTTGCTCACCCGGCAGCCAGCCCCGCTGTCCCAGAAGCAGCGGTCATTT 120
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Qy        121 GTCACATTCCGAGGAGAGCCCGCCGAGGGTTTCAATCACCTGGTGGTGGATGAGAGGACA 180
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Qy        181 GGACACATTTACTTGGGGGCCGTCAATCGGATTTACAAGCTCTCCAGCGACCTGAAGGTC 240
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Qy        241 TTGGTGACGCATGAGACAGGGCCGGACGAGGACAACCCCAAGTGTTACCCACCCCGCATC 300
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Qy        901 GAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGCCTACCTGTCCAAAGCGGGGGCC 960
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Db       1278 GAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGCCTACCTGTCCAAAGCGGGGGCC 1337

Qy        961 GTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGACCTGCTCTTCACCGTCTTCTCC 1020
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Qy       1021 AAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTCGGCCCTGTGCATCTTCATCTTG 1080
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Qy       1081 AAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTCTTGTTACCGGGGCGAGGGCACG 1140
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Qy       1141 CTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTGCAGCAGTGCGCTCTTAACCATT 1200
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Qy       1201 GACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCTGGGAGTGTCCGACATGGTGCGT 1260
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Db       1578 GACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCTGGGAGTGTCCGACATGGTGCGT 1637

Qy       1261 GGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGACGTCTGTCATCGCATATGTCTAC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1638 GGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGACGTCTGTCATCGCATATGTCTAC 1697

Qy       1321 AAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGGCAAGCTGAAGAAG 1371
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Db       1698 AAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGGCAAGCTGAAGAAG 1748


RESULT 5
AK123428
LOCUS       AK123428               3310 bp    mRNA    linear   PRI 09-SEP-2003
DEFINITION  Homo sapiens cDNA FLJ41434 fis, clone BRHIP2007616, moderately
            similar to Plexin 2.
ACCESSION   AK123428
VERSION     AK123428.1  GI:34528974
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
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  AUTHORS   Kawakami,B., Sugiyama,A., Takemoto,M., Sugiyama,T., Irie,R.,
            Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y.,
            Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H.,
            Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K.,
            Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
            Oshima,A., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K.
            and Isogai,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3310)
  AUTHORS   Isogai,T. and Yamamoto,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JUL-2003) Takao Isogai, FLJ Project(HRI Team); 2-6-7
            Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
            HRI, and Biotechnology Center, National Institute of Technology and
            Evaluation; clone selection for full insert sequencing: HRI and
            RAB; annotation: HRI and RAB.
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                     /tissue_type="hippocampus"
                     /clone_lib="BRHIP2"
                     /note="cloning vector: pME18SFL3"
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                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="BAC85615.1"
                     /db_xref="GI:34528975"
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                     SGVNESGSVFGVIVSYSNLDDKLFIATAVDGKPEYFPTISSRKLTKNSEADGMFAYVF
                     HDEFVASMIKIPSDTFTIIPDFDIYYVYGFSSGNFVYFLTLQPEMVSPPGSTTKEQVY
                     TSKLVRLCKEDTAFNSYVEVPIGCERSGVEYRLLQAAYLSKAGAVLGRTLGVHPDDDL
                     LFTVFSKGQKRKMKSLDESALCIFILKQINDRIKERLQSCYRGEGTLDLAWLKVKDIP
                     CSSALLTIDDNFCGLDMNAPLGVSDMVRGIPVFTEDRDRMTSVIAYVYKNHSLAFVGT
                     KSGKLKKVPGTSLCPTLELQTGPRSHRATVTLELLFSSCSSN"
ORIGIN

  Query Match             24.1%;  Score 1371;  DB 9;  Length 3310;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1371;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        136 ATGAAAGCCATGCCCTGGAACTGGACCTGCCTTCTCTCCCACCTCCTCATGGTGGGCATG 195

Qy         61 GGCTCCTCCACTTTGCTCACCCGGCAGCCAGCCCCGCTGTCCCAGAAGCAGCGGTCATTT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 GGCTCCTCCACTTTGCTCACCCGGCAGCCAGCCCCGCTGTCCCAGAAGCAGCGGTCATTT 255

Qy        121 GTCACATTCCGAGGAGAGCCCGCCGAGGGTTTCAATCACCTGGTGGTGGATGAGAGGACA 180
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Db        256 GTCACATTCCGAGGAGAGCCCGCCGAGGGTTTCAATCACCTGGTGGTGGATGAGAGGACA 315

Qy        181 GGACACATTTACTTGGGGGCCGTCAATCGGATTTACAAGCTCTCCAGCGACCTGAAGGTC 240
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Db        316 GGACACATTTACTTGGGGGCCGTCAATCGGATTTACAAGCTCTCCAGCGACCTGAAGGTC 375

Qy        241 TTGGTGACGCATGAGACAGGGCCGGACGAGGACAACCCCAAGTGTTACCCACCCCGCATC 300
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Qy        301 GTCCAGACCTGCAATGAGCCCCTGACCACCACCAACAATGTCAACAAGATGCTCCTCATA 360
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Qy        361 GACTACAAGGAGAACAGGCTGATTGCCTGTGGGAGCCTGTACCAAGGCATCTGCAAGCTG 420
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Db        496 GACTACAAGGAGAACAGGCTGATTGCCTGTGGGAGCCTGTACCAAGGCATCTGCAAGCTG 555

Qy        421 CTGAGGCTGGAGGACCTCTTCAAGCTGGGGGAGCCTTATCATAAGAAGGAGCACTATCTG 480
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Db        556 CTGAGGCTGGAGGACCTCTTCAAGCTGGGGGAGCCTTATCATAAGAAGGAGCACTATCTG 615

Qy        481 TCAGGTGTCAACGAGAGCGGCTCAGTCTTTGGAGTGATCGTCTCCTACAGCAACCTGGAT 540
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Db        616 TCAGGTGTCAACGAGAGCGGCTCAGTCTTTGGAGTGATCGTCTCCTACAGCAACCTGGAT 675

Qy        541 GACAAGCTGTTCATTGCCACGGCAGTGGATGGGAAGCCCGAGTATTTTCCCACCATCTCC 600
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Qy        661 GAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACACCTTCACCATCATCCCTGACTTT 720
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Db        856 GATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTTTGTCTACTTTTTGACCCTCCAA 915

Qy        781 CCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGAGCAGGTGTATACATCCAAGCTC 840
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Db        976 GTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTATGTAGAGGTGCCCATTGGCTGT 1035

Qy        901 GAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGCCTACCTGTCCAAAGCGGGGGCC 960
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Qy       1021 AAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTCGGCCCTGTGCATCTTCATCTTG 1080
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Qy       1081 AAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTCTTGTTACCGGGGCGAGGGCACG 1140
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Db       1216 AAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTCTTGTTACCGGGGCGAGGGCACG 1275

Qy       1141 CTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTGCAGCAGTGCGCTCTTAACCATT 1200
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Qy       1261 GGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGACGTCTGTCATCGCATATGTCTAC 1320
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Qy       1321 AAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGGCAAGCTGAAGAAG 1371
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RESULT 6
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AC009785/c
LOCUS       AC009785              179145 bp    DNA     linear   PRI 26-MAY-2002
DEFINITION  Homo sapiens chromosome 7 clone RP11-198E23, complete sequence.
ACCESSION   AC009785
VERSION     AC009785.8  GI:21217401
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 179145)
  AUTHORS   Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
            Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.
            and Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 179145)
  AUTHORS   Bubb,K.L., Desmarais,C.L., Ramsey,S.A. and Hubley,R.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-SEP-1999) Human Genome Center, University of
            Washington, Box 352145, Seattle, WA 98195, USA
REFERENCE   3  (bases 1 to 179145)
  AUTHORS   Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Raymond,C.,
            Clendenning,J., Ivey,R.G. and Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUN-2001) Genome Center, University of Washington,
            Box 352145, Seattle, WA 98195, USA
REFERENCE   4  (bases 1 to 179145)
  AUTHORS   Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
            Saenphimmachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-APR-2002) Genome Center, University of Washington,
            Box 352145, Seattle, WA 98195, USA
REFERENCE   5  (bases 1 to 179145)
  AUTHORS   Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
            Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.
            and Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAY-2002) Genome Center, University of Washington,
            Box 352145, Seattle, WA 98195, USA
COMMENT     On May 26, 2002 this sequence version replaced gi:20066281.
            -------------- Genome Center
                Center: University of Washington Genome Center
                Center Code: UWGC
                Web site: http://www.genome.washington.edu
                Contact: uwgchtgs@u.washington.edu
            -------------- Project Information
                Center project name: chr-7
                Center clone name: RP11-198E23 (djs380)
            ------------- Summary Statistics
                Sequencing vector: plasmid; X52328; 100% of reads
                Chemistry: Dye-terminator Big Dye; 100% of reads
                Assembly program: Phrap; version 0.990319
                Consensus quality: 178850 bases at least Q40
                Consensus quality: 179053 bases at least Q30
                Consensus quality: 179141 bases at least Q20
                Insert size: 179145; sum-of-contigs
                Quality coverage: 11.8x in Q20 bases; sum-of-contigs
            --------------.
            Overlapping Sequences:
                5':  RP11-341C17 (UWGC:djs301) AC011625 73322-bp overlap
                3':  RP11-335B7 (UWGC:djs542) AC026239 38206-bp overlap
            --------------------
            Sequence Quality Assessment:
             This entry has been annotated with sequence quality
             estimates computed by the Phrap assembly program.
             All manually edited bases have been reduced to quality zero.
             Quality levels above 40 are expected to have less than
             1 error in 10,000 bp.
             Base-by-base quality values are not generally visible from the
             GenBank flat file format but are available as part
             of this entry's ASN.1 file.
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

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1854	1895	449	<800	6918	7002
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658	<800	7224	7291	2089	2069
26398	26593	1005	1033	550	<800
537	<800	1020	1033	4191	4187
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1928	2045	2237	2276	629	<800
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6707	6816	6349	6347	18266	18041
1884	1895	6669	6652	3099	3165
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13944	13827	5398	5641	2425	2425
4275	4287	599	<800	3767	3773
2057	2209	4055	4127	1506	1485
2293	2209	299	<800	3639	3773
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9916	9943	6964	6903	6894	7002
7673	7645	5766	5641	11819	11807

115	<800	4281	4127	837	821
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1071	1096	1032	1033	3280	3312
18341	18612	1591	1546	3780	3773
7618	7645	955	954	623	<800
1733	1700	330	<800	202	<800
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7616	7645	6261	6347	10775	10621
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19080	18612	3869	3877	9445	9461
114	<800	4148	4127	1694	1646
7	<800	3828	3877	3745	3773
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		1561	1546	9893	9817
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		4960	4943	998	1011
		9109	8931	1318	1283
		929	954	94	<800
		7844	7901	796	821
		535	<800	111	<800
		5397	5408	1029	1011
		1905	1916	1491	1485
		113	<800	20564	20918
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		750	735		
		1264	1248		

FEATURES Location/Qualifiers
source 1. .179145
/organism="Homo sapiens"

Query Match 20.9%; Score 1188; DB 9; Length 179145;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        1 ATGAAAGCCATGCCCTGGAACTGGACCTGCCTTCTCTCCCACCTCCTCATGGTGGGCATG 60
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Db    61796 ATGAAAGCCATGCCCTGGAACTGGACCTGCCTTCTCTCCCACCTCCTCATGGTGGGCATG 61737

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Db    61556 TTGGTGACGCATGAGACAGGGCCGGACGAGGACAACCCCAAGTGTTACCCACCCCGCATC 61497

Qy      301 GTCCAGACCTGCAATGAGCCCCTGACCACCACCAACAATGTCAACAAGATGCTCCTCATA 360
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Db    61496 GTCCAGACCTGCAATGAGCCCCTGACCACCACCAACAATGTCAACAAGATGCTCCTCATA 61437

Qy      361 GACTACAAGGAGAACAGGCTGATTGCCTGTGGGAGCCTGTACCAAGGCATCTGCAAGCTG 420
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Qy      421 CTGAGGCTGGAGGACCTCTTCAAGCTGGGGGAGCCTTATCATAAGAAGGAGCACTATCTG 480
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Db    61376 CTGAGGCTGGAGGACCTCTTCAAGCTGGGGGAGCCTTATCATAAGAAGGAGCACTATCTG 61317

Qy      481 TCAGGTGTCAACGAGAGCGGCTCAGTCTTTGGAGTGATCGTCTCCTACAGCAACCTGGAT 540
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Db    61316 TCAGGTGTCAACGAGAGCGGCTCAGTCTTTGGAGTGATCGTCTCCTACAGCAACCTGGAT 61257

Qy      541 GACAAGCTGTTCATTGCCACGGCAGTGGATGGGAAGCCCGAGTATTTTCCCACCATCTCC 600
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Qy      601 AGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCATGTTCGCGTACGTCTTCCATGAT 660
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Db    61196 AGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCATGTTCGCGTACGTCTTCCATGAT 61137

Qy      661 GAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACACCTTCACCATCATCCCTGACTTT 720
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Db    61136 GAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACACCTTCACCATCATCCCTGACTTT 61077

Qy      721 GATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTTTGTCTACTTTTTGACCCTCCAA 780
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Db    61076 GATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTTTGTCTACTTTTTGACCCTCCAA 61017

Qy      781 CCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGAGCAGGTGTATACATCCAAGCTC 840
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Db    61016 CCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGAGCAGGTGTATACATCCAAGCTC 60957

Qy      841 GTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTATGTAGAGGTGCCCATTGGCTGT 900
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Qy      901 GAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGCCTACCTGTCCAAAGCGGGGGCC 960
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Qy     1081 AAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTCTTGTTACCGGGGCGAGGGCACG 1140
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Db    60716 AAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTCTTGTTACCGGGGCGAGGGCACG 60657

Qy     1141 CTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTGCAGCAGTGCG 1188
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RESULT 7
AX833678
LOCUS AX833678 3666 bp DNA linear PAT 15-DEC-2003
DEFINITION Sequence 802 from Patent EP1347046.
ACCESSION AX833678

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VERSION     AX833678.1  GI:39919813
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
            Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
            Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
            Masuho,Y.
  TITLE     Full-length cDNA sequences
  JOURNAL   Patent: EP 1347046-A 802 24-SEP-2003;
            Research Association for Biotechnology (JP)
FEATURES             Location/Qualifiers
     source          1. .3666
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ORIGIN

  Query Match             19.5%;  Score 1108;  DB 6;  Length 3666;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1158;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db        1081 CCACGACGACCAGTGTGGGAAGCAGAAACTGGCCTACAAACTAGAACAAGTCATAACCCT 1140

Qy       5667 CATGAGCTTAGACAGCTGA 5685
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RESULT 8
AK095606
LOCUS       AK095606               3666 bp    mRNA    linear   PRI 15-JUL-2002
DEFINITION  Homo sapiens cDNA FLJ38287 fis, clone FCBBF3008362, moderately
            similar to PLEXIN 4 PRECURSOR.
ACCESSION   AK095606
VERSION     AK095606.1  GI:21754899
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Suzuki,O., Sasaki,N., Aotsuka,S., Shoji,T., Ichihara,T.,
            Shiohata,N., Matsumoto,K., Hirano,M., Sano,S., Nomura,R.,
            Yoshikawa,Y., Matsumura,Y., Moriya,S., Chiba,E., Momiyama,H.,
            Onogawa,S., Kaeriyama,S., Satoh,N., Matsunawa,H., Takahashi,E.,
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            Terashima,Y., Watanabe,M., Sugiyama,T., Irie,R., Otsuki,T.,
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            Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
            Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
            Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3666)
  AUTHORS   Isogai,T. and Yamamoto,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
            Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
            HRI, and Biotechnology Center, National Institute of Technology and
            Evaluation; clone selection for full insert sequencing: HRI and
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          RAB; annotation: HRI and RAB.
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ORIGIN

  Query Match             19.5%;  Score 1108;  DB 9;  Length 3666;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1158;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy       4887 CAGCCCCGACAGCCTCCGCTCACGGACACCTATGATCACTCCTGACCTGGAGAGTGGAGT 4946
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Qy       5667 CATGAGCTTAGACAGCTGA 5685
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RESULT 9
AC011625/c
LOCUS       AC011625              188090 bp    DNA     linear   PRI 08-DEC-1999
DEFINITION  Homo sapiens clone RP11-341C17 from 7q31, complete sequence.
ACCESSION   AC011625
VERSION     AC011625.2  GI:6539285
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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REFERENCE   1  (bases 1 to 188090)
  AUTHORS   Kaul,R.K., Yu,J., Wong,G.K.-S., Magness,C.L., Green,E.D., Green,P.
            and Olson,M.V.
  TITLE     Large-scale MCD Mapping and Sequencing of Human Chromosome 7
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 188090)
  AUTHORS   Bubb,K.L., Desmarais,C.L., Ramsey,S.A. and Hubley,R.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-OCT-1999) Human Genome Center, University of
            Washington, Box 352145, Seattle, WA 98195, USA
REFERENCE   3  (bases 1 to 188090)
  AUTHORS   Kaul,R.K. and Desmarais,C.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-DEC-1999) Human Genome Center, University of
            Washington, Box 352145, Seattle, WA 98195, USA
COMMENT     On Dec 8, 1999 this sequence version replaced gi:6016750.

             -------------- Genome Center:
             University of Washington Genome Center
            Center code: UWGC
            Web site: http://genome.washington.edu
             Contact: uwgchelp@u.washington.edu
             -------------- Project Information
            Center project name: chr-7
            Center clone name: djs301 (RP11-341C17)
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---------- Summary Statistics
Sequencing vector: M13; 100% of reads
Chemistry: Dye-primer Bodipy; 93% of reads Chemistry:
Dye-terminator Big Dye; 7% of reads
Assembly program: Phrap; version 0.990319
Insert size: 188 094; sum-of-contigs
Quality coverage: 7.78X in Q20 bases; sum-of-contigs
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Overlapping Sequences:
5': UWGC:djs302
3': UWGC:djs380

Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

Double stranded (DS) coverage: 70.4%
DS or two chemistry coverage: 100.0%
Single stranded regions: 0

Sequence Validation:
This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-600 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

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2231.00	2189.00	16729.00	16537.00	4194.00	4094.00
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     repeat_region   complement(2131. .2409)
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     repeat_region   11525. .11795
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Qy        181 GGACACATTTACTTGGGGGCCGTCAATCGGATTTACAAGCTCTCCAGCGACCTGAAGGTC 240
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Qy        361 GACTACAAGGAGAACAGGCTGATTGCCTGTGGGAGCCTGTACCAAGGCATCTGCAAGCTG 420
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Qy        421 CTGAGGCTGGAGGACCTCTTCAAGCTGGGGGAGCCTTATCATAAGAAGGAGCACTATCTG 480
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Qy        481 TCAGGTGTCAACGAGAGCGGCTCAGTCTTTGGAGTGATCGTCTCCTACAGCAACCTGGAT 540
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Db     176084 TCAGGTGTCAACGAGAGCGGCTCGGTCTTTGGAGTGATCGTCTCCTACAGCAACCTGGAT 176025

Qy        541 GACAAGCTGTTCATTGCCACGGCAGTGGATGGGAAGCCCGAGTATTTTCCCACCATCTCC 600
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RESULT 10
AC009723/c
LOCUS       AC009723              179592 bp    DNA     linear   HTG 08-NOV-2000
DEFINITION  Homo sapiens clone RP11-44F19, WORKING DRAFT SEQUENCE, 25 unordered
            pieces.
ACCESSION   AC009723
VERSION     AC009723.4  GI:9965551
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 179592)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens, clone RP11-44F19
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 179592)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
            Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Brown,A.,
            Castle,A., Cerny,J., Colangelo,M., Collins,S., Collymore,A.,
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            Naylor,J., Niloff,M., O'Connor,T., O'Donnell,P., Pavlin,B.,
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            Stange-Thomann,N., Stojanovic,N., Stone,C., Subramanian,A.,
            Tesfaye,S., Torruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A.,
            Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-AUG-1999) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Sep 3, 2000 this sequence version replaced gi:7770419.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            ---------- Genome Center
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    Center: Whitehead Institute/ MIT Center for Genome Research
    Center code: WIBR
    Web site: http://www-seq.wi.mit.edu
    Contact: sequence_submissions@genome.wi.mit.edu
-------------- Project Information
    Center project name: L1062
    Center clone name: 44_F_19
-------------- Summary Statistics
    Sequencing vector: M13; M77815; 95% of reads
    Sequencing vector: Plasmid; n/a; 5% of reads
    Chemistry: Dye-primer-amersham; 5% of reads
    Chemistry: Dye-terminator Big Dye; 95% of reads
    Assembly program: Phrap; version 0.960731
    Consensus quality: 159631 bases at least Q40
    Consensus quality: 169781 bases at least Q30
    Consensus quality: 174012 bases at least Q20
    Insert size: 176000; agarose-fp
    Insert size: 177192; sum-of-contigs
    Quality coverage: 4.2 in Q20 bases.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 25 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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*     3334     3433: gap of 100 bp
*     3434     4557: contig of 1124 bp in length
*     4558     4657: gap of 100 bp
*     4658     5689: contig of 1032 bp in length
*     5690     5789: gap of 100 bp
*     5790     7161: contig of 1372 bp in length
*     7162     7261: gap of 100 bp
*     7262     8676: contig of 1415 bp in length
*     8677     8776: gap of 100 bp
*     8777     9951: contig of 1175 bp in length
*     9952    10051: gap of 100 bp
*    10052    11777: contig of 1726 bp in length
*    11778    11877: gap of 100 bp
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*    13013    13112: gap of 100 bp
*    13113    14573: contig of 1461 bp in length
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*    17179    18544: contig of 1366 bp in length
*    18545    18644: gap of 100 bp
*    18645    20233: contig of 1589 bp in length
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ORIGIN

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Qy        421 CTGAGGCTGGAGGACCTCTTCAAGCTGGGGGAGCCTTATCATAAGAAGGAGCACTATCTG 480
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Qy        481 TCAGGTGTCAACGAGAGCGGCTCAGTCTTTGGAGTGATCGTCTCCTACAGCAACCTGGAT 540
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LOCUS       HSM805617               3556 bp    mRNA    linear   PRI 12-JUL-2002
DEFINITION  Homo sapiens mRNA; cDNA DKFZp566O0546 (from clone DKFZp566O0546).
ACCESSION   AL834504
VERSION     AL834504.1  GI:21740304
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3556)
  AUTHORS   Ottenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
            Wiemann,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JUL-2002) 1, D-85764 Neuherberg, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by MediGenomix (Martinsried/Germany) within the cDNA
            sequencing consortium of the German Genome Project. This clone
            (DKFZp566O0546) is available at the RZPD in Berlin. Please contact
            the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
            information about the clone and the sequencing project is available
            at http://mips.gsf.de/proj/cDNA/.
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match           15.4%;  Score 878;  DB 9;  Length 3556;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 1028;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4655 ATCTGGAGTGGCGACAAGGAAGTGGGGCAAGGATGATCTTGCAGGATGAAGACATCACCA 4714
Db          1 ATCTGGAGTGGCGACAAGGAAGTGGGGCAAGGATGATCTTGCAGGATGAAGACATCACCA 60

Qy       4715 CCAAGATTGAGAATGATTGGAAGCGACTGAACACACTGGCCCACTACCAGGTGCCAGATG 4774
Db         61 CCAAGATTGAGAATGATTGGAAGCGACTGAACACACTGGCCCACTACCAGGTGCCAGATG 120
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Qy       4775 GTTCCGTGGTGGCATTAGTGTCCAAGCAGGTGACAGCCTATAACGCAGTGAACAACTCCA 4834
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Qy       4835 CCGTCTCCAGGACCTCAGCAAGTAAATATGAAAACATGATCCGGTACACGGGCAGCCCCG 4894
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Db        181 CCGTCTCCAGGACCTCAGCAAGTAAATATGAAAACATGATCCGGTACACGGGCAGCCCCG 240

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Db        241 ACAGCCTCCGCTCACGGACACCTATGATCACTCCTGACCTGGAGAGTGGAGTCAAGATGT 300

Qy       4955 GGCACCTAGTGAAGAACCACGAGCACGGAGACCAGAAGGAGGGGGACCGGGGGAGCAAGA 5014
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Qy       5015 TGGTGTCTGAAATCTACCTGACCCGACTCCTGGCCACTAAGGGCACACTGCAGAAGTTTG 5074
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Db        361 TGGTGTCTGAAATCTACCTGACCCGACTCCTGGCCACTAAGGGCACACTGCAGAAGTTTG 420

Qy       5075 TGGATGACCTCTTTGAGACCATCTTCAGCACGGCACACCGTGGCTCTGCCCTGCCCCTGG 5134
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Qy       5135 CCATCAAGTACATGTTTGACTTCCTGGATGAGCAGGCTGATAAACATGGCATTCATGACC 5194
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Qy       5255 TCAAGAACCCGCAGTTTGTGTTTGACATCCATAAGAACAGCATCACAGACGCCTGCCTCT 5314
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Qy       5315 CTGTGGTGGCTCAGACCTTCATGGACTCTTGCTCCACGTCAGAGCACCGGCTGGGCAAGG 5374
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Db        661 CTGTGGTGGCTCAGACCTTCATGGACTCTTGCTCCACGTCAGAGCACCGGCTGGGCAAGG 720

Qy       5375 ACTCGCCCTCCAACAAGCTGCTGTATGCCAAGGACATCCCCAGCTACAAGAATTGGGTGG 5434
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Qy       5435 AGAGGTATTACTCAGACATAGGGAAGATGCCAGCCATCAGCGACCAAGACATGAACGCAT 5494
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Qy       5495 ACCTGGCTGAGCAGTCCCGGATGCACATGAATGAGTTCAACACCATGAGTGCACTCTCAG 5554
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Db        841 ACCTGGCTGAGCAGTCCCGGATGCACATGAATGAGTTCAACACCATGAGTGCACTCTCAG 900

Qy       5555 AGATCTTCTCCTATGTGGGCAAATACAGCGAGGAGATCCTTGGACCTCTGGACCACGATG 5614
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Db        901 AGATCTTCTCCTATGTGGGCAAATACAGCGAGGAGATCCTTGGACCTCTGGACCACGACG 960

Qy       5615 ACCAGTGTGGGAAGCAGAAACTGGCCTACAAACTAGAACAAGTCATAACCCTCATGAGCT 5674
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Db        961 ACCAGTGTGGGAAGCAGAAACTGGCCTACAAACTAGAACAAGTCATAACCCTCATGAGCT 1020

Qy       5675 TAGACAGCTGA 5685
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RESULT 12
AX574564
LOCUS       AX574564               2597 bp    DNA     linear   PAT 07-JAN-2003
DEFINITION  Sequence 91 from Patent WO0224888.
ACCESSION   AX574564
VERSION     AX574564.1  GI:27551835
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baker,K.P., Eaton,D.L., Filvaroff,E., Goddard,A., Grimaldi,J.C.,
            Gurney,A.L., Smith,V., Stephan,J.P., Watanabe,C.K., Wood,W.I.,
            Zhang,Z. and Fong,S.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: WO 0224888-A 91 28-MAR-2002;
            GENENTECH, INC. (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             13.9%;  Score 793;  DB 6;  Length 2597;
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  Matches  793;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        579 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 638
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Db          1 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 60

Qy        639 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 698
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Qy        699 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 758
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Qy       1059 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 1118
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Qy       1119 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 1178
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Db        541 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 600

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Qy       1239 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 1298
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Db        661 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 720

Qy       1299 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 1358
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Db        721 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 780

Qy       1359 CAAGCTGAAGAAG 1371
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Db        781 CAAGCTGAAGAAG 793


RESULT 13
AY358850
LOCUS       AY358850               2597 bp    mRNA    linear   PRI 03-OCT-2003
DEFINITION  Homo sapiens clone DNA190803 FAYV2820 (UNQ2820) mRNA, complete cds.
ACCESSION   AY358850
VERSION     AY358850.1  GI:37182817
KEYWORDS    FLI_CDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2597)
  AUTHORS   Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
            Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
            Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
            Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
            Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
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            Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
            Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
            Goddard,A., Wood,W.I. and Godowski,P.
  TITLE     The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
            Effort to Identify Novel Human Secreted and Transmembrane Proteins:
            A Bioinformatics Assessment
  JOURNAL   Genome Res. 13 (10), 2265-2270 (2003)
   PUBMED   12975309
REFERENCE   2  (bases 1 to 2597)
  AUTHORS   Clark,H.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
            Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             13.9%;  Score 793;  DB 9;  Length 2597;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  793;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        579 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 638
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Db          1 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 60

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Db        121 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 180

Qy        759 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 818
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Db        181 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 240

Qy        819 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 878
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Qy        879 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 938
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Qy        939 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 998
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Db        421 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 480

Qy       1059 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 1118
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Qy       1179 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 1238
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Qy       1359 CAAGCTGAAGAAG 1371
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Db        781 CAAGCTGAAGAAG 793


RESULT 14
HSM802037
LOCUS       HSM802037              1029 bp    mRNA    linear   PRI 18-FEB-2000
DEFINITION  Homo sapiens mRNA; cDNA DKFZp434G0625 (from clone DKFZp434G0625);
            partial cds.
ACCESSION   AL137352
VERSION     AL137352.1  GI:6807867
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1029)
  AUTHORS   Ansorge,W., Wirkner,U., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JAN-2000) MIPS, Am Klopferspitz 18a, D-82152
            Martinsried, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by EMBL (European Molecular Biology Laboratories,
            Heidelberg/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            This clone (DKFZp434G0625) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
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            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
            information about the clone and the sequencing project is available
            at http://www.mips.biochem.mpg.de/proj/cDNA/.
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ORIGIN

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Qy        795 TCCACCAGGCTCCACCACCAAGGAGCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAA 854
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Db        181 TCCACCAGGCTCCACCACCAAGGAGCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAA 240

Qy        855 GGAGGACACAGCCTTCAACTCCTATGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGT 914
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGAGGACACAGCCTTCAACTCCTATGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGT 300

Qy        915 GGAGTACCGCCTGCTGCAGGCTGCCTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGAC 974
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Db        301 GGAGTACCGCCTGCTGCAGGCTGCCTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGAC 360

Qy        975 CCTTGGAGTCCATCCAGATGATGACCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCG 1034
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCTTGGAGTCCATCCAGATGATGACCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCG 420

Qy       1035 GAAAATGAAATCCCTGGATGAGTCGGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGA 1094
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GAAAATGAAATCCCTGGATGAGTCGGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGA 480

Qy       1095 CCGCATTAAGGAGCGGCTGCAGTCTTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTG 1154
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Db        481 CCGCATTAAGGAGCGGCTGCAGTCTTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTG 540

Qy       1155 GCTCAAGGTGAAGGACATCCCCTGCAGCAGTGCGCTCTTAACCATTGACGATAACTTCTG 1214
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Db        541 GCTTAAGGTGAAGGACATCCCCTGCAGCAGTGCGCTCTTAACCATTGACGATAACTTCTG 600

Qy       1215 TGGCCTGGACATGAATGCTCCCCTGGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTT 1274
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Db        601 TGGCCTGGACATGAATGCTCCCCTGGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTT 660

Qy       1275 CACGGAGGACAGGGACCGCATGACGTCTGTCATCGCATATGTCTACAAGAACCACTCTCT 1334
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Db        661 CACGGAGGACAGGGACCGCATGACGTCTGTCATCGCATATGTCTACAAGAACCACTCTCT 720

Qy       1335 GGCCTTTGTGGGCACCAAAAGTGGCAAGCTGAAGAAG 1371
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Db        721 GGCCTTTGTGGGCACCAAAAGTGGCAAGCTGAAGAAG 757


RESULT 15
AC025595/c
LOCUS       AC025595               74655 bp    DNA     linear   HTG 26-JUL-2000
DEFINITION  Homo sapiens clone RP11-24E10, LOW-PASS SEQUENCE SAMPLING.
ACCESSION   AC025595
VERSION     AC025595.2  GI:7341984
KEYWORDS    HTG; HTGS_PHASE0.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 74655)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens, clone RP11-24E10
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 74655)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
            Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
            Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
            Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
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            Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
            Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
            Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
            Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J.,
            Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
            McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
            Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
            Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
            O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N.,
            Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
            Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
            Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
            Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
            Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
            Young,G., Zainoun,J., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-MAR-2000) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Mar 30, 2000 this sequence version replaced gi:7229794.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L4440
                Center clone name: 24_E_10
            --------------.
            * NOTE: This record contains 90 individual
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
*        1      727: contig of 727 bp in length
*      728      827: gap of 100 bp
*      828     1590: contig of 763 bp in length
*     1591     1690: gap of 100 bp
*     1691     2443: contig of 753 bp in length
*     2444     2543: gap of 100 bp
*     2544     3286: contig of 743 bp in length
*     3287     3386: gap of 100 bp
*     3387     4099: contig of 713 bp in length
*     4100     4199: gap of 100 bp
*     4200     4924: contig of 725 bp in length
*     4925     5024: gap of 100 bp
*     5025     5745: contig of 721 bp in length
*     5746     5845: gap of 100 bp
*     5846     6567: contig of 722 bp in length
*     6568     6667: gap of 100 bp
*     6668     7409: contig of 742 bp in length
*     7410     7509: gap of 100 bp
*     7510     8239: contig of 730 bp in length
*     8240     8339: gap of 100 bp
*     8340     9048: contig of 709 bp in length
*     9049     9148: gap of 100 bp
*     9149     9902: contig of 754 bp in length
*     9903    10002: gap of 100 bp
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*    13241    13340: gap of 100 bp
*    13341    14074: contig of 734 bp in length
*    14075    14174: gap of 100 bp
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*    14907    15006: gap of 100 bp
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*    15729    15828: gap of 100 bp
*    15829    16542: contig of 714 bp in length
*    16543    16642: gap of 100 bp
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*    18226    18325: gap of 100 bp
*    18326    19056: contig of 731 bp in length
*    19057    19156: gap of 100 bp
*    19157    19894: contig of 738 bp in length
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*    19995    20729: contig of 735 bp in length
*    20730    20829: gap of 100 bp
*    20830    21569: contig of 740 bp in length
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*    21670    22401: contig of 732 bp in length
*    22402    22501: gap of 100 bp
*    22502    23225: contig of 724 bp in length
*    23226    23325: gap of 100 bp
*    23326    24053: contig of 728 bp in length
*    24054    24153: gap of 100 bp
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*    24893    24992: gap of 100 bp
*    24993    25727: contig of 735 bp in length
*    25728    25827: gap of 100 bp
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*    26567    26666: gap of 100 bp
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*    50693    51419: contig of 727 bp in length
*    51420    51519: gap of 100 bp
*    51520    52272: contig of 753 bp in length
*    52273    52372: gap of 100 bp
*    52373    53123: contig of 751 bp in length
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*    54881    55621: contig of 741 bp in length
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*    56459    56558: gap of 100 bp
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 Query Match             8.9%;  Score 509;  DB 2;  Length 74655;
 Best Local Similarity   99.8%;  Pred. No. 9.9e-283;
 Matches  559;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         94 CCGCTGTCCCAGAAGCAGCGGTCATTTGTCACATTCCGAGGAGAGCCCGCCGAGGGTTTC 153
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Db      33970 CCGCTGTCCCAGAAGCAGCGGTCATTTGTCACATTCCGAGGAGAGCCCGCCGAGGGTTTC 33911

Qy        154 AATCACCTGGTGGTGGATGAGAGGACAGGACACATTTACTTGGGGGCCGTCAATCGGATT 213
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Qy        214 TACAAGCTCTCCAGCGACCTGAAGGTCTTGGTGACGCATGAGACAGGGCCGGACGAGGAC 273
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Qy        334 AACAATGTCAACAAGATGCTCCTCATAGACTACAAGGAGAACAGGCTGATTGCCTGTGGG 393
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Qy        394 AGCCTGTACCAAGGCATCTGCAAGCTGCTGAGGCTGGAGGACCTCTTCAAGCTGGGGGAG 453
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Qy        454 CCTTATCATAAGAAGGAGCACTATCTGTCAGGTGTCAACGAGAGCGGCTCAGTCTTTGGA 513
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Db      33610 CCTTATCATAAGAAGGAGCACTATCTGTCAGGTGTCAACGAGAGCGGCTCGGTCTTTGGA 33551

Qy        514 GTGATCGTCTCCTACAGCAACCTGGATGACAAGCTGTTCATTGCCACGGCAGTGGATGGG 573
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Qy        574 AAGCCCGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGAT 633
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Db      33490 AAGCCCGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGAT 33431

Qy        634 GGCATGTTCGCGTACGTCTT 653
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Db      33430 GGCATGTTCGCGTACGTCTT 33411


Search completed: February 20, 2004, 07:08:38
Job time : 14204 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 19, 2004, 23:14:05 ; Search time 1340 Seconds
(without alignments)
18042.161 Million cell updates/sec

Title: US-09-964-956-12
Perfect score: 5691
Sequence: 1 atgaaagccatgccctggaa.....gcttagacagctgaaataaa 5691

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
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4: geneseqn2001as:*
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9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5691	100.0	5691	6	ABS63437	Abs63437 Human cDN
2	5532	97.2	6367	6	ABA00062	Aba00062 CADHP-9 c
3	793	13.9	2597	6	ABK70006	Abk70006 cDNA enco
4	793	13.9	2597	8	ADA01359	Ada01359 Human PRO
5	793	13.9	2597	8	ADA43788	Ada43788 Human cDN
6	793	13.9	2597	8	ADA43556	Ada43556 Human cDN
7	793	13.9	2597	8	ADA01231	Ada01231 Human PRO
8	793	13.9	2597	8	ADA01115	Ada01115 Human cDN
9	793	13.9	2597	8	ADA43672	Ada43672 Human cDN
10	793	13.9	2597	8	ADA06934	Ada06934 Human PRO
11	793	13.9	2597	8	ADA08422	Ada08422 Novel hum
12	793	13.9	2597	8	ADB99715	Adb99715 Human PRO
13	793	13.9	2597	8	ADB86998	Adb86998 Human PRO
14	793	13.9	2597	8	ADB66153	Adb66153 Human cDN
15	793	13.9	2597	9	ADB99831	Adb99831 Human PRO
16	793	13.9	2597	9	ADB99486	Adb99486 Novel hum
17	793	13.9	2597	9	ADB66037	Adb66037 Human cDN
18	793	13.9	2597	9	ADC23435	Adc23435 Human cDN
19	793	13.9	2597	9	ADC26128	Adc26128 Human PRO
20	793	13.9	2597	9	ADE04955	Ade04955 Human PRO
21	793	13.9	2597	9	ADE11261	Ade11261 Human PRO
22	793	13.9	2597	9	ADD88192	Add88192 Human PRO
23	793	13.9	2597	9	ADD95487	Add95487 Human cDN
24	793	13.9	2597	9	ADE06417	Ade06417 Human PRO
25	793	13.9	2597	9	ADE38192	Ade38192 Human PRO
26	793	13.9	2597	9	ADD88308	Add88308 Human PRO
27	793	13.9	2597	9	ADD90889	Add90889 Human cDN
28	793	13.9	2597	10	ADE51742	Ade51742 Human cDN
29	793	13.9	2597	10	ADE51858	Ade51858 Human cDN
30	793	13.9	2597	10	ADE37716	Ade37716 Human cDN
31	793	13.9	2597	10	ADE37600	Ade37600 Human cDN
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37	793	13.9	2597	10	ADE39884	Ade39884 Human PRO
38	793	13.9	2597	10	ADE19749	Ade19749 Human PRO
39	793	13.9	2597	10	ADE77327	Ade77327 Human cDN
40	793	13.9	2597	10	ADE65435	Ade65435 Human PRO
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44	793	13.9	2597	10	ADE38900	Ade38900 Human PRO
45	793	13.9	2597	10	ADE51974	Ade51974 Human cDN
46	793	13.9	2597	10	ADD91005	Add91005 Human cDN
47	793	13.9	2597	10	ADE38784	Ade38784 Human PRO
48	793	13.9	2597	10	ADE37484	Ade37484 Human cDN
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51	793	13.9	2597	10	ADE38668	Ade38668 Human PRO
52	793	13.9	2597	10	ADE39599	Ade39599 Human PRO
53	793	13.9	2597	10	ADD89204	Add89204 Human PRO
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56	793	13.9	2597	10	ADE77443	Ade77443 Human cDN
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58	793	13.9	2597	10	ADE39367	Ade39367 Human PRO
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c 61	503	8.8	598	4	AAK36939	Aak36939 Human bon
c 62	503	8.8	598	4	AAK11122	Aak11122 Human bra
c 63	503	8.8	598	4	ABS36611	Abs36611 Human liv
64	491	8.6	601	4	AAS00023	Aas00023 Human cDN
c 65	481	8.5	495	4	AAI55806	Aai55806 Probe #24
c 66	481	8.5	495	4	AAK49882	Aak49882 Human bon
c 67	481	8.5	495	4	AAK23792	Aak23792 Human bra
c 68	481	8.5	495	4	ABS49520	Abs49520 Human liv
69	479	8.4	3560	9	ADB62416	Adb62416 Human cDN
70	185	3.3	477	5	AAS68294	Aas68294 DNA encod
71	185	3.3	477	7	ACD05873	Acd05873 Novel hum
72	183	3.2	1314	5	AAS68296	Aas68296 DNA encod
73	183	3.2	1314	7	ACD05552	Acd05552 cDNA enco
74	49	0.9	570	3	AAC74352	Aac74352 Human sec
75	49	0.9	6826	8	ADA09914	Ada09914 Human rec
76	47	0.8	418	3	AAA44628	Aaa44628 Human sec
77	47	0.8	5895	6	ABT06294	Abt06294 Human NOV
78	39	0.7	995	5	ABV29002	Abv29002 Human pro
79	39	0.7	995	5	ABV23162	Abv23162 Human pro
80	39	0.7	3914	6	ABV76746	Abv76746 Human ple
81	39	0.7	6387	6	ABN59899	Abn59899 Novel hum
82	39	0.7	7136	7	ABX34698	Abx34698 Human mdd
83	35	0.6	1088	4	ABA08997	Aba08997 Human NOV
84	33	0.6	306	4	AAI55494	Aai55494 Probe #24
85	33	0.6	306	4	AAK23470	Aak23470 Human bra
86	33	0.6	306	6	ABS23099	Abs23099 Human gen
87	33	0.6	518	4	AAI42422	Aai42422 Probe #11
88	33	0.6	518	4	AAK10787	Aak10787 Human bra
89	33	0.6	518	6	ABS10659	Abs10659 Human gen
90	30	0.5	932	6	ABN74259	Abn74259 Bovine em
91	29	0.5	459	8	ACH40941	Ach40941 Human foe
92	29	0.5	499	8	ACH35856	Ach35856 Human end
93	29	0.5	768	4	AAH03972	Aah03972 Human cDN
94	29	0.5	1767	4	AAH15398	Aah15398 Human cDN
95	26	0.5	26	6	ABS63465	Abs63465 Real-time
96	25	0.4	6730	6	ABI99504	Abi99504 Mouse isc

97	23	0.4	190	3	AAC16570	Aac16570	Human sec
98	23	0.4	201	4	AAI56420	Aai56420	Probe #25
99	23	0.4	201	6	ABS23899	Abs23899	Human gen
100	23	0.4	600	4	AAI43440	Aai43440	Probe #12
101	23	0.4	600	6	ABS11541	Abs11541	Human gen
102	22	0.4	22	6	ABS63464	Abs63464	Real-time
c 103	21	0.4	21	6	ABS63466	Abs63466	Real-time
104	21	0.4	154	5	ABV04995	Abv04995	Human pro
105	21	0.4	205	5	ABV35258	Abv35258	Human pro
106	21	0.4	205	5	ABV44095	Abv44095	Human pro
107	21	0.4	522	5	ABV14164	Abv14164	Human pro
108	21	0.4	3111	4	AAS04276	Aas04276	Rat gluta
109	21	0.4	3111	9	ADB58570	Adb58570	Toxicity-
110	21	0.4	3111	9	ADB53197	Adb53197	Primary r
c 111	21	0.4	135638	7	ABX34289	Abx34289	S. atrool
c 112	20	0.4	274	6	ABL72690	Abl72690	Corn tass
c 113	20	0.4	311	7	ABX88561	Abx88561	Corn ear-
c 114	20	0.4	318	3	AAZ42602	Aaz42602	Human 5'
c 115	20	0.4	324	6	ABN94554	Abn94554	Gene #105
c 116	20	0.4	328	4	AAS57777	Aas57777	cDNA #453
c 117	20	0.4	345	5	AAS82885	Aas82885	DNA encod
c 118	20	0.4	369	8	ACH21424	Ach21424	Human adu
c 119	20	0.4	382	3	AAC07272	Aac07272	Human sec
c 120	20	0.4	386	8	ACH29631	Ach29631	Human tes
c 121	20	0.4	412	3	AAC07271	Aac07271	Human sec
c 122	20	0.4	414	8	ACH29208	Ach29208	Human adu
123	20	0.4	419	6	ABK45224	Abk45224	cDNA enco
c 124	20	0.4	456	3	AAC07270	Aac07270	Human sec
c 125	20	0.4	462	3	AAA77885	Aaa77885	cDNA enco
c 126	20	0.4	462	4	AAI28623	Aai28623	Colon tum
c 127	20	0.4	462	7	ABZ32809	Abz32809	Human col
c 128	20	0.4	476	8	ACH44821	Ach44821	Human foe
c 129	20	0.4	482	8	ACH33668	Ach33668	Human end
c 130	20	0.4	486	3	AAC07273	Aac07273	Human sec
c 131	20	0.4	495	8	ACH50755	Ach50755	Human mam
c 132	20	0.4	500	7	ACD93147	Acd93147	Human col
133	20	0.4	506	9	ADD19817	Add19817	Seabass p
c 134	20	0.4	615	3	AAC00732	Aac00732	Human sec
c 135	20	0.4	616	3	AAA16233	Aaa16233	Human col
c 136	20	0.4	670	3	AAC10893	Aac10893	Human sec
c 137	20	0.4	689	3	AAC10890	Aac10890	Human sec
c 138	20	0.4	700	6	ABN96801	Abn96801	Gene #329
c 139	20	0.4	736	5	AAS69768	Aas69768	DNA encod
c 140	20	0.4	744	3	AAC10882	Aac10882	Human sec
c 141	20	0.4	746	5	AAS69769	Aas69769	DNA encod
c 142	20	0.4	750	3	AAA01845	Aaa01845	Human col
c 143	20	0.4	792	6	ABQ56140	Abq56140	Human ova
c 144	20	0.4	824	4	AAH05487	Aah05487	Human cDN
c 145	20	0.4	1320	4	AAS56182	Aas56182	Salmonell
c 146	20	0.4	1320	7	ACA51334	Aca51334	Prokaryot
147	20	0.4	1636	2	AAT39794	Aat39794	Mouse SH3
c 148	20	0.4	2060	4	AAH15894	Aah15894	Human cDN
c 149	20	0.4	2074	3	AAC76166	Aac76166	Human ORF
150	20	0.4	2153	4	AAI60597	Aai60597	Human pol
c 151	20	0.4	2214	6	ABK34791	Abk34791	Human cDN
c 152	20	0.4	2444	3	AAA90083	Aaa90083	Human neg
c 153	20	0.4	2522	4	AAI58811	Aai58811	Human pol
c 154	20	0.4	2522	8	ADB48792	Adb48792	Novel hum
c 155	20	0.4	2564	9	ADB62125	Adb62125	Human cDN
156	20	0.4	2971	4	AAK94342	Aak94342	Human cDN
c 157	20	0.4	3849	4	AAF25795	Aaf25795	S. chryso
158	20	0.4	6252	4	AAS00020	Aas00020	Human cDN
159	20	0.4	6252	5	AAH81745	Aah81745	Human dif
160	20	0.4	6252	6	ABL67279	Abl67279	Thyroid c
c 161	20	0.4	6329	4	AAH98400	Aah98400	Human EST
c 162	20	0.4	6329	4	ABA09062	Aba09062	Human ple
163	20	0.4	6561	5	AAS85204	Aas85204	DNA encod
c 164	20	0.4	13842	3	AAZ87297	Aaz87297	S. venezu
c 165	20	0.4	36778	3	AAZ87318	Aaz87318	S. venezu
c 166	20	0.4	37948	3	AAZ87285	Aaz87285	S. venezu
c 167	20	0.4	38506	3	AAA75633	Aaa75633	Nucleotid
c 168	20	0.4	38506	3	AAZ56001	Aaz56001	Recombina
c 169	20	0.4	38506	7	ABS56090	Abs56090	S. venezu
c 170	20	0.4	38506	7	ADA09418	Ada09418	Cosmid pK
c 171	20	0.4	88421	6	AAL40781	Aal40781	88421nt g
172	20	0.4	110000	7	ABX16390_5	Continuation (6 of	
c 173	19	0.3	132	3	AAA41395	Aaa41395	Human sec
c 174	19	0.3	294	7	ACD92078	Acd92078	Human col
c 175	19	0.3	360	6	AAS17588	Aas17588	DNA encod
c 176	19	0.3	436	3	AAC69658	Aac69658	Human mic
177	19	0.3	464	8	ACH44098	Ach44098	Human foe
178	19	0.3	503	5	AAF59651	Aaf59651	Eel ghrel
c 179	19	0.3	512	5	AAS65908	Aas65908	DNA encod
180	19	0.3	531	2	AAT01576	Aat01576	Human leu
181	19	0.3	558	5	AAH97972	Aah97972	Murine 7-
c 182	19	0.3	588	2	AAV22147	Aav22147	Mouse BH3
c 183	19	0.3	689	3	AAF08602	Aaf08602	Fusarium
c 184	19	0.3	720	5	AAS74665	Aas74665	DNA encod
185	19	0.3	735	7	ACF67304	Acf67304	Photorhab
186	19	0.3	739	4	AAK92012	Aak92012	Human cDN
187	19	0.3	739	4	AAK93668	Aak93668	Human cDN
c 188	19	0.3	791	6	AAL38167	Aal38167	DNA from
189	19	0.3	900	2	AAQ61558	Aaq61558	Genomic s
c 190	19	0.3	1059	6	ABQ42478	Abq42478	Oligonucl
191	19	0.3	1059	6	ABQ42479	Abq42479	Oligonucl
c 192	19	0.3	1059	6	ABQ20484	Abq20484	Oligonucl
193	19	0.3	1059	6	ABQ20485	Abq20485	Oligonucl
194	19	0.3	1176	5	AAS76846	Aas76846	DNA encod
c 195	19	0.3	1233	7	ACA21173	Aca21173	Prokaryot
c 196	19	0.3	1236	8	ADA32039	Ada32039	DNA encod
197	19	0.3	1296	6	ABZ32409	Abz32409	Candida a
198	19	0.3	1317	6	AAS62393	Aas62393	cDNA sequ
199	19	0.3	1467	7	AAD55828	Aad55828	Micromono
200	19	0.3	1599	9	ADE07844	Ade07844	Novel cod
201	19	0.3	2000	7	ADA72625	Ada72625	Rice gene
202	19	0.3	2036	4	ABL11823	Abl11823	Drosophil
c 203	19	0.3	2206	4	AAS02663	Aas02663	Human sec
c 204	19	0.3	2206	7	ABZ67186	Abz67186	Human sec
c 205	19	0.3	2206	7	ABZ73589	Abz73589	Secreted
c 206	19	0.3	2206	7	ADA98098	Ada98098	Human sec
c 207	19	0.3	2237	2	AAQ89779	Aaq89779	Cotranspo
208	19	0.3	2414	4	AAK94356	Aak94356	Human ful
c 209	19	0.3	2444	7	ADA52653	Ada52653	Human cod
210	19	0.3	2466	9	ADB58952	Adb58952	Toxicity-
211	19	0.3	2466	9	ADB53694	Adb53694	Primary r
212	19	0.3	2477	2	AAX52244	Aax52244	Protein P
213	19	0.3	2477	3	AAC58585	Aac58585	Human PRO
214	19	0.3	2477	3	AAA77558	Aaa77558	Human PRO
215	19	0.3	2477	3	ADC78489	Adc78489	Human PRO
216	19	0.3	2477	4	AAF72402	Aaf72402	Human PRO
217	19	0.3	2477	4	AAS21409	Aas21409	Human cDN
218	19	0.3	2477	7	ACA59035	Aca59035	Human PRO
219	19	0.3	2477	7	ACD24018	Acd24018	Novel hum
220	19	0.3	2477	7	ACA58432	Aca58432	cDNA enco
221	19	0.3	2477	7	ACA67159	Aca67159	cDNA enco
222	19	0.3	2477	7	ACA60139	Aca60139	Human cDN
223	19	0.3	2477	7	ACD07539	Acd07539	Novel hum
224	19	0.3	2477	7	ACA03768	Aca03768	cDNA enco
225	19	0.3	2477	7	ABX71587	Abx71587	Human cDN
226	19	0.3	2477	7	ACH06919	Ach06919	Human sec
227	19	0.3	2477	7	ABX89306	Abx89306	DNA encod
228	19	0.3	2477	7	ACD41960	Acd41960	Human sec
229	19	0.3	2477	7	ABX96156	Abx96156	Human sec
230	19	0.3	2477	7	ACA05477	Aca05477	cDNA enco
231	19	0.3	2477	7	ACD20144	Acd20144	Human sec
232	19	0.3	2477	7	ACA04189	Aca04189	Human cDN
233	19	0.3	2477	7	ACA54947	Aca54947	Novel hum
234	19	0.3	2477	8	ACD19782	Acd19782	Human sec
235	19	0.3	2477	8	ADA45850	Ada45850	Novel hum
236	19	0.3	2477	8	ADA76281	Ada76281	Human PRO
237	19	0.3	2477	8	ADB29374	Adb29374	Human sec
238	19	0.3	2477	8	ADA18931	Ada18931	Human PRO
239	19	0.3	2477	8	ADA61554	Ada61554	Homo sapi
240	19	0.3	2477	8	ADB19339	Adb19339	Novel hum
241	19	0.3	2477	8	ADB27880	Adb27880	cDNA enco
242	19	0.3	2477	8	ADA86359	Ada86359	Novel hum

243	19	0.3	2477	8	ADB15923	Adb15923 Human PRO
244	19	0.3	2477	8	ADA47709	Ada47709 Human PRO
245	19	0.3	2477	8	ADA18230	Ada18230 Human sec
246	19	0.3	2477	8	ACD66929	Acd66929 Human cDN
247	19	0.3	2477	8	ADA67504	Ada67504 Human PRO
248	19	0.3	2477	8	ADB30511	Adb30511 cDNA enco
249	19	0.3	2477	8	ADA85807	Ada85807 Novel hum
250	19	0.3	2477	8	ADA97019	Ada97019 Human PRO
251	19	0.3	2477	8	ADA79323	Ada79323 Human PRO
252	19	0.3	2477	8	ADA87462	Ada87462 Novel hum
253	19	0.3	2477	8	ADB16664	Adb16664 Human PRO
254	19	0.3	2477	8	ACD83090	Acd83090 Human PRO
255	19	0.3	2477	8	ADA16205	Ada16205 Human sec
256	19	0.3	2477	8	ADA91756	Ada91756 Novel hum
257	19	0.3	2477	8	ADB14819	Adb14819 Human PRO
258	19	0.3	2477	8	ADB18780	Adb18780 Novel hum
259	19	0.3	2477	8	ADA93995	Ada93995 Human PRO
260	19	0.3	2477	8	ADB19891	Adb19891 Novel hum
261	19	0.3	2477	8	ADB13203	Adb13203 Human PRO
262	19	0.3	2477	8	ACD98589	Acd98589 Novel hum
263	19	0.3	2477	8	ADA74457	Ada74457 Human PRO
264	19	0.3	2477	8	ADA42350	Ada42350 Human sec
265	19	0.3	2477	8	ADB24690	Adb24690 Human PRO
266	19	0.3	2477	8	ADA82214	Ada82214 Human PRO
267	19	0.3	2477	8	ADA75177	Ada75177 Human PRO
268	19	0.3	2477	8	ADA85255	Ada85255 Novel hum
269	19	0.3	2477	8	ADA84703	Ada84703 Novel hum
270	19	0.3	2477	8	ACD23268	Acd23268 Human PRO
271	19	0.3	2477	8	ADB29959	Adb29959 cDNA enco
272	19	0.3	2477	8	ADA80487	Ada80487 Human PRO
273	19	0.3	2477	8	ADA75729	Ada75729 Human PRO
274	19	0.3	2477	8	ADA46954	Ada46954 Human PRO
275	19	0.3	2477	8	ADB25250	Adb25250 Human PRO
276	19	0.3	2477	8	ADA93426	Ada93426 Human PRO
277	19	0.3	2477	8	ADB26776	Adb26776 cDNA enco
278	19	0.3	2477	8	ADB31063	Adb31063 cDNA enco
279	19	0.3	2477	8	ADA60991	Ada60991 Homo sapi
280	19	0.3	2477	8	ADB24138	Adb24138 Human PRO
281	19	0.3	2477	8	ADA96467	Ada96467 Human PRO
282	19	0.3	2477	8	ADA81039	Ada81039 Human PRO
283	19	0.3	2477	8	ADA95915	Ada95915 Human PRO
284	19	0.3	2477	8	ADB26224	Adb26224 cDNA enco
285	19	0.3	2477	8	ADB21709	Adb21709 Novel hum
286	19	0.3	2477	8	ADA77488	Ada77488 Human PRO
287	19	0.3	2477	8	ADB18228	Adb18228 cDNA enco
288	19	0.3	2477	8	ADA86911	Ada86911 Novel hum
289	19	0.3	2477	8	ADA16629	Ada16629 Human sec
290	19	0.3	2477	8	ADA13058	Ada13058 Human sec
291	19	0.3	2477	8	ADA41926	Ada41926 Human sec
292	19	0.3	2477	8	ADA88014	Ada88014 Novel hum
293	19	0.3	2477	8	ADA46402	Ada46402 Novel hum
294	19	0.3	2477	8	ADA17273	Ada17273 Human sec
295	19	0.3	2477	8	ADA42776	Ada42776 Human sec
296	19	0.3	2477	8	ADB28432	Adb28432 cDNA enco
297	19	0.3	2477	8	ADB28984	Adb28984 cDNA enco
298	19	0.3	2477	8	ADA76936	Ada76936 Human PRO
299	19	0.3	2477	8	ADA88566	Ada88566 Novel hum
300	19	0.3	2477	8	ADA97571	Ada97571 Human PRO
301	19	0.3	2477	8	ADB27328	Adb27328 cDNA enco
302	19	0.3	2477	8	ADB22261	Adb22261 Novel hum
303	19	0.3	2477	8	ACD23630	Acd23630 Human PRO
304	19	0.3	2477	8	ADA66952	Ada66952 Human PRO
305	19	0.3	2477	8	ADB22813	Adb22813 Human PRO
306	19	0.3	2477	8	ADB23586	Adb23586 Human PRO
307	19	0.3	2477	8	ADA92308	Ada92308 Novel hum
308	19	0.3	2477	8	ADB15371	Adb15371 Human PRO
309	19	0.3	2477	8	ADB38623	Adb38623 Novel hum
310	19	0.3	2477	8	ADB38071	Adb38071 Novel hum
311	19	0.3	2477	8	ADB66543	Adb66543 Novel hum
312	19	0.3	2477	9	ADB89623	Adb89623 Human PRO
313	19	0.3	2477	9	ADB90355	Adb90355 Human PRO
314	19	0.3	2477	9	ADB77695	Adb77695 Human sec
315	19	0.3	2477	9	ADB39456	Adb39456 Novel hum
316	19	0.3	2477	9	ADB74831	Adb74831 Human sec
317	19	0.3	2477	9	ADB47079	Adb47079 Novel hum
318	19	0.3	2477	9	ADB86686	Adb86686 Human PRO
319	19	0.3	2477	9	ADB77291	Adb77291 Novel hum
320	19	0.3	2477	9	ADB34448	Adb34448 Human PRO
321	19	0.3	2477	9	ADB35552	Adb35552 Human PRO
322	19	0.3	2477	9	ADB33896	Adb33896 Human PRO
323	19	0.3	2477	9	ADB35000	Adb35000 Human PRO
324	19	0.3	2477	9	ADB36104	Adb36104 Human PRO
325	19	0.3	2477	9	ADB46499	Adb46499 Novel hum
326	19	0.3	2477	9	ADC28477	Adc28477 Human sec
327	19	0.3	2477	9	ADC39677	Adc39677 Human sec
328	19	0.3	2477	9	ADC40191	Adc40191 Human sec
329	19	0.3	2477	9	ADC19015	Adc19015 Human sec
330	19	0.3	2477	9	ADC34315	Adc34315 Human sec
331	19	0.3	2477	9	ADC29370	Adc29370 Human sec
332	19	0.3	2477	9	ADC28901	Adc28901 Human sec
333	19	0.3	2477	9	ADC40786	Adc40786 Human sec
334	19	0.3	2477	9	ADC19443	Adc19443 Human sec
335	19	0.3	2477	9	ADC33891	Adc33891 Human sec
336	19	0.3	2477	9	ADC12961	Adc12961 Human sec
337	19	0.3	2477	9	ADC50372	Adc50372 Novel hum
338	19	0.3	2477	9	ADC71919	Adc71919 Novel hum
339	19	0.3	2477	9	ADC59898	Adc59898 Novel hum
340	19	0.3	2477	9	ADC52905	Adc52905 Novel hum
341	19	0.3	2477	9	ADC57259	Adc57259 Novel hum
342	19	0.3	2477	9	ADC60450	Adc60450 Novel hum
343	19	0.3	2477	9	ADC50925	Adc50925 Novel hum
344	19	0.3	2477	9	ADC65452	Adc65452 Human PRO
345	19	0.3	2477	9	ADC54550	Adc54550 Novel hum
346	19	0.3	2477	9	ADC53511	Adc53511 Novel hum
347	19	0.3	2477	9	ADC59034	Adc59034 Novel hum
348	19	0.3	2477	9	ADC55912	Adc55912 Novel hum
349	19	0.3	2477	9	ADC58482	Adc58482 Novel hum
350	19	0.3	2477	9	ADC12413	Adc12413 Human sec
351	19	0.3	2477	9	ADD03156	Add03156 Novel hum
352	19	0.3	2477	9	ADC90148	Adc90148 Novel hum
353	19	0.3	2477	9	ADC69567	Adc69567 cDNA enco
354	19	0.3	2477	9	ADC48456	Adc48456 Human PRO
355	19	0.3	2477	9	ADD09985	Add09985 Human PRO
356	19	0.3	2477	9	ADD04560	Add04560 Novel hum
357	19	0.3	2477	9	ADC80516	Adc80516 Novel hum
358	19	0.3	2477	9	ADD11023	Add11023 Human PRO
359	19	0.3	2477	9	ADC47904	Adc47904 Human PRO
360	19	0.3	2477	9	ADD04968	Add04968 Human sec
361	19	0.3	2477	9	ADC79964	Adc79964 Novel hum
362	19	0.3	2477	9	ADD09433	Add09433 Human PRO
363	19	0.3	2477	9	ADD03974	Add03974 Human sec
364	19	0.3	2477	9	ADD03550	Add03550 Human sec
365	19	0.3	2477	9	ADD41146	Add41146 Novel hum
366	19	0.3	2477	9	ADD52285	Add52285 cDNA enco
367	19	0.3	2477	9	ADD53025	Add53025 cDNA enco
368	19	0.3	2477	9	ADD53577	Add53577 Novel hum
369	19	0.3	2477	9	ADD51733	Add51733 cDNA enco
370	19	0.3	2477	9	ADD02532	Add02532 Human PRO
371	19	0.3	2477	9	ADD01966	Add01966 Human PRO
372	19	0.3	2477	9	ADD54148	Add54148 Novel hum
373	19	0.3	2477	9	ADD92465	Add92465 Human PRO
374	19	0.3	2477	9	ADD91361	Add91361 Human PRO
375	19	0.3	2477	9	ADE03975	Ade03975 Human PRO
376	19	0.3	2477	9	ADE32272	Ade32272 Novel hum
377	19	0.3	2477	9	ADE22204	Ade22204 cDNA enco
378	19	0.3	2477	9	ADD79428	Add79428 cDNA enco
379	19	0.3	2477	9	ADE41964	Ade41964 Human PRO
380	19	0.3	2477	9	ADE17781	Ade17781 Human PRO
381	19	0.3	2477	9	ADD91913	Add91913 Human PRO
382	19	0.3	2477	9	ADE33376	Ade33376 Novel hum
383	19	0.3	2477	9	ADE33928	Ade33928 Novel hum
384	19	0.3	2477	9	ADD79980	Add79980 cDNA enco
385	19	0.3	2477	9	ADD93017	Add93017 Human PRO
386	19	0.3	2477	9	ADE19437	Ade19437 Human PRO
387	19	0.3	2477	9	ADE34802	Ade34802 Human sec
388	19	0.3	2477	9	ADE18885	Ade18885 Human PRO

	389	19	0.3	2477	9	ADE43081 Ade43081 Human PRO
	390	19	0.3	2477	9	ADD95870 Add95870 Human PRO
	391	19	0.3	2477	9	ADE22756 Ade22756 cDNA enco
	392	19	0.3	2477	9	ADD78874 Add78874 cDNA enco
	393	19	0.3	2477	9	ADE32824 Ade32824 Novel hum
	394	19	0.3	2477	9	ADE42516 Ade42516 Human PRO
	395	19	0.3	2477	9	ADD80532 Add80532 cDNA enco
	396	19	0.3	2477	9	ADD89560 Add89560 Human PRO
	397	19	0.3	2477	9	ADE40844 Ade40844 Human PRO
	398	19	0.3	2477	9	ADE04643 Ade04643 Human PRO
	399	19	0.3	2477	10	ADC81068 Adc81068 Novel hum
	400	19	0.3	2477	10	ADE79247 Ade79247 Human sec
	401	19	0.3	2477	10	ADD76516 Add76516 Human PRO
	402	19	0.3	2477	10	ADD87880 Add87880 Human PRO
	403	19	0.3	2477	10	ADD86284 Add86284 Human PRO
	404	19	0.3	2477	10	ADE79671 Ade79671 Human sec
	405	19	0.3	2477	10	ADE75732 Ade75732 Human PRO
	406	19	0.3	2477	10	ADE73347 Ade73347 Human sec
	407	19	0.3	2477	10	ADE23308 Ade23308 cDNA enco
	408	19	0.3	2477	10	ADE23860 Ade23860 cDNA enco
	409	19	0.3	2477	10	ADE24503 Ade24503 cDNA enco
	410	19	0.3	2477	10	ADD87328 Add87328 Human PRO
	411	19	0.3	2477	10	ADE89194 Ade89194 Human PRO
	412	19	0.3	2477	10	ADE73882 Ade73882 Human sec
	413	19	0.3	2477	10	ADE18333 Ade18333 Human PRO
	414	19	0.3	2477	10	ADE88642 Ade88642 Human PRO
	415	19	0.3	2649	7	ACF69734 Acf69734 Photorhab
c	416	19	0.3	2764	7	ADA53084 Ada53084 Human cod
c	417	19	0.3	2777	4	AAH32536 Aah32536 Human sec
c	418	19	0.3	2777	7	ADA55915 Ada55915 Gene enco
c	419	19	0.3	2777	7	ADA39721 Ada39721 Human sec
c	420	19	0.3	2777	7	ACC50392 Acc50392 Human sec
	421	19	0.3	2997	7	ADA52505 Ada52505 Human cod
	422	19	0.3	3156	6	ABZ11988 Abz11988 Human pol
	423	19	0.3	3195	5	AAS87692 Aas87692 DNA encod
	424	19	0.3	3458	7	ADA53359 Ada53359 Human cod
	425	19	0.3	3671	5	AAD02591 Aad02591 Human cyt
	426	19	0.3	4426	2	AAV09064 Aav09064 Bovine cG
	427	19	0.3	4474	2	AAQ79703 Aaq79703 Cyclic gu
	428	19	0.3	4474	2	AAX99381 Aax99381 Bovine cG
	429	19	0.3	5031	4	ABL11822 Abl11822 Drosophil
c	430	19	0.3	5440	4	AAL05240 Aal05240 Human rep
c	431	19	0.3	5440	4	AAL05242 Aal05242 Human rep
c	432	19	0.3	5440	4	ABL98123 Abl98123 Human tes
c	433	19	0.3	5440	4	ABL98125 Abl98125 Human tes
	434	19	0.3	5526	5	AAS76845 Aas76845 DNA encod
	435	19	0.3	5778	4	AAK53086 Aak53086 Human pol
	436	19	0.3	5804	4	AAK52102 Aak52102 Human pol
	437	19	0.3	6042	5	AAS76844 Aas76844 DNA encod
c	438	19	0.3	9594	4	ABL10394 Abl10394 Drosophil
c	439	19	0.3	15856	4	AAL05552 Aal05552 Human rep
	440	19	0.3	18663	4	AAK75859 Aak75859 Human imm
c	441	19	0.3	20300	6	ABK47337 Abk47337 Genomic n
c	442	19	0.3	30310	6	AAL38253 Aal38253 Genomic D
c	443	19	0.3	30781	6	AAD46712 Aad46712 Human DBH
	444	19	0.3	51705	8	ADA02723 Ada02723 Mouse Syk
	445	19	0.3	51705	9	ADB72461 Adb72461 Mouse Syk
	446	19	0.3	60196	7	AAD55810 Aad55810 Micromono
c	447	19	0.3	67571	7	AAD53224_5 Continuation (6 of
c	448	19	0.3	110000	2	AAV30458_4 Continuation (5 of
c	449	19	0.3	110000	2	AAV30459_4 Continuation (5 of
	450	19	0.3	110000	4	AAI99682_02 Continuation (3 of
	451	19	0.3	110000	4	AAI99683_02 Continuation (3 of
	452	19	0.3	110000	7	ACF67367_27 Continuation (28 o
c	453	19	0.3	110000	7	ACF65386_1 Continuation (2 of
	454	19	0.3	178896	6	ABQ88146 Abq88146 Human ost
c	455	19	0.3	268685	6	ABS56563 Abs56563 Human SUL
c	456	19	0.3	334462	9	ADC24763 Adc24763 Human wil
c	457	18	0.3	71	2	AAT65326 Aat65326 Human ker
	458	18	0.3	132	7	AAL52257 Aal52257 184P1E2 g
	459	18	0.3	164	4	AAI25048 Aai25048 Probe #14
	460	18	0.3	164	4	ABA70673 Aba70673 Human foe
	461	18	0.3	164	4	AAI50840 Aai50840 Probe #19
	462	18	0.3	164	4	ABA37215 Aba37215 Probe #15
	463	18	0.3	164	4	AAK44864 Aak44864 Human bon
	464	18	0.3	164	4	AAK18919 Aak18919 Human bra
	465	18	0.3	164	4	ABS44526 Abs44526 Human liv
	466	18	0.3	164	6	ABS19105 Abs19105 Human gen
	467	18	0.3	209	4	ABL22363 Abl22363 Drosophil
	468	18	0.3	248	4	AAL00188 Aal00188 Human rep
c	469	18	0.3	258	7	ABX91685 Abx91685 Murine ge
	470	18	0.3	262	3	AAA42325 Aaa42325 Human sec
c	471	18	0.3	278	2	AAT22474 Aat22474 Human gen
	472	18	0.3	288	7	ABX87821 Abx87821 Corn ear-
	473	18	0.3	298	4	AAF31739 Aaf31739 Novel rat
	474	18	0.3	326	4	AAH50812 Aah50812 Human tum
c	475	18	0.3	326	4	AAH50810 Aah50810 Human tum
c	476	18	0.3	382	6	ABK64256 Abk64256 Human ben
c	477	18	0.3	384	6	ABN21187 Abn21187 Human ORF
	478	18	0.3	414	4	AAK56382 Aak56382 Human imm
c	479	18	0.3	420	6	ABK45931 Abk45931 cDNA enco
	480	18	0.3	429	4	AAI13250 Aai13250 Probe #31
	481	18	0.3	429	4	ABA54948 Aba54948 Human foe
	482	18	0.3	429	4	AAI34602 Aai34602 Probe #32
	483	18	0.3	429	4	ABA44507 Aba44507 Human bre
	484	18	0.3	429	4	ABA24714 Aba24714 Probe #31
	485	18	0.3	429	4	AAK28673 Aak28673 Human bon
	486	18	0.3	429	4	AAK03220 Aak03220 Human bra
	487	18	0.3	429	4	ABS28273 Abs28273 Human liv
	488	18	0.3	429	5	AAI03154 Aai03154 Probe #31
	489	18	0.3	429	6	ABS03184 Abs03184 Human gen
c	490	18	0.3	434	4	AAI88275 Aai88275 Human pol
	491	18	0.3	435	9	ADB37411 Adb37411 Rat stem
	492	18	0.3	439	4	AAI81242 Aai81242 Human pol
c	493	18	0.3	444	4	AAH78200 Aah78200 Nucleotid
c	494	18	0.3	445	4	AAH78198 Aah78198 Nucleotid
c	495	18	0.3	447	4	AAD16363 Aad16363 Human sbg
c	496	18	0.3	464	8	ACH34389 Ach34389 Human end
c	497	18	0.3	468	9	ADE15977 Ade15977 G-coupled
	498	18	0.3	470	4	AAI15829 Aai15829 Probe #57
	499	18	0.3	470	4	ABA58069 Aba58069 Human foe
	500	18	0.3	470	4	AAI37670 Aai37670 Probe #63
	501	18	0.3	470	4	ABA27308 Aba27308 Probe #57
	502	18	0.3	470	4	AAK31795 Aak31795 Human bon
	503	18	0.3	470	4	AAK06141 Aak06141 Human bra
	504	18	0.3	470	4	ABS31481 Abs31481 Human liv
	505	18	0.3	470	6	ABS06553 Abs06553 Human gen
	506	18	0.3	471	8	ACH22905 Ach22905 Human adu
c	507	18	0.3	477	4	AAH78199 Aah78199 Nucleotid
	508	18	0.3	480	7	ACA36832 Aca36832 Prokaryot
	509	18	0.3	483	6	ABV86973 Abv86973 Human col
c	510	18	0.3	486	7	ACA49535 Aca49535 Prokaryot
	511	18	0.3	489	4	ABL22153 Abl22153 Drosophil
	512	18	0.3	492	8	ACH44940 Ach44940 Human foe
	513	18	0.3	501	3	AAC44336 Aac44336 Arabidops
c	514	18	0.3	501	8	ACH42397 Ach42397 Human foe
	515	18	0.3	528	3	AAC36143 Aac36143 Arabidops
	516	18	0.3	537	3	AAC35899 Aac35899 Arabidops
c	517	18	0.3	546	6	ABS53641 Abs53641 Human DNA
c	518	18	0.3	546	6	AAI73010 Aai73010 Zcys7 cod
	519	18	0.3	553	7	ABX57155 Abx57155 Arabidops
	520	18	0.3	604	6	ABT10350 Abt10350 Human bre
c	521	18	0.3	605	9	ADD16691 Add16691 DNA (SeqI
c	522	18	0.3	619	9	ADB51386 Adb51386 Primary r
c	523	18	0.3	624	3	AAF09593 Aaf09593 Fusarium
	524	18	0.3	633	7	ACA39739 Aca39739 Prokaryot
c	525	18	0.3	633	8	ADB08469 Adb08469 Alloiococ
c	526	18	0.3	633	8	ADB08467 Adb08467 Alloiococ
c	527	18	0.3	637	4	AAS30870 Aas30870 Human cDN
c	528	18	0.3	642	4	AAL00039 Aal00039 Human rep
c	529	18	0.3	666	3	AAF11941 Aaf11941 Aspergill
	530	18	0.3	686	3	AAF14604 Aaf14604 Aspergill
	531	18	0.3	724	4	ABL16707 Abl16707 Drosophil
c	532	18	0.3	726	3	AAZ36370 Aaz36370 DNA encod
c	533	18	0.3	729	8	ADB08475 Adb08475 Alloiococ
c	534	18	0.3	729	8	ADB08471 Adb08471 Alloiococ

c	535	18	0.3	729	8	ADB08473	Adb08473 Alloiococ
	536	18	0.3	742	9	ADB67959	Adb67959 Human lun
	537	18	0.3	746	2	AAX40036	Aax40036 Prostate
	538	18	0.3	759	6	ABK30714	Abk30714 Plant dwa
	539	18	0.3	759	6	ABL49515	Abl49515 Sequence
	540	18	0.3	797	9	ADB58500	Adb58500 Toxicity-
	541	18	0.3	797	9	ADB53098	Adb53098 Primary r
	542	18	0.3	808	4	AAH06598	Aah06598 Human cDN
	543	18	0.3	814	5	AAS11362	Aas11362 Soybean D
	544	18	0.3	816	4	ABA69602	Aba69602 Human foe
	545	18	0.3	816	4	ABS43312	Abs43312 Human liv
c	546	18	0.3	831	9	ADD17516	Add17516 DNA (SeqI
	547	18	0.3	832	6	ABK09490	Abk09490 Human ova
c	548	18	0.3	833	2	AAX40033	Aax40033 Prostate
c	549	18	0.3	840	6	ABQ68625	Abq68625 Listeria
	550	18	0.3	845	4	AAH98771	Aah98771 Human EST
c	551	18	0.3	849	6	ABK75468	Abk75468 Bacillus
c	552	18	0.3	873	6	ABS67310	Abs67310 Breast sp
	553	18	0.3	882	5	AAD08650	Aad08650 Mouse can
c	554	18	0.3	899	7	ABT15733	Abt15733 Human can
c	555	18	0.3	921	3	AAA26406	Aaa26406 Human sec
c	556	18	0.3	921	5	AAS87191	Aas87191 DNA encod
c	557	18	0.3	921	7	ADA55984	Ada55984 Gene enco
c	558	18	0.3	921	7	ADA39795	Ada39795 Human sec
c	559	18	0.3	921	7	ACC50432	Acc50432 Human sec
c	560	18	0.3	921	9	ADC73491	Adc73491 Human sec
c	561	18	0.3	961	4	AAF92129	Aaf92129 Human PRO
c	562	18	0.3	961	6	ABK33646	Abk33646 cDNA enco
c	563	18	0.3	961	6	ABS74449	Abs74449 Human cDN
c	564	18	0.3	961	7	ACA66951	Aca66951 cDNA enco
c	565	18	0.3	961	7	ACD68703	Acd68703 Novel hum
c	566	18	0.3	961	7	ACA91235	Aca91235 Novel hum
c	567	18	0.3	961	7	ACD81612	Acd81612 Human cDN
c	568	18	0.3	961	7	ACA60434	Aca60434 Novel hum
c	569	18	0.3	961	7	ACA58881	Aca58881 cDNA enco
c	570	18	0.3	961	7	ACA64057	Aca64057 cDNA enco
c	571	18	0.3	961	7	ACA91321	Aca91321 cDNA enco
c	572	18	0.3	961	7	ACD45220	Acd45220 Human sec
c	573	18	0.3	961	7	ACA93768	Aca93768 Human cDN
c	574	18	0.3	961	7	ACA67342	Aca67342 cDNA enco
c	575	18	0.3	961	7	ACA68607	Aca68607 Novel hum
c	576	18	0.3	961	7	ACH66315	Ach66315 Novel hum
c	577	18	0.3	961	7	ACD02369	Acd02369 Novel hum
c	578	18	0.3	961	7	ACA89360	Aca89360 Novel hum
c	579	18	0.3	961	7	ACA68997	Aca68997 Novel hum
c	580	18	0.3	961	7	ACA98519	Aca98519 Human PRO
c	581	18	0.3	961	8	ACA63444	Aca63444 cDNA enco
c	582	18	0.3	961	8	ABT44336	Abt44336 Human PRO
c	583	18	0.3	961	8	ADB17200	Adb17200 Human cDN
c	584	18	0.3	961	8	ACH03647	Ach03647 Human sec
c	585	18	0.3	961	8	ADA20005	Ada20005 Novel hum
c	586	18	0.3	961	8	ADB17388	Adb17388 Human cDN
c	587	18	0.3	961	8	ADA20177	Ada20177 Novel hum
c	588	18	0.3	961	8	ACD82161	Acd82161 Human sec
c	589	18	0.3	961	8	ABT44619	Abt44619 Human PRO
c	590	18	0.3	961	8	ACD82286	Acd82286 Human sec
c	591	18	0.3	961	8	ADA00474	Ada00474 Human sec
c	592	18	0.3	961	8	ABT43992	Abt43992 Human mem
c	593	18	0.3	961	8	ADB85716	Adb85716 Novel hum
c	594	18	0.3	961	8	ADB83711	Adb83711 Novel hum
c	595	18	0.3	961	8	ADB80817	Adb80817 Novel hum
c	596	18	0.3	961	8	ADB73358	Adb73358 Novel hum
c	597	18	0.3	961	8	ADB78440	Adb78440 Novel hum
c	598	18	0.3	961	9	ADB85088	Adb85088 Human PRO
c	599	18	0.3	961	9	ADB78194	Adb78194 Novel hum
c	600	18	0.3	961	9	ADB87260	Adb87260 Human PRO
c	601	18	0.3	961	9	ADB84842	Adb84842 Human PRO
c	602	18	0.3	961	9	ADB68395	Adb68395 Human PRO
c	603	18	0.3	961	9	ADB68202	Adb68202 Human PRO
c	604	18	0.3	961	9	ADB83957	Adb83957 Novel hum
c	605	18	0.3	961	9	ADB73112	Adb73112 Novel hum
c	606	18	0.3	961	9	ADB91019	Adb91019 Novel hum
c	607	18	0.3	961	9	ADC07099	Adc07099 Human PRO
c	608	18	0.3	961	9	ADC17278	Adc17278 cDNA sequ
c	609	18	0.3	961	9	ADC14976	Adc14976 Novel hum
c	610	18	0.3	961	9	ADC36950	Adc36950 Human PRO
c	611	18	0.3	961	9	ADC52471	Adc52471 Novel hum
c	612	18	0.3	961	9	ADC21940	Adc21940 Human PRO
c	613	18	0.3	961	9	ADC49971	Adc49971 Novel hum
c	614	18	0.3	961	9	ADC49170	Adc49170 Novel hum
c	615	18	0.3	961	9	ADC49687	Adc49687 Novel hum
c	616	18	0.3	961	9	ADC47548	Adc47548 Novel hum
c	617	18	0.3	961	9	ADC47293	Adc47293 Novel hum
c	618	18	0.3	961	9	ADC78168	Adc78168 Novel hum
c	619	18	0.3	961	9	ADD06403	Add06403 Novel hum
c	620	18	0.3	961	9	ADC77922	Adc77922 Novel hum
c	621	18	0.3	961	9	ADD50885	Add50885 Novel hum
c	622	18	0.3	961	9	ADD51131	Add51131 Novel hum
c	623	18	0.3	961	9	ADD36147	Add36147 Novel hum
c	624	18	0.3	961	9	ADD50612	Add50612 Human PRO
c	625	18	0.3	961	9	ADD50366	Add50366 Human PRO
c	626	18	0.3	961	9	ADD51377	Add51377 Novel hum
c	627	18	0.3	961	10	ADC48924	Adc48924 Novel hum
c	628	18	0.3	961	10	ADC52281	Adc52281 Novel hum
c	629	18	0.3	961	10	ADE21095	Ade21095 Novel hum
c	630	18	0.3	961	10	ADE05939	Ade05939 Human PRO
c	631	18	0.3	961	10	ADD75168	Add75168 Human PRO
c	632	18	0.3	961	10	ADD75914	Add75914 Novel hum
c	633	18	0.3	961	10	ADD85146	Add85146 Novel hum
c	634	18	0.3	961	10	ADD86972	Add86972 Novel hum
c	635	18	0.3	961	10	ADE20849	Ade20849 Novel hum
c	636	18	0.3	961	10	ADE39146	Ade39146 Novel hum
c	637	18	0.3	961	10	ADE05693	Ade05693 Human PRO
c	638	18	0.3	961	10	ADD73678	Add73678 Human PRO
c	639	18	0.3	961	10	ADD78518	Add78518 Novel hum
c	640	18	0.3	961	10	ADE21341	Ade21341 Novel hum
c	641	18	0.3	961	10	ADD77456	Add77456 Novel hum
c	642	18	0.3	961	10	ADE20603	Ade20603 Novel hum
c	643	18	0.3	961	10	ADD75668	Add75668 Human PRO
c	644	18	0.3	961	10	ADD74184	Add74184 Human PRO
c	645	18	0.3	961	10	ADD74430	Add74430 Human PRO
c	646	18	0.3	961	10	ADD76160	Add76160 Novel hum
c	647	18	0.3	961	10	ADD85652	Add85652 Novel hum
c	648	18	0.3	961	10	ADE05201	Ade05201 Human PRO
c	649	18	0.3	961	10	ADD75414	Add75414 Human PRO
c	650	18	0.3	961	10	ADD76958	Add76958 Novel hum
c	651	18	0.3	961	10	ADD86726	Add86726 Novel hum
c	652	18	0.3	961	10	ADD78194	Add78194 Novel hum
c	653	18	0.3	961	10	ADD77702	Add77702 Novel hum
c	654	18	0.3	961	10	ADD77948	Add77948 Novel hum
c	655	18	0.3	961	10	ADD85406	Add85406 Novel hum
c	656	18	0.3	961	10	ADD73938	Add73938 Human PRO
c	657	18	0.3	961	10	ADD74676	Add74676 Human PRO
c	658	18	0.3	961	10	ADD77204	Add77204 Novel hum
c	659	18	0.3	961	10	ADD85898	Add85898 Novel hum
c	660	18	0.3	961	10	ADE05447	Ade05447 Human PRO
c	661	18	0.3	961	10	ADD74922	Add74922 Human PRO
c	662	18	0.3	969	4	AAS53900	Aas53900 Klebsiell
c	663	18	0.3	986	7	ABZ51974	Abz51974 Aspergill
c	664	18	0.3	1000	9	ADC03553	Adc03553 Human Na/
	665	18	0.3	1020	8	ADA03013	Ada03013 Mouse Ncf
	666	18	0.3	1020	9	ADB72751	Adb72751 Mouse Ncf
	667	18	0.3	1020	9	ADC85493	Adc85493 Mouse Ncf
	668	18	0.3	1023	8	ADA48577	Ada48577 Rice gene
c	669	18	0.3	1036	7	ABT23209	Abt23209 Human pro
	670	18	0.3	1040	2	AAQ92530	Aaq92530 P. commun
	671	18	0.3	1051	6	ABL69977	Abl69977 Pancreas
c	672	18	0.3	1084	4	AAI85851	Aai85851 Human pol
c	673	18	0.3	1090	2	AAV84040	Aav84040 Human HTX
c	674	18	0.3	1113	4	ABL22035	Abl22035 Drosophil
	675	18	0.3	1119	7	ACA46946	Aca46946 Prokaryot
	676	18	0.3	1129	7	ABZ80037	Abz80037 Human AGE
c	677	18	0.3	1131	2	AAQ89633	Aaq89633 Human apo
c	678	18	0.3	1131	2	AAQ40029	Aaq40029 Sequence
	679	18	0.3	1161	6	ABN91470	Abn91470 Staphyloc
	680	18	0.3	1214	4	AAL24443	Aal24443 Human bre

c	681	18	0.3	1236	4	AAK78770	Aak78770 Human imm
c	682	18	0.3	1236	4	AAK78769	Aak78769 Human imm
	683	18	0.3	1242	5	AAS87318	Aas87318 DNA encod
	684	18	0.3	1242	6	AAK99392	Aak99392 DNA of th
c	685	18	0.3	1317	7	ACA36042	Aca36042 Prokaryot
c	686	18	0.3	1317	7	ACA31646	Aca31646 Prokaryot
	687	18	0.3	1335	4	AAK61707	Aak61707 Human imm
c	688	18	0.3	1362	7	ACA30833	Aca30833 Prokaryot
	689	18	0.3	1385	4	AAH99262	Aah99262 Human pro
	690	18	0.3	1395	8	ADB12712	Adb12712 Alloiococ
c	691	18	0.3	1405	6	AAL48815	Aal48815 Murine an
c	692	18	0.3	1406	7	ABX05078	Abx05078 Human nov
	693	18	0.3	1425	8	ADA03012	Ada03012 Mouse Ncf
	694	18	0.3	1425	9	ADB72750	Adb72750 Mouse Ncf
	695	18	0.3	1425	9	ADC85492	Adc85492 Mouse Ncf
	696	18	0.3	1427	7	ACD07381	Acd07381 Rice Myb-
	697	18	0.3	1460	2	AAT38075	Aat38075 Sequence
	698	18	0.3	1461	8	ACD26032	Acd26032 Human cDN
	699	18	0.3	1507	9	ADC30526	Adc30526 Human nov
c	700	18	0.3	1517	6	ABQ70450	Abq70450 Listeria
	701	18	0.3	1520	3	AAA52343	Aaa52343 Wild-type
	702	18	0.3	1520	6	ABS54411	Abs54411 Fruit fly
	703	18	0.3	1520	8	ABX16504	Abx16504 Fruitfly
	704	18	0.3	1554	7	ACF70169	Acf70169 Photorhab
	705	18	0.3	1559	4	ABL22362	Abl22362 Drosophil
	706	18	0.3	1581	5	AAH21791	Aah21791 Mouse G4S
	707	18	0.3	1604	9	ADB59144	Adb59144 Toxicity-
	708	18	0.3	1607	3	AAC54954	Aac54954 Arabidops
	709	18	0.3	1609	3	AAC53307	Aac53307 Arabidops
	710	18	0.3	1617	4	AAD12576	Aad12576 Human pro
c	711	18	0.3	1633	7	ABQ77395	Abq77395 Human RNA
c	712	18	0.3	1648	6	ABQ60809	Abq60809 Unidentif
c	713	18	0.3	1751	4	AAI58611	Aai58611 Human pol
c	714	18	0.3	1751	8	ADB48589	Adb48589 Novel hum
	715	18	0.3	1771	9	ADB58986	Adb58986 Toxicity-
	716	18	0.3	1771	9	ADB53738	Adb53738 Primary r
	717	18	0.3	1771	9	ADB37410	Adb37410 Rat stem
	718	18	0.3	1771	9	ADB37412	Adb37412 Rat stem
	719	18	0.3	1827	3	AAF18251	Aaf18251 Lung canc
	720	18	0.3	1840	4	AAK94394	Aak94394 Human ful
	721	18	0.3	1882	2	AAT08702	Aat08702 Rat OCT-1
	722	18	0.3	1882	7	ABT41827	Abt41827 Toxicity
	723	18	0.3	1882	9	ADB59238	Adb59238 Toxicity-
	724	18	0.3	1882	9	ADB52575	Adb52575 Primary r
c	725	18	0.3	1926	2	AAV82522	Aav82522 Sphingomo
	726	18	0.3	1948	4	ABA57042	Aba57042 Human foe
	727	18	0.3	1948	4	ABS30328	Abs30328 Human liv
	728	18	0.3	1959	5	AAF26317	Aaf26317 Pseudomon
	729	18	0.3	2000	4	ABL20725	Abl20725 Drosophil
c	730	18	0.3	2006	9	ADC32458	Adc32458 Human nov
c	731	18	0.3	2014	3	AAC69630	Aac69630 Human sec
c	732	18	0.3	2084	7	ACA23442	Aca23442 Prokaryot
	733	18	0.3	2109	4	ABL03833	Abl03833 Drosophil
	734	18	0.3	2233	4	ABL17591	Abl17591 Drosophil
c	735	18	0.3	2253	6	ABZ14355	Abz14355 Arabidops
	736	18	0.3	2321	4	ABL20727	Abl20727 Drosophil
	737	18	0.3	2339	7	ACC51207	Acc51207 Human Plk
	738	18	0.3	2346	4	ABL22154	Abl22154 Drosophil
	739	18	0.3	2346	4	ABL20130	Abl20130 Drosophil
c	740	18	0.3	2379	6	ABZ14366	Abz14366 Arabidops
	741	18	0.3	2414	4	ABL22150	Abl22150 Drosophil
c	742	18	0.3	2415	6	ABK73868	Abk73868 Bacillus
c	743	18	0.3	2430	5	AAS90898	Aas90898 DNA encod
	744	18	0.3	2484	4	ABL03465	Abl03465 Drosophil
	745	18	0.3	2489	4	ABL22152	Abl22152 Drosophil
	746	18	0.3	2505	2	AAV69865	Aav69865 Human gro
	747	18	0.3	2510	6	ABK83456	Abk83456 Human cDN
c	748	18	0.3	2544	9	ADC30652	Adc30652 Human nov
c	749	18	0.3	2596	4	AAI86538	Aai86538 Human pol
c	750	18	0.3	2602	4	ABL26431	Abl26431 Drosophil
	751	18	0.3	2613	6	ABK28647	Abk28647 Human cDN
	752	18	0.3	2626	9	ADB63577	Adb63577 Human cDN
	753	18	0.3	2670	9	ADB69916	Adb69916 C. neofor
c	754	18	0.3	2724	4	ABL16706	Abl16706 Drosophil
c	755	18	0.3	2810	7	ABZ24708	Abz24708 Human cel
	756	18	0.3	2888	4	ABL16825	Abl16825 Drosophil
c	757	18	0.3	2940	4	AAI60397	Aai60397 Human pol
c	758	18	0.3	3000	2	AAX84399	Aax84399 S. capsul
	759	18	0.3	3044	4	ABL06599	Abl06599 Drosophil
	760	18	0.3	3093	6	ABZ13765	Abz13765 Arabidops
c	761	18	0.3	3183	7	AAL52258	Aal52258 184P1E2 g
c	762	18	0.3	3183	7	AAL52269	Aal52269 184P1E2-r
c	763	18	0.3	3183	7	AAL52259	Aal52259 184P1E2 g
c	764	18	0.3	3183	7	AAL52262	Aal52262 184P1E2 g
c	765	18	0.3	3183	7	AAL52268	Aal52268 184P1E2-r
c	766	18	0.3	3183	7	AAL52260	Aal52260 184P1E2 g
c	767	18	0.3	3183	7	AAL52265	Aal52265 184P1E2 g
c	768	18	0.3	3183	7	AAL52263	Aal52263 184P1E2 g
c	769	18	0.3	3183	7	AAL52267	Aal52267 184P1E2 g
c	770	18	0.3	3183	7	AAL52264	Aal52264 184P1E2 g
c	771	18	0.3	3183	7	AAL52261	Aal52261 184P1E2 g
c	772	18	0.3	3183	7	AAL52266	Aal52266 184P1E2 g
	773	18	0.3	3227	4	AAK80792	Aak80792 Human imm
	774	18	0.3	3227	4	AAK80791	Aak80791 Human imm
	775	18	0.3	3251	4	ABL13875	Abl13875 Drosophil
	776	18	0.3	3289	9	ADB69555	Adb69555 C. neofor
	777	18	0.3	3347	4	ABL19736	Abl19736 Drosophil
c	778	18	0.3	3366	6	ABT07269	Abt07269 Human CpG
c	779	18	0.3	3408	4	ABL21092	Abl21092 Drosophil
	780	18	0.3	3437	9	ADB47716	Adb47716 A. gossyp
	781	18	0.3	3510	2	AAZ07545	Aaz07545 Human vit
	782	18	0.3	3622	4	ABL18286	Abl18286 Drosophil
c	783	18	0.3	3659	1	AAN60204	Aan60204 Interfero
	784	18	0.3	3688	4	ABL22034	Abl22034 Drosophil
	785	18	0.3	3854	9	ADB79946	Adb79946 Rat Tspan
c	786	18	0.3	3969	6	AAD38860	Aad38860 Human kin
	787	18	0.3	3985	4	AAH17848	Aah17848 Human cDN
	788	18	0.3	4077	8	ACF35658	Acf35658 Human nuc
c	789	18	0.3	4189	7	AAD53178	Aad53178 Human kin
	790	18	0.3	4202	7	ABX70939	Abx70939 Novel hum
c	791	18	0.3	4233	4	ABL17590	Abl17590 Drosophil
	792	18	0.3	4287	4	AAK53303	Aak53303 Human pol
	793	18	0.3	4304	4	AAK52319	Aak52319 Human pol
	794	18	0.3	4408	7	ACF34477	Acf34477 Gene enco
c	795	18	0.3	4461	4	AAL02765	Aal02765 Human rep
	796	18	0.3	4473	9	ADB99954	Adb99954 Human vit
	797	18	0.3	4594	9	ADB99955	Adb99955 Human vit
	798	18	0.3	4596	2	AAV03326	Aav03326 DNA seque
	799	18	0.3	4596	5	AAS79490	Aas79490 DNA encod
	800	18	0.3	4596	6	ABK51171	Abk51171 cDNA enco
	801	18	0.3	4596	9	ADE85075	Ade85075 Farnesyl
	802	18	0.3	4599	5	AAS79301	Aas79301 DNA encod
	803	18	0.3	4604	2	AAV41327	Aav41327 Human vit
	804	18	0.3	4604	5	AAS69305	Aas69305 DNA encod
	805	18	0.3	4604	6	ABZ34981	Abz34981 Human gen
	806	18	0.3	4604	9	ADB99864	Adb99864 Human vit
	807	18	0.3	4604	9	ADE84901	Ade84901 Farnesyl
	808	18	0.3	4673	2	AAT12787	Aat12787 Pea phyto
	809	18	0.3	4727	4	ABL13386	Abl13386 Drosophil
	810	18	0.3	4733	9	ADB99953	Adb99953 Human vit
	811	18	0.3	4794	4	ABL19928	Abl19928 Drosophil
	812	18	0.3	4847	2	AAV58943	Aav58943 Rat GRIP2
c	813	18	0.3	5019	4	ABL26430	Abl26430 Drosophil
	814	18	0.3	5049	4	AAL04696	Aal04696 Human rep
	815	18	0.3	5049	4	ABL97603	Abl97603 Human tes
	816	18	0.3	5135	4	ABL03464	Abl03464 Drosophil
c	817	18	0.3	5168	6	ABK94716	Abk94716 Neurodege
	818	18	0.3	5211	5	AAS65560	Aas65560 DNA encod
	819	18	0.3	5289	9	ADB69194	Adb69194 C. neofor
c	820	18	0.3	5350	4	ABL06598	Abl06598 Drosophil
c	821	18	0.3	5359	9	ADC01427	Adc01427 Enterohae
	822	18	0.3	5423	9	ADE53664	Ade53664 Human pro
	823	18	0.3	5433	9	ADB53693	Adb53693 Primary r
c	824	18	0.3	5484	4	ABL13874	Abl13874 Drosophil
	825	18	0.3	5557	5	AAH21794	Aah21794 Human SH2
c	826	18	0.3	5699	5	AAS89500	Aas89500 DNA encod

	827	18	0.3	5721	4	ABL11973 Abl11973 Drosophil
c	828	18	0.3	5938	6	ABK84688 Abk84688 Human cDN
c	829	18	0.3	6196	7	ABT19929 Abt19929 Aspergill
c	830	18	0.3	6196	7	ABT18115 Abt18115 Aspergill
	831	18	0.3	6242	9	ADD71201 Add71201 Human int
c	832	18	0.3	6601	7	ABT19996 Abt19996 Aspergill
c	833	18	0.3	6601	7	ABT18182 Abt18182 Aspergill
c	834	18	0.3	6679	4	ABL20726 Abl20726 Drosophil
	835	18	0.3	6690	4	ABL16769 Abl16769 Drosophil
	836	18	0.3	7033	3	AAZ36989 Aaz36989 Human per
c	837	18	0.3	7060	4	ABL20724 Abl20724 Drosophil
c	838	18	0.3	7079	4	ABL03832 Abl03832 Drosophil
	839	18	0.3	7228	4	AAL04695 Aal04695 Human rep
	840	18	0.3	7228	4	ABL97602 Abl97602 Human tes
c	841	18	0.3	7330	4	ABL06499 Abl06499 Drosophil
c	842	18	0.3	7568	5	AAS80823 Aas80823 DNA encod
	843	18	0.3	8087	4	ABL11972 Abl11972 Drosophil
	844	18	0.3	8254	5	ABA17475 Aba17475 Human ner
c	845	18	0.3	9220	5	ABV24414 Abv24414 Human pro
c	846	18	0.3	9220	5	ABV25265 Abv25265 Human pro
c	847	18	0.3	9416	6	ABK83800 Abk83800 Human cDN
c	848	18	0.3	9416	7	ACF34559 Acf34559 Gene enco
	849	18	0.3	10543	4	ABL06498 Abl06498 Drosophil
	850	18	0.3	11304	4	AAL03113 Aal03113 Human rep
c	851	18	0.3	11950	9	ADE53871 Ade53871 Human pro
c	852	18	0.3	13993	9	ADB31304 Adb31304 Testoster
c	853	18	0.3	14070	2	AAZ09525 Aaz09525 Human Apo
c	854	18	0.3	14070	7	ACA64742 Aca64742 Apolipopr
c	855	18	0.3	14121	6	ABT13015 Abt13015 Human apo
c	856	18	0.3	14121	7	ACC62114 Acc62114 Human ali
	857	18	0.3	15254	4	AAK83135 Aak83135 Human imm
	858	18	0.3	15254	4	AAK83137 Aak83137 Human imm
	859	18	0.3	15255	4	AAK83136 Aak83136 Human imm
	860	18	0.3	15256	4	AAK83134 Aak83134 Human imm
	861	18	0.3	22873	9	ADC87198 Adc87198 Human GPC
	862	18	0.3	24259	4	AAS46691 Aas46691 Tumour su
	863	18	0.3	28315	9	ADC86254 Adc86254 Human GPC
	864	18	0.3	30610	5	ABA15643 Aba15643 Human ner
c	865	18	0.3	31871	4	ABK42516 Abk42516 Genomic s
c	866	18	0.3	31871	8	ADB60672 Adb60672 Connectiv
c	867	18	0.3	32200	4	ABK42917 Abk42917 Genomic s
c	868	18	0.3	32200	8	ADB61073 Adb61073 Connectiv
c	869	18	0.3	34269	4	AAK68677 Aak68677 Human imm
c	870	18	0.3	34269	4	AAK85168 Aak85168 Human imm
	871	18	0.3	36776	4	AAK86321 Aak86321 Human imm
	872	18	0.3	38643	8	ADA03011 Ada03011 Mouse Ncf
	873	18	0.3	38643	9	ADB72749 Adb72749 Mouse Ncf
	874	18	0.3	38643	9	ADC85491 Adc85491 Mouse Ncf
c	875	18	0.3	40328	3	AAZ92584 Aaz92584 Human DAZ
c	876	18	0.3	40742	4	AAK68089 Aak68089 Human imm
c	877	18	0.3	40742	4	AAK79886 Aak79886 Human imm
c	878	18	0.3	43795	3	AAZ92583 Aaz92583 Human DAZ
	879	18	0.3	44979	9	ADC86188 Adc86188 Human GPC
	880	18	0.3	45000	9	ADB99873 Adb99873 Partial g
	881	18	0.3	47670	4	ABL16824 Abl16824 Drosophil
	882	18	0.3	50368	4	ABL16768 Abl16768 Drosophil
c	883	18	0.3	53522	6	AAD30228 Aad30228 Human PKD
c	884	18	0.3	53526	2	AAT94101 Aat94101 Human PKD
c	885	18	0.3	53577	2	AAT18551 Aat18551 Human pol
c	886	18	0.3	53577	2	AAT94108 Aat94108 Human PKD
	887	18	0.3	67571	7	AAD53224_5 Continuation (6 of
	888	18	0.3	72149	9	ADE81173 Ade81173 ML-236B s
	889	18	0.3	96594	9	ADC85476 Adc85476 Human Msf
	890	18	0.3	96595	8	ADA02996 Ada02996 Human Msf
	891	18	0.3	96595	9	ADB72734 Adb72734 Human Msf
	892	18	0.3	110000	2	AAX91990_00 Aax91990 Nucleotid
c	893	18	0.3	110000	4	AAI99682_10 Continuation (11 o
c	894	18	0.3	110000	4	AAI99682_21 Continuation (22 o
c	895	18	0.3	110000	4	AAI99682_22 Continuation (23 o
c	896	18	0.3	110000	4	AAI99683_10 Continuation (11 o
c	897	18	0.3	110000	4	AAI99683_21 Continuation (22 o
	898	18	0.3	110000	6	ABQ69245_03 Continuation (4 of
	899	18	0.3	110000	6	ABQ67197_02 Continuation (3 of
	900	18	0.3	110000	6	ABA03041_03 Continuation (4 of
c	901	18	0.3	110000	7	ACF65385_3 Continuation (4 of
c	902	18	0.3	110000	7	ACF67367_32 Continuation (33 o
c	903	18	0.3	110000	8	ADB12064_06 Continuation (7 of
c	904	18	0.3	110000	8	ADB12064_15 Continuation (16 o
	905	18	0.3	122186	4	AAC89560 Aac89560 Human his
	906	18	0.3	123219	4	AAH88703 Aah88703 Human DNA
	907	18	0.3	165199	6	ABK83460 Abk83460 Human cDN
	908	18	0.3	188888	6	ABQ75562 Abq75562 Human rel
c	909	18	0.3	197997	7	AAL54074 Aal54074 Human tra
c	910	18	0.3	198161	6	ABK83564 Abk83564 Human cDN
c	911	18	0.3	220895	6	ABK84798 Abk84798 Human cDN
	912	18	0.3	349980	6	ABQ81847 Abq81847 Bifidobac
c	913	17	0.3	20	6	AAD35759 Aad35759 Human hIb
c	914	17	0.3	20	6	AAD35758 Aad35758 Human hIb
	915	17	0.3	22	7	ADA06040 Ada06040 Human NOV
	916	17	0.3	22	7	ABT33573 Abt33573 NOV probe
	917	17	0.3	25	6	ABT06340 Abt06340 Human NOV
	918	17	0.3	25	6	ABT06367 Abt06367 Human NOV
	919	17	0.3	25	6	ABT06370 Abt06370 Human NOV
	920	17	0.3	25	6	ABT06343 Abt06343 Human NOV
c	921	17	0.3	32	2	AAT42078 Aat42078 Human ery
c	922	17	0.3	54	2	AAQ42517 Aaq42517 Sequence
	923	17	0.3	60	6	ABN42958 Abn42958 Human spl
c	924	17	0.3	100	7	ACD76585 Acd76585 E. coli K
c	925	17	0.3	116	3	AAC32592 Aac32592 Human sec
	926	17	0.3	117	4	ABA74494 Aba74494 Human foe
	927	17	0.3	117	4	AAI54965 Aai54965 Probe #23
	928	17	0.3	117	4	AAK49135 Aak49135 Human bon
	929	17	0.3	117	4	AAK22962 Aak22962 Human bra
	930	17	0.3	117	4	ABS48786 Abs48786 Human liv
c	931	17	0.3	135	4	AAF75398 Aaf75398 Codon-opt
c	932	17	0.3	138	4	AAI49333 Aai49333 Probe #18
c	933	17	0.3	138	4	ABA51150 Aba51150 Human bre
c	934	17	0.3	138	4	AAK43260 Aak43260 Human bon
c	935	17	0.3	138	4	AAK17456 Aak17456 Human bra
c	936	17	0.3	138	5	AAI09615 Aai09615 Probe #96
	937	17	0.3	162	2	AAT42549 Aat42549 Chloropla
	938	17	0.3	193	6	ABK14569 Abk14569 Human pap
	939	17	0.3	211	7	ACD96588 Acd96588 Human col
c	940	17	0.3	215	5	ABA17523 Aba17523 Human ner
c	941	17	0.3	215	5	ABA17522 Aba17522 Human ner
c	942	17	0.3	218	6	ABL66693 Abl66693 Lung canc
c	943	17	0.3	221	3	AAC14831 Aac14831 Human sec
	944	17	0.3	222	2	AAT21690 Aat21690 Human gen
	945	17	0.3	225	5	AAH52284 Aah52284 Human AFP
c	946	17	0.3	236	4	AAI23132 Aai23132 Probe #13
c	947	17	0.3	236	4	ABA68227 Aba68227 Human foe
c	948	17	0.3	236	4	AAI48442 Aai48442 Probe #17
c	949	17	0.3	236	4	ABA50287 Aba50287 Human bre
c	950	17	0.3	236	4	ABA35237 Aba35237 Probe #13
c	951	17	0.3	236	4	AAK42363 Aak42363 Human bon
c	952	17	0.3	236	4	AAK16608 Aak16608 Human bra
c	953	17	0.3	236	4	ABS41973 Abs41973 Human liv
c	954	17	0.3	236	5	AAI08787 Aai08787 Probe #87
c	955	17	0.3	236	6	ABS16418 Abs16418 Human gen
c	956	17	0.3	238	8	ADA60132 Ada60132 Soybean s
c	957	17	0.3	242	4	AAK63236 Aak63236 Human imm
c	958	17	0.3	249	2	AAX52018 Aax52018 Human sec
	959	17	0.3	258	3	AAA10218 Aaa10218 Rat liver
c	960	17	0.3	261	8	ACH44287 Ach44287 Human foe
c	961	17	0.3	273	4	ABL23265 Abl23265 Drosophil
c	962	17	0.3	273	6	ABL62999 Abl62999 Breast ca
	963	17	0.3	277	6	ABN77360 Abn77360 Human ORF
	964	17	0.3	278	7	ABX83460 Abx83460 Corn ear-
	965	17	0.3	284	6	ABN19394 Abn19394 Human ORF
	966	17	0.3	303	7	ACD97447 Acd97447 Human col
	967	17	0.3	303	9	ACF04665 Acf04665 Rat endob
	968	17	0.3	307	5	AAS34504 Aas34504 Human DNA
	969	17	0.3	315	5	ABV01349 Abv01349 Human pro
	970	17	0.3	321	4	ABA74039 Aba74039 Human foe
	971	17	0.3	321	4	AAI54489 Aai54489 Probe #23
	972	17	0.3	321	4	AAK48661 Aak48661 Human bon

973	17	0.3	321	4	AAK22493	Aak22493 Human bra
974	17	0.3	321	4	ABS48341	Abs48341 Human liv
c 975	17	0.3	321	6	ABN94568	Abn94568 Gene #106
c 976	17	0.3	326	6	ABN21344	Abn21344 Human ORF
977	17	0.3	338	5	ABA13835	Aba13835 Human ner
c 978	17	0.3	345	6	ABV96346	Abv96346 Human pan
c 979	17	0.3	346	4	AAK55956	Aak55956 Human imm
980	17	0.3	349	7	ABX52688	Abx52688 Bovine ES
c 981	17	0.3	351	2	AAV86902	Aav86902 EST clone
982	17	0.3	351	7	ACC44893	Acc44893 Mouse TSH
c 983	17	0.3	354	8	ACL24576	Acl24576 DNA clone
984	17	0.3	356	4	AAD03894	Aad03894 Human tar
985	17	0.3	363	4	AAK92899	Aak92899 Human cDN
986	17	0.3	366	3	AAC03240	Aac03240 Human sec
c 987	17	0.3	371	6	ABV95176	Abv95176 Human pan
988	17	0.3	372	8	ACH47740	Ach47740 Human inf
c 989	17	0.3	373	6	ABV95612	Abv95612 Human pan
c 990	17	0.3	374	6	ABV95943	Abv95943 Human pan
c 991	17	0.3	377	8	ACL24578	Acl24578 DNA clone
c 992	17	0.3	378	4	AAI13465	Aai13465 Probe #33
c 993	17	0.3	378	4	ABA55162	Aba55162 Human foe
c 994	17	0.3	378	4	AAI34821	Aai34821 Probe #35
c 995	17	0.3	378	4	ABA44706	Aba44706 Human bre
c 996	17	0.3	378	4	ABA24907	Aba24907 Probe #33
c 997	17	0.3	378	4	AAK28874	Aak28874 Human bon
c 998	17	0.3	378	4	AAK03423	Aak03423 Human bra
c 999	17	0.3	378	4	ABS28491	Abs28491 Human liv
c1000	17	0.3	378	5	AAI03344	Aai03344 Probe #33

ALIGNMENTS

RESULT 1
ABS63437
ID ABS63437 standard; cDNA; 5691 BP.
XX
AC ABS63437;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human cDNA, homologous to plexin, designated NOV4.
XX
KW Human; gene; ss; NOV; NOVX; NOVX-associated disorder; cardiomyopathy;
KW atherosclerosis; diabetes; cell signalling; metabolic pathway;
KW cellular receptor; downstream effector; cancer; gene therapy;
KW hypertension; congenital heart defect; aortic stenosis; obesity;
KW infectious disease; anorexia; Alzheimer's disease; Parkinson's disease;
KW neurodegenerative disorder; haemophilia; dyslipidemia; vaccine;
KW haematopoietic disease; scleroderma; fertility; immunogen;
KW idiopathic thrombocytopenic purpura; graft versus host disease;
KW Crohn's disease; multiple sclerosis; cirrhosis; autoimmune disease;
KW systemic lupus erythematosus; asthma; arthritis; psoriasis; allergy;
KW stroke; anxiety; Lesch-Nyhan syndrome; schizophrenia; cerebellar ataxia;
KW pain; alcoholism; transgenic.
XX
OS Homo sapiens.
XX
PN WO200226826-A2.
XX
PD 04-APR-2002.
XX
PF 27-SEP-2001; 2001WO-US042336.
XX
PR 27-SEP-2000; 2000US-0235631P.
PR 27-SEP-2000; 2000US-0235633P.
PR 27-SEP-2000; 2000US-0235808P.
PR 27-SEP-2000; 2000US-0236064P.
PR 27-SEP-2000; 2000US-0236065P.
PR 27-SEP-2000; 2000US-0236066P.
PR 28-SEP-2000; 2000US-0236135P.
PR 03-OCT-2000; 2000US-0237434P.
PR 05-OCT-2000; 2000US-0238321P.
PR 06-OCT-2000; 2000US-0238396P.
PR 06-OCT-2000; 2000US-0238399P.
PR 16-MAR-2001; 2001US-0276667P.
PR 31-MAY-2001; 2001US-0294823P.
PR 12-JUL-2001; 2001US-0304868P.
PR 26-SEP-2001; 2001US-00235631.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Gerlach VL, Macdougall JR, Smithson G, Millet I, Stone D;
PI Gunther E, Ellerman K, Grosse WM, Alsobrook JP, Lepley DM;
PI Burgess CE, Padigaru M, Kekuda R, Spytek KA, Leach MD, Shimkets RA;
XX
DR WPI; 2002-499860/53.
DR P-PSDB; ABG78364.
XX
PT Novel isolated NOVX polypeptides and polynucleotides homologous to
PT attractin, plexin, papin-like family of proteins, useful for treating
PT atherosclerosis, diabetes, cancer, Alzheimer's disease, hemophilia and
PT stroke.
XX
PS Claim 8; Page 58-59; 308pp; English.
XX
CC The invention discloses the isolated human polypetides, and
CC polynucleotides encoding them, that have been designated NOVX. The
CC polypeptides, polynucleotides and antibodies are useful in treating or
CC preventing a NOVX-associated disorder which is cardiomyopathy,
CC atherosclerosis and diabetes in a human, where the disorder is related to
CC cell signal processing and metabolic pathway modulation. They can also be
CC used in determining the presence of, or predisposition to, a disease
CC associated with altered levels of the polypeptides and polynucleotides of
CC any one of the 13 sequences (NOV1-NOV8), for raising antibodies, for
CC identifying an agent that binds to, or that modulates the expression or
CC activity of the polypeptide, for identifying an agent which is cellular
CC receptor or downstream effector, for treating or preventing a NOVX-
CC associated disorder and as a pharmaceutical composition comprising the
CC polypeptide, polynucleotide or the antibody. The polypeptides and
CC polynucleotides are useful in diagnostic applications (e.g. as a marker
CC for cancerous cells or tissue types) where their amounts are assessed, or
CC for the manufacture of a medicament (e.g. gene therapy) for treating or
CC preventing disorders or syndromes such as hypertension, congenital heart
CC defects, aortic stenosis, obesity, infectious disease, anorexia, cancer,
CC Alzheimer's disease, Parkinson's disorders, neurodegenerative disorders,
CC haemophilia, dyslipidemias, haematopoietic diseases, scleroderma,
CC fertility, idiopathic thrombocytopenic purpura, graft versus host
CC diseases, Crohn's disease, multiple sclerosis, cirrhosis, autoimmune
CC disease, systemic lupus erythematosus, asthma, arthritis, psoriasis,
CC allergy, stroke, anxiety, Lesch-Nyhan syndrome, schizophrenia, cerebellar
CC ataxia, pain and alcoholism. They may also be used as immunogens to
CC produce antibodies specific for the invention, and as vaccines.
CC Transgenic cells containing a NOVX expressing construct are useful to
CC produce non-human transgenic animals for studying the function and/or
CC activity of the NOVX proteins and for identifying and/or evaluating
CC modulators of NOVX protein activity. Transgenic cells containing a NOVX
CC expressing construct are useful to produce non-human transgenic animals
CC for studying the function and/or activity of the NOVX proteins and for
CC identifying and/or evaluating modulators of NOVX protein activity. The
CC sequences presented in ABS63431-ABS63444 are the human NOV1-NOV8 cDNAs
XX
SQ Sequence 5691 BP; 1318 A; 1658 C; 1574 G; 1141 T; 0 U; 0 Other;

Query Match 100.0%; Score 5691; DB 6; Length 5691;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5691; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAAGCCATGCCCTGGAACTGGACCTGCCTTCTCTCCCACCTCCTCATGGTGGGCATG 60
Db 1 ATGAAAGCCATGCCCTGGAACTGGACCTGCCTTCTCTCCCACCTCCTCATGGTGGGCATG 60

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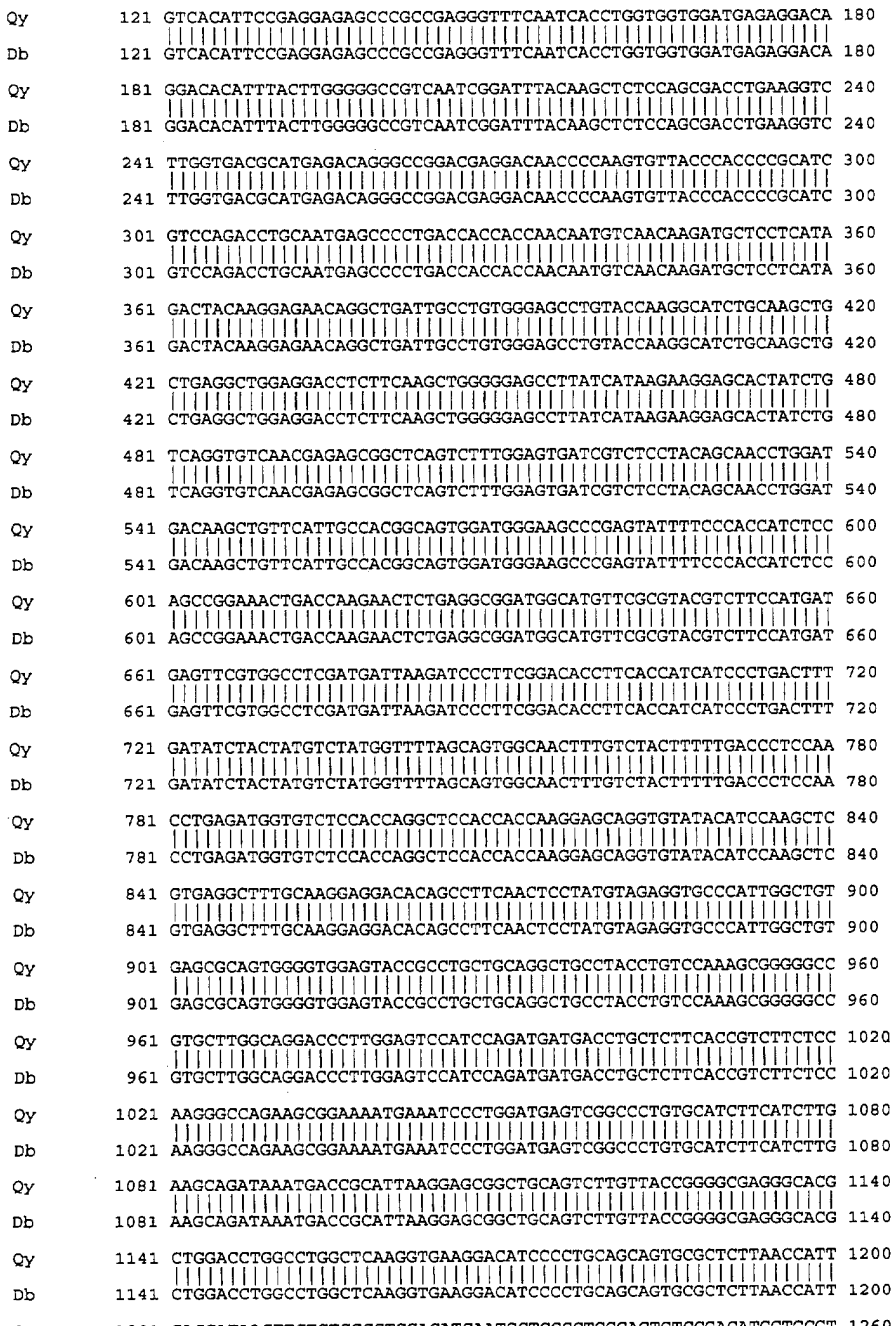
Db 61 GGCTCCTCCACTTTGCTCACCCGGCAGCCAGCCCCGCTGTCCCAGAAGCAGCGGTCATTT 120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Db 121 GTCACATTCCGAGGAGAGCCCGCCGAGGGTTTCAATCACCTGGTGGTGGATGAGAGGACA 180
Qy 181 GGACACATTTACTTGGGGGCCGTCAATCGGATTTACAAGCTCTCCAGCGACCTGAAGGTC 240
Db 181 GGACACATTTACTTGGGGGCCGTCAATCGGATTTACAAGCTCTCCAGCGACCTGAAGGTC 240
Qy 241 TTGGTGACGCATGAGACAGGGCCGGACGAGGACAACCCCAAGTGTTACCCACCCCGCATC 300
Db 241 TTGGTGACGCATGAGACAGGGCCGGACGAGGACAACCCCAAGTGTTACCCACCCCGCATC 300
Qy 301 GTCCAGACCTGCAATGAGCCCCTGACCACCACCAACAATGTCAACAAGATGCTCCTCATA 360
Db 301 GTCCAGACCTGCAATGAGCCCCTGACCACCACCAACAATGTCAACAAGATGCTCCTCATA 360
Qy 361 GACTACAAGGAGAACAGGCTGATTGCCTGTGGGAGCCTGTACCAAGGCATCTGCAAGCTG 420
Db 361 GACTACAAGGAGAACAGGCTGATTGCCTGTGGGAGCCTGTACCAAGGCATCTGCAAGCTG 420
Qy 421 CTGAGGCTGGAGGACCTCTTCAAGCTGGGGGAGCCTTATCATAAGAAGGAGCACTATCTG 480
Db 421 CTGAGGCTGGAGGACCTCTTCAAGCTGGGGGAGCCTTATCATAAGAAGGAGCACTATCTG 480
Qy 481 TCAGGTGTCAACGAGAGCGGCTCAGTCTTTGGAGTGATCGTCTCCTACAGCAACCTGGAT 540
Db 481 TCAGGTGTCAACGAGAGCGGCTCAGTCTTTGGAGTGATCGTCTCCTACAGCAACCTGGAT 540
Qy 541 GACAAGCTGTTCATTGCCACGGCAGTGGATGGGAAGCCCGAGTATTTTCCCACCATCTCC 600
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Qy 601 AGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCATGTTCGCGTACGTCTTCCATGAT 660
Db 601 AGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCATGTTCGCGTACGTCTTCCATGAT 660
Qy 661 GAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACACCTTCACCATCATCCCTGACTTT 720
Db 661 GAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACACCTTCACCATCATCCCTGACTTT 720
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Qy 781 CCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGAGCAGGTGTATACATCCAAGCTC 840
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Db 1081 AAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTCTTGTTACCGGGGCGAGGGCACG 1140
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Db 1141 CTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTGCAGCAGTGCGCTCTTAACCATT 1200
Qy 1201 GACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCTGGGAGTGTCCGACATGGTGCGT 1260
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Db 1261 GGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGACGTCTGTCATCGCATATGTCTAC 1320
Qy 1321 AAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGGCAAGCTGAAGAAGATCCGGGTG 1380
Db 1321 AAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGGCAAGCTGAAGAAGATCCGGGTG 1380
Qy 1381 GATGGACCCAGGGGCAACGCCCTCCAGTATGAGACGGTGCAGGTGGTGGACCCCGGCCCA 1440
Db 1381 GATGGACCCAGGGGCAACGCCCTCCAGTATGAGACGGTGCAGGTGGTGGACCCCGGCCCA 1440
Qy 1441 GTCCTCCGGGATATGGCCTTCTCCAAGGACCACGAGCAACTCTACATCATGTCAGAGAGG 1500
Db 1441 GTCCTCCGGGATATGGCCTTCTCCAAGGACCACGAGCAACTCTACATCATGTCAGAGAGG 1500
Qy 1501 CAGCTCACCAGAGTCCCTGTGGAGTCCTGTGGTCAGTATCAGAGCTGCGGCGAGTGCCTT 1560
Db 1501 CAGCTCACCAGAGTCCCTGTGGAGTCCTGTGGTCAGTATCAGAGCTGCGGCGAGTGCCTT 1560
Qy 1561 GGCTCAGGCGACCCCCACTGTGGCTGGTGTGTGCTGCACAACACGTGCACCCGGAAGGAG 1620
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Qy 1681 CTGACGGTCCATCCCAACAATATCTCCGTCTCTCAGTACAACGTGCTGCTGGTCCTGGAG 1740
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Db 1741 ACGTACAATGTCCCGGAGCTGTCAGCTGGCGTCAACTGCACCTTTGAGGACCTGTCAGAG 1800
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Db 1801 ATGGATGGGCTGGTCGTGGGCAATCAGATCCAGTGCTACTCCCCTGCAGCCAAGGAGGTG 1860
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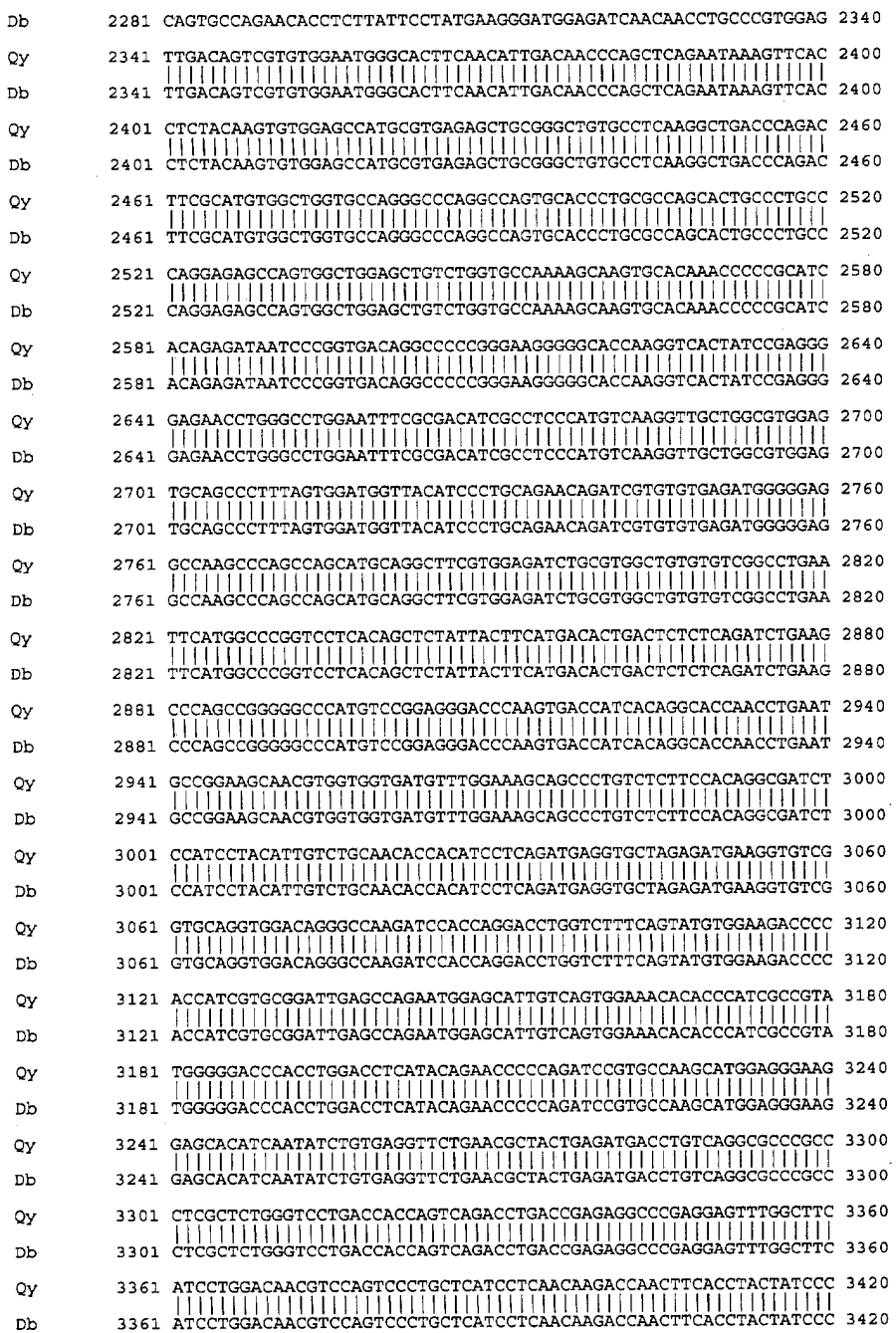
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Qy 2461 TTCGCATGTGGCTGGTGCCAGGGCCCAGGCCAGTGCACCCTGCGCCAGCACTGCCCTGCC 2520
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Db       4501 GTCCTGAGCTGTGTCAGCCCAGACAATGCCAACAGCCCCGAGGTCCCAGTAAAGATCCTC 4560

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Qy       4621 CCTTGCTCCCACCGGCCCAAAGCTGCAGATATGGATCTGGAGTGGCGACAAGGAAGTGGG 4680
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Db       4741 CTGAACACACTGGCCCACTACCAGGTGCCAGATGGTTCCGTGGTGGCATTAGTGTCCAAG 4800

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Qy       5161 GATGAGCAGGCTGATAAACATGGCATTCATGACCCGCACGTCCGCCATACCTGGAAGAGC 5220
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Qy       5281 ATCCATAAGAACAGCATCACAGACGCCTGCCTCTCTGTGGTGGCTCAGACCTTCATGGAC 5340
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Qy       5341 TCTTGCTCCACGTCAGAGCACCGGCTGGGCAAGGACTCGCCCTCCAACAAGCTGCTGTAT 5400
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Qy       5461 ATGCCAGCCATCAGCGACCAAGACATGAACGCATACCTGGCTGAGCAGTCCCGGATGCAC 5520
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RESULT 2
ABA00062
ID ABA00062 standard; cDNA; 6367 BP.
XX
AC ABA00062;
XX
DT 25-OCT-2002 (first entry)
XX
DE CADHP-9 coding sequence, Incyte ID No: 7156379CB1.
XX
KW Gene; human; cell adhesion protein; CADHP; AIDS; Alzheimer's disease;
KW acquired immunodeficiency syndrome; thymic dysplasia; epilepsy;
KW renal tubular acidosis; congenital glaucoma; cancer; atherosclerosis;
KW Parkinson's disease; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 566. .6250
FT /*tag= a
FT /product= "CADHP-9"
XX
PN WO200259312-A2.
XX
PD 01-AUG-2002.
XX
PF 18-DEC-2001; 2001WO-US049206.
XX
PR 18-DEC-2000; 2000US-0256542P.
PR 22-DEC-2000; 2000US-0259604P.
PR 05-JAN-2001; 2001US-0260101P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Duggan BM, Xu Y, Lee EA, Lee S, Lu DAM, Warren BA, Yue H;
PI Gietzen KJ, Honchell CD, Burford N, Baughn MR, Tang TY, Hillman JL;
PI Gandhi AR, Kallick DA, Bandman O, Graul RC, Walia NK, Lu Y;
PI Ramkumar J, Yao MG, Lal PG;
XX
DR WPI; 2002-590826/63.
DR P-PSDB; AAG79420.
XX
PT New human cell adhesion proteins (CADHP) useful for treating, diagnosing
PT and preventing diseases or conditions associated with the aberrant CADPH
PT expression e.g. cancer, acquired immunodeficiency syndrome, Alzheimer's
PT disease and epilepsy.
XX
PS Claim 5; Page 146-48; 149pp; English.
XX
CC The sequences given in ABA00054-63 encode novel human cell adhesion
CC proteins (CADHP). The CADHP polypeptides and polynucleotides are useful
CC in treating, diagnosing and preventing diseases or conditions associated
CC with the decreased expression or overexpression of CADHP, e.g. immune
CC system (acquired immunodeficiency syndrome, thymic dysplasia),
CC neurological (Alzheimer's disease, Parkinson's disease, epilepsy),
CC developmental (renal tubular acidosis, congenital glaucoma) and cell
CC proliferative (cancer, atherosclerosis) disorders. They are also useful
CC in assessing the effects of exogenous compounds on the expression of
CC nucleic acid and amino acid sequences of CADHP. The CADHP or its
CC fragments are useful in screening compounds for effectiveness as agonist
CC or antagonist of the polypeptides, or in altering the expression of the
CC target polynucleotide and compounds that specifically bind to or modulate
CC the activity of the polypeptide. The protein encoded by this cDNA
CC sequence shows homology to mouse plexin-2
XX

```
SQ   Sequence 6367 BP; 1423 A; 1885 C; 1799 G; 1259 T; 0 U; 1 Other;

  Query Match             97.2%;  Score 5532;  DB 6;  Length 6367;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 5682;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

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Qy        121 GTCACATTCCGAGGAGAGCCCGCCGAGGGTTTCAATCACCTGGTGGTGGATGAGAGGACA 180
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Qy        181 GGACACATTTACTTGGGGGCCGTCAATCGGATTTACAAGCTCTCCAGCGACCTGAAGGTC 240
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Qy        361 GACTACAAGGAGAACAGGCTGATTGCCTGTGGGAGCCTGTACCAAGGCATCTGCAAGCTG 420
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Qy        541 GACAAGCTGTTCATTGCCACGGCAGTGGATGGGAAGCCCGAGTATTTTCCCACCATCTCC 600
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Db       1286 GATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTTTGTCTACTTTTTGACCCTCCAA 1345

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Db       1526 GTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGACCTGCTCTTCACCGTCTTCTCC 1585

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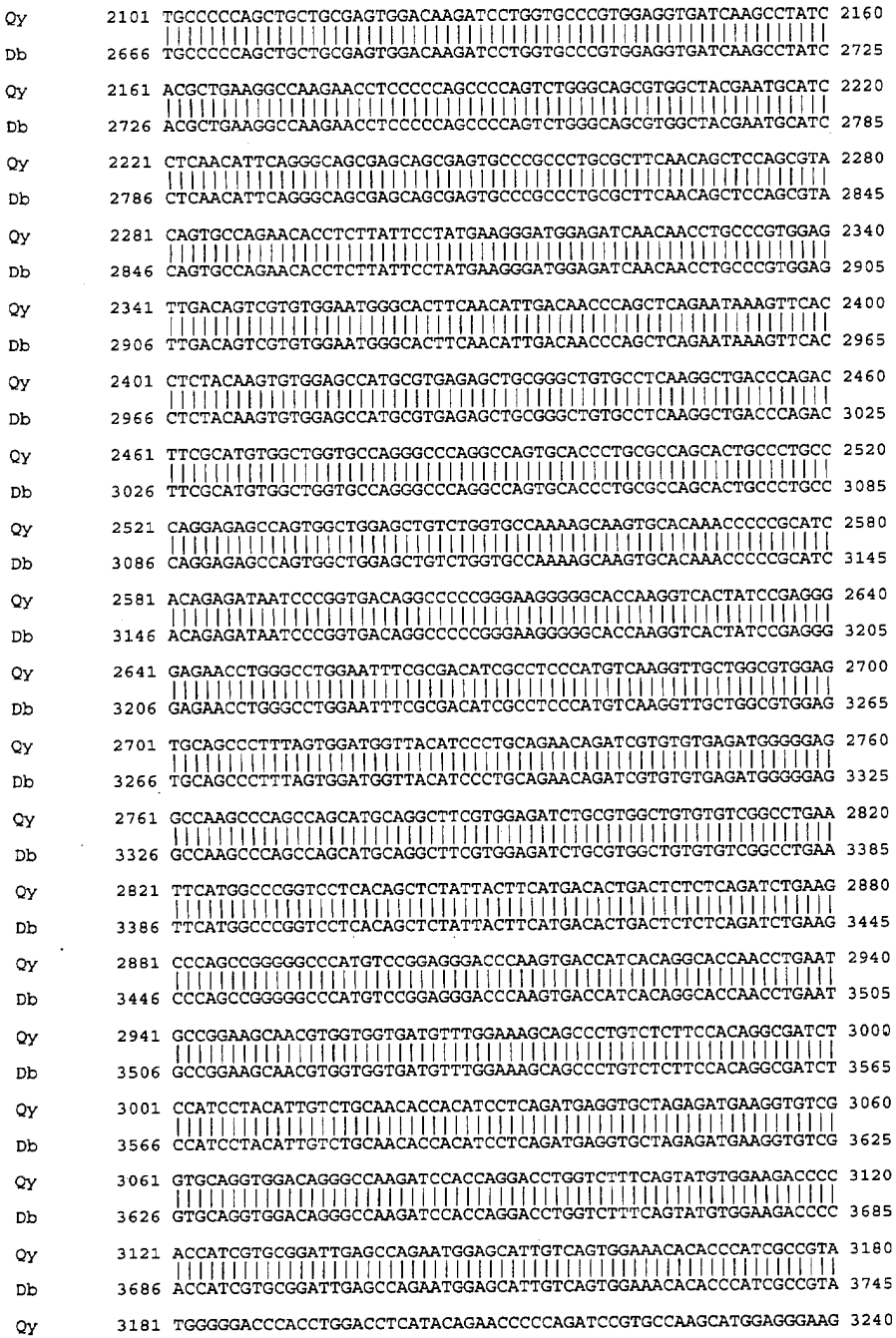
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Qy 3961 ACCATGCGGGTGCTGTTCCCAGGAATTGAAGACCACCCTGTCCTCCGGGACCTTGAGGTC 4020
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Db 4586 CCGGGCTACCGGCAGGAGCGTGTGGAGAAAGGCCTGAAGCTCTTCGCCCAGCTCATCAAC 4645
Qy 4081 AACAAGGTGTTCCTGCTGTCCTTCATCCGCACGCTTGAGTCCCAGCGTAGCTTCTCCATG 4140
Db 4646 AACAAGGTGTTCCTGCTGTCCTTCATCCGCACGCTTGAGTCCCAGCGTAGCTTCTCCATG 4705
Qy 4141 CGCGACCGTGGCAACGTGGCCTCACTCATCATGACCGTGCTGCAGAGCAAGCTGGAGTAC 4200
Db 4706 CGCGACCGTGGCAACGTGGCCTCACTCATCATGACCGTGCTGCAGAGCAAGCTGGAGTAC 4765
Qy 4201 GCCACTGATGTGCTGAAGCAGCTGCTGGCCGACCTCATTGACAAGAACCTGGAGAGCAAG 4260
Db 4766 GCCACTGATGTGCTGAAGCAGCTGCTGGCCGACCTCATTGACAAGAACCTGGAGAGCAAG 4825
Qy 4261 AACCACCCTAAGCTGCTGCTCAGGAGGACTGAGTCAGTGGCTGAGAAGATGCTGACCAAT 4320

```
Db       4826 AACCACCCTAAGCTGCTGCTCAGGAGGACTGAGTCAGTGGCTGAGAAGATGCTGACCAAT 4885
Qy       4321 TGGTTTACTTTCCTCCTCTACAAGTTCCTCAAGGAGTGTGCTGGGGAGCCCCTCTTCTCC 4380
Db       4886 TGGTTTACTTTCCTCCTCTACAAGTTCCTCAAGGAGTGTGCTGGGGAGCCCCTCTTCTCC 4945
Qy       4381 CTGTTCTGTGCCATCAAGCAGCAGATGGAGAAGGGCCCCATTGACGCCATCACGGGCGAG 4440
Db       4946 CTGTTCTGTGCCATCAAGCAGCAGATGGAGAAGGGCCCCATTGACGCCATCACGGGCGAG 5005
Qy       4441 GCCCGCTACTCCTTGAGCGAGGACAAGCTCATCCGCCAGCAGATTGACTACAAAACCCTG 4500
Db       5006 GCCCGCTACTCCTTGAGCGAGGACAAGCTCATCCGCCAGCAGATTGACTACAAAACCCTG 5065
Qy       4501 GTCCTGAGCTGTGTCAGCCCAGACAATGCCAACAGCCCCGAGGTCCCAGTAAAGATCCTC 4560
Db       5066 GTCCTGAGCTGTGTCAGCCCAGACAATGCCAACAGCCCCGAGGTCCCAGTAAAGATCCTC 5125
Qy       4561 AACTGTGACACCATCACTCAGGTCAAGGAGAAGATTCTGGATGCCATCTTCAAGAATGTG 4620
Db       5126 AACTGTGACACCATCACTCAGGTCAAGGAGAAGATTCTGGATGCCATCTTCAAGAATGTG 5185
Qy       4621 CCTTGCTCCCACCGGCCCAAAGCTGCAGATATGGATCTGGAGTGGCGACAAGGAAGTGGG 4680
Db       5186 CCTTGCTCCCACCGGCCCAAAGCTGCAGATATGGATCTGGAGTGGCGACAAGGAAGTGGG 5245
Qy       4681 GCAAGGATGATCTTGCAGGATGAAGACATCACCACCAAGATTGAGAATGATTGGAAGCGA 4740
Db       5246 GCAAGGATGATCTTGCAGGATGAAGACATCACCACCAAGATTGAGAATGATTGGAAGCGA 5305
Qy       4741 CTGAACACACTGGCCCACTACCAGGTGCCAGATGGTTCCGTGGTGGCATTAGTGTCCAAG 4800
Db       5306 CTGAACACACTGGCCCACTACCAGGTGCCAGATGGTTCCGTGGTGGCATTAGTGTCCAAG 5365
Qy       4801 CAGGTGACAGCCTATAACGCAGTGAACAACTCCACCGTCTCCAGGACCTCAGCAAGTAAA 4860
Db       5366 CAGGTGACAGCCTATAACGCAGTGAACAACTCCACCGTCTCCAGGACCTCAGCAAGTAAA 5425
Qy       4861 TATGAAAACATGATCCGGTACACGGGCAGCCCCGACAGCCTCCGCTCACGGACACCTATG 4920
Db       5426 TATGAAAACATGATCCGGTACACGGGCAGCCCCGACAGCCTCCGCTCACGGACACCTATG 5485
Qy       4921 ATCACTCCTGACCTGGAGAGTGGAGTCAAGATGTGGCACCTAGTGAAGAACCACGAGCAC 4980
Db       5486 ATCACTCCTGACCTGGAGAGTGGAGTCAAGATGTGGCACCTAGTGAAGAACCACGAGCAC 5545
Qy       4981 GGAGACCAGAAGGAGGGGGGACCGGGGGAGCAAGATGGTGTCTGAAATCTACCTGACCCGA 5040
Db       5546 GGAGACCAGAAGGAGGGGGGACCGGGGGAGCAAGATGGTGTCTGAAATCTACCTGACCCGA 5605
Qy       5041 CTCCTGGCCACTAAGGGCACACTGCAGAAGTTTGTGGATGACCTCTTTGAGACCATCTTC 5100
Db       5606 CTCCTGGCCACTAAGGGCACACTGCAGAAGTTTGTGGATGACCTCTTTGAGACCATCTTC 5665
Qy       5101 AGCACGGCACACCGTGGCTCTGCCCTGCCCCTGGCCATCAAGTACATGTTTGACTTCCTG 5160
Db       5666 AGCACGGCACACCGTGGCTCTGCCCTGCCCCTGGCCATCAAGTACATGTTTGACTTCCTG 5725
Qy       5161 GATGAGCAGGCTGATAAACATGGCATTCATGACCCGCACGTCCGCCATACCTGGAAGAGC 5220
Db       5726 GATGAGCAGGCTGATAAACATGGCATTCATGACCCGCACGTCCGCCATACCTGGAAGAGC 5785
Qy       5221 AATTGCCTGCCCCTGAGGTTTTGGGTCAACATGATCAAGAACCCGCAGTTTGTGTTTGAC 5280
Db       5786 AATTGCCTGCCCCTGAGGTTTTGGGTCAACATGATCAAGAACCCGCAGTTTGTGTTTGAC 5845
Qy       5281 ATCCATAAGAACAGCATCACAGACGCCTGCCTCTCTGTGGTGGCTCAGACCTTCATGGAC 5340
Db       5846 ATCCATAAGAACAGCATCACAGACGCCTGCCTCTCTGTGGTGGCTCAGACCTTCATGGAC 5905
Qy       5341 TCTTGCTCCACGTCAGAGCACCGGCTGGGCAAGGACTCGCCCTCCAACAAGCTGCTGTAT 5400
Db       5906 TCTTGCTCCACGTCAGAGCACCGGCTGGGCAAGGACTCGCCCTCCAACAAGCTGCTGTAT 5965
Qy       5401 GCCAAGGACATCCCCAGCTACAAGAATTGGGTGGAGAGGTATTACTCAGACATAGGGAAG 5460
Db       5966 GCCAAGGACATCCCCAGCTACAAGAATTGGGTGGAGAGGTATTACTCAGACATAGGGAAG 6025
Qy       5461 ATGCCAGCCATCAGCGACCAAGACATGAACGCATACCTGGCTGAGCAGTCCCGGATGCAC 5520
Db       6026 ATGCCAGCCATCAGCGACCAAGACATGAACGCATACCTGGCTGAGCAGTCCCGGATGCAC 6085
Qy       5521 ATGAATGAGTTCAACACCATGAGTGCACTCTCAGAGATCTTCTCCTATGTGGGCAAATAC 5580
Db       6086 ATGAATGAGTTCAACACCATGAGTGCACTCTCAGAGATCTTCTCCTATGTGGGCAAATAC 6145
Qy       5581 AGCGAGGAGATCCTTGGACCTCTGGACCACGATGACCAGTGTGGGAAGCAGAAACTGGCC 5640
Db       6146 AGCGAGGAGATCCTTGGACCTCTGGACCACGACGACCAGTGTGGGAAGCAGAAACTGGCC 6205
Qy       5641 TACAAACTAGAACAAGTCATAACCCTCATGAGCTTAGACAGCTGA 5685
Db       6206 TACAAACTAGAACAAGTCATAACCCTCATGAGCTTAGACAGCTGA 6250
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RESULT 3
ABK70006
ID   ABK70006 standard; DNA; 2597 BP.
XX
AC   ABK70006;
XX
DT   15-JUL-2002  (first entry)
XX
DE   cDNA encoding human Pro peptide #46.
XX
KW   Human; ss; gene; PRO; secreted protein; transmembrane protein;
KW   genetic disorder; tumour; cancer.
XX
OS   Homo sapiens.
XX
PN   WO200224888-A2.
XX
PD   28-MAR-2002.
XX
PF   29-AUG-2001; 2001WO-US027099.
XX
PR   01-SEP-2000; 2000US-0229896P.
PR   05-SEP-2000; 2000US-0230621P.
PR   22-SEP-2000; 2000US-0235147P.
PR   10-NOV-2000; 2000WO-US030873.
PR   12-JAN-2001; 2001US-0261878P.
PR   16-JAN-2001; 2001US-0261910P.
PR   16-JAN-2001; 2001US-0261939P.
PR   16-JAN-2001; 2001US-0262150P.
PR   25-JAN-2001; 2001US-0264395P.
PR   02-FEB-2001; 2001US-0266421P.
PR   09-FEB-2001; 2001US-0267623P.
PR   28-FEB-2001; 2001WO-US006520.
PR   09-MAR-2001; 2001US-0274399P.
PR   03-APR-2001; 2001US-0280982P.
PR   04-APR-2001; 2001US-0282129P.
PR   04-APR-2001; 2001US-0282199P.
PR   09-MAY-2001; 2001US-0290589P.
PR   25-MAY-2001; 2001WO-US017092.
PR   01-JUN-2001; 2001WO-US017800.
PR   20-JUN-2001; 2001WO-US019692.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-JUL-2001; 2001WO-US021735.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Eaton DL,  Filvaroff E,  Goddard A,  Grimaldi JC;
PI   Gurney AL,  Smith V,  Stephan J,  Watanabe CK,  Wood WI,  Zhang Z;
PI   Fong S;
XX
DR   WPI; 2002-362426/39.
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DR   P-PSDB; ABG34075.
XX
PT   New PRO polypeptides and polynucleotides encoding the polypeptides,
PT   useful in gene therapy, chromosome identification, tissue typing, or for
PT   genetic analysis of individuals with genetic disorders.
XX
PS   Claim 2; Fig 91; 218pp; English.
XX
CC   This invention relates to the cDNA and protein sequences of novel
CC   secreted and transmembrane polypeptides PRO polypeptides. The invention
CC   also comprises a method for producing the proteins of the invention by
CC   recombinant means and antibodies specific for the protein of the
CC   invention. The antibody may be used for detecting the PRO proteins of the
CC   invention and may be used to modify their activity. polynucleotides may
CC   be used as hybridisation probes for a cDNA library to isolate the full-
CC   length PRO cDNA or to isolate other cDNAs, to construct hybridisation
CC   probes for mapping the gene which encodes that PRO and for genetic
CC   analysis of individuals with genetic disorders, in assays to identify
CC   other proteins or molecules involved in binding reaction, to generate
CC   transgenic animals or knock-out animals which in turn are useful in the
CC   development and screening of therapeutically useful reagents, for
CC   chromosome identification, and tissue typing. The PRO polypeptides are
CC   useful in gene therapy, and as molecular weight markers for protein
CC   electrophoresis purposes. The sequences may also be used to detect
CC   overexpression on PRO polypeptides in cancerous tumours and for screening
CC   for differentially expressed genes using microarray technology. The
CC   present sequence represents a cDNA encoding a human PRO protein of the
CC   invention
XX
SQ   Sequence 2597 BP; 688 A; 570 C; 642 G; 697 T; 0 U; 0 Other;

  Query Match             13.9%;  Score 793;  DB 6;  Length 2597;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  793;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        579 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 60

Qy        639 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 120

Qy        699 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 180

Qy        759 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 240

Qy        819 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 300

Qy        879 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 938
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 360

Qy        939 CTACCTGTCCAAAGCGGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTACCTGTCCAAAGCGGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 420

Qy        999 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 480

Qy       1059 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 540

Qy       1119 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 1178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 600

Qy       1179 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 1238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 660

Qy       1239 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 1298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 720

Qy       1299 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 1358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 780

Qy       1359 CAAGCTGAAGAAG 1371
              |||||||||||||
Db        781 CAAGCTGAAGAAG 793


RESULT 4
ADA01359
ID   ADA01359 standard; cDNA; 2597 BP.
XX
AC   ADA01359;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Human PRO polynucleotide #46.
XX
KW   Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide;
KW   tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
KW   adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;
KW   microvascular endothelial cell; endothelial cell tube formation;
KW   sports-related joint problem; articular cartilage defect; osteoarthritis;
KW   rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.
XX
OS   Homo sapiens.
XX
PN   US2003068779-A1.
XX
PD   10-APR-2003.
XX
PF   16-SEP-2002; 2002US-00245107.
XX
PR   09-MAY-2001; 2001US-0290589P.
PR   29-AUG-2001; 2001WO-US027099.
PR   18-JUL-2002; 2002US-00197942.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Eaton DL,  Filvaroff E,  Goddard A,  Grimaldi JC;
PI   Gurney AL,  Smith V,  Stephan JP,  Watanabe CK,  Wood WI,  Zhang Z;
PI   Fong S;
XX
DR   WPI; 2003-625484/59.
DR   P-PSDB; ADA01360.
XX
PT   Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for
PT   stimulating proliferation of human microvascular endothelial cells, and
PT   PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
PT   cells.
XX
PS   Claim 2; Fig 91; 307pp; English.
XX
CC   The invention relates to isolated human PRO polypeptides (secreted and
CC   transmembrane polypeptides) and the polynucleotides encoding them. The
CC   invention also relates to an antibody which specifically binds to a PRO
CC   polypeptide, a method for stimulating the release of tumour necrosis
CC   factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC   proliferation or differentiation of chondrocyte cells and a method for
CC   detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
CC   colon, breast, prostate, rectal, cervical and liver tumours). The
CC   polynucleotides are useful in molecular biology, including uses as
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CC   hybridisation probes, in chromosome and gene mapping, in generating
CC   antisense RNA and DNA and in gene therapy. The polynucleotides may also
CC   be used in preparing PRO polypeptides by recombinant techniques and in
CC   generating either transgenic animals or knock-out animals which are
CC   useful in the development and screening of therapeutically useful
CC   reagents. The PRO polypeptides or antibodies are used in preparing a
CC   medicament for treating a condition responsive to the polypeptides or
CC   antibodies, such as tumours, for stimulating and inhibiting proliferation
CC   of human microvascular endothelial cells, for inducing endothelial cell
CC   tube formation and for treating sports-related joint problems, articular
CC   cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence
CC   represents a human PRO polynucleotide of the invention.
XX
SQ   Sequence 2597 BP; 688 A; 570 C; 642 G; 697 T; 0 U; 0 Other;

  Query Match             13.9%;  Score 793;  DB 8;  Length 2597;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  793;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        579 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 60

Qy        639 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 120

Qy        699 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 180

Qy        759 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 240

Qy        819 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 300

Qy        879 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 938
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 360

Qy        939 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 420

Qy        999 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 480

Qy       1059 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 540

Qy       1119 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 1178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 600

Qy       1179 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 1238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 660

Qy       1239 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 1298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 720

Qy       1299 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 1358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 780

Qy       1359 CAAGCTGAAGAAG 1371
              |||||||||||||
Db        781 CAAGCTGAAGAAG 793


RESULT 5
ADA43788
ID   ADA43788 standard; cDNA; 2597 BP.
XX
AC   ADA43788;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human cDNA encoding secreted/transmembrane polypeptide PRO34003.
XX
KW   ss; gene; human; PRO; secreted protein; transmembrane protein;
KW   endothelial cell tube formation; chondrocyte cell differentiation;
KW   microvascular endothelial cell; tumour; lung tumour; colon tumour;
KW   breast tumour; prostate tumour; rectal tumour; kidney tumour;
KW   liver tumour; cytostatic; vaccine.
XX
OS   Homo sapiens.
XX
PN   US2003064474-A1.
XX
PD   03-APR-2003.
XX
PF   16-SEP-2002; 2002US-00245859.
XX
PR   29-AUG-2001; 2001WO-US027099.
PR   18-JUL-2002; 2002US-00197942.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Eaton DL,  Filvaroff E,  Goddard A,  Grimaldi JC;
PI   Gurney AL,  Smith V,  Stephan JP,  Watanabe CK,  Wood WI,  Zhang Z;
PI   Fong S;
XX
DR   WPI; 2003-605867/57.
DR   P-PSDB; ADA43789.
XX
PT   New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
PT   PRO21383, useful in molecular biology, chromosome and gene mapping, in
PT   generating antisense RNA and DNA, and in gene therapy.
XX
PS   Claim 2; Fig 91; 308pp; English.
XX
CC   The invention relates to an isolated secreted/transmembrane (PRO)
CC   polypeptide, having at least 80% sequence identity to a sequence selected
CC   from any one of the 57 amino acid sequences given in specification, or to
CC   a sequence encoded by a nucleic acid molecule selected from any one of
CC   the nucleic acids deposited under any of the ATCC accession numbers given
CC   in specification, or a sequence having at least 80% identity to PRO
CC   lacking its associated signal peptide, an extracellular domain of PRO
CC   with or without its associated signal peptide. Also included are vectors,
CC   transformed host cells, anti-PRO antibodies, the nucleic acids encoding
CC   PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
CC   administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
CC   PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
CC   an oligonucleotide probe derived from any one of the above nucleotide
CC   sequences. PRO6018 polypeptide is useful for stimulating the
CC   proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
CC   and PRO21383 polypeptides are useful for stimulating the proliferation of
CC   human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
CC   polypeptides are useful for inhibiting the proliferation of human
CC   microvascular endothelial cells. PRO polypeptides are useful for
CC   detecting the presence of tumour in a mammal, including tumours of lung,
CC   colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
CC   PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
CC   PRO34274 polypeptides are useful for inducing endothelial cell tube
CC   formation. PRO or the antibody are useful in the preparation of a
CC   medicament for treating a condition responsive to PRO polypeptide. The
CC   oligonucleotide probes are useful for isolating genomic and cDNA
CC   nucleotide sequences, for measuring or detecting the expression of an
CC   associated gene, and as antisense probes. PRO nucleic acid is useful as a
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CC   hybridisation probe, in chromosome and gene mapping, in the generation of
CC   antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
CC   PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
CC   present sequence encodes a PRO protein.
XX
SQ   Sequence 2597 BP; 688 A; 570 C; 642 G; 697 T; 0 U; 0 Other;

  Query Match             13.9%;  Score 793;  DB 8;  Length 2597;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  793;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        579 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 60

Qy        639 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 120

Qy        699 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 180

Qy        759 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 240

Qy        819 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 300

Qy        879 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 938
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 360

Qy        939 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 420

Qy        999 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 480

Qy       1059 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 540

Qy       1119 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 1178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 600

Qy       1179 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 1238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 660

Qy       1239 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 1298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 720

Qy       1299 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 1358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 780

Qy       1359 CAAGCTGAAGAAG 1371
              |||||||||||||
Db        781 CAAGCTGAAGAAG 793


RESULT 6
ADA43556
ID   ADA43556 standard; cDNA; 2597 BP.
XX
AC   ADA43556;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human cDNA encoding secreted/transmembrane polypeptide PRO34003.
XX
KW   ss; gene; human; PRO; secreted protein; transmembrane protein;
KW   endothelial cell tube formation; chondrocyte cell differentiation;
KW   microvascular endothelial cell; tumour; lung tumour; colon tumour;
KW   breast tumour; prostate tumour; rectal tumour; kidney tumour;
KW   liver tumour; cytostatic; vaccine.
XX
OS   Homo sapiens.
XX
PN   US2003073196-A1.
XX
PD   17-APR-2003.
XX
PF   18-SEP-2002; 2002US-00246210.
XX
PR   04-APR-2001; 2001US-0282199P.
PR   29-AUG-2001; 2001WO-US027099.
PR   18-JUL-2002; 2002US-00197942.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Eaton DL,  Filvaroff E,  Goddard A,  Grimaldi JC;
PI   Gurney AL,  Smith V,  Stephan JP,  Watanabe CK,  Wood WI,  Zhang Z;
PI   Fong S;
XX
DR   WPI; 2003-743814/70.
DR   P-PSDB; ADA43557.
XX
PT   New secreted and transmembrane PRO polypeptides, e.g. PRO20080 or
PT   PRO21383 useful for stimulating the proliferation or differentiation of
PT   chondrocyte cells and detecting the presence of a tumor in a mammal.
XX
PS   Claim 2; Fig 91; 307pp; English.
XX
CC   The invention relates to an isolated secreted/transmembrane (PRO)
CC   polypeptide, having at least 80% sequence identity to a sequence selected
CC   from any one of the 57 amino acid sequences given in specification, or to
CC   a sequence encoded by a nucleic acid molecule selected from any one of
CC   the nucleic acids deposited under any of the ATCC accession numbers given
CC   in specification, or a sequence having at least 80% identity to PRO
CC   lacking its associated signal peptide, an extracellular domain of PRO
CC   with or without its associated signal peptide. Also included are vectors,
CC   transformed host cells, anti-PRO antibodies, the nucleic acids encoding
CC   PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
CC   administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
CC   PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
CC   an oligonucleotide probe derived from any one of the above nucleotide
CC   sequences. PRO6018 polypeptide is useful for stimulating the
CC   proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
CC   and PRO21383 polypeptides are useful for stimulating the proliferation of
CC   human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
CC   polypeptides are useful for inhibiting the proliferation of human
CC   microvascular endothelial cells. PRO polypeptides are useful for
CC   detecting the presence of tumour in a mammal, including tumours of lung,
CC   colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
CC   PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
CC   PRO34274 polypeptides are useful for inducing endothelial cell tube
CC   formation. PRO or the antibody are useful in the preparation of a
CC   medicament for treating a condition responsive to PRO polypeptide. The
CC   oligonucleotide probes are useful for isolating genomic and cDNA
CC   nucleotide sequences, for measuring or detecting the expression of an
CC   associated gene, and as antisense probes. PRO nucleic acid is useful as a
CC   hybridisation probe, in chromosome and gene mapping, in the generation of
CC   antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
CC   PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
CC   present sequence encodes a PRO protein.
XX
SQ   Sequence 2597 BP; 688 A; 570 C; 642 G; 697 T; 0 U; 0 Other;
```

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  Query Match             13.9%;  Score 793;  DB 8;  Length 2597;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  793;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        579 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 60

Qy        639 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 120

Qy        699 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 180

Qy        759 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 240

Qy        819 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 300

Qy        879 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 938
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 360

Qy        939 CTACCTGTCCAAAGCGGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 420

Qy        999 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 480

Qy       1059 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 540

Qy       1119 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 1178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 600

Qy       1179 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 1238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 660

Qy       1239 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 1298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 720

Qy       1299 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 1358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 780

Qy       1359 CAAGCTGAAGAAG 1371
              |||||||||||||
Db         781 CAAGCTGAAGAAG 793


RESULT 7
ADA01231
ID   ADA01231 standard; cDNA; 2597 BP.
XX
AC   ADA01231;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Human PRO polynucleotide #46.
XX
KW   Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide;
KW   tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
KW   cancer; lung; colon; breast; prostate; rectum; kidney; liver;
KW   microvascular endothelial cell; endothelial cell tube formation.
XX
OS   Homo sapiens.
XX
PN   US2003068782-A1.
XX
PD   10-APR-2003.
XX
PF   16-SEP-2002; 2002US-00245851.
XX
PR   27-APR-1999;   99US-0131271P.
PR   29-OCT-1999;   99US-0162506P.
PR   02-DEC-1999;   99WO-US028551.
PR   29-AUG-2001; 2001WO-US027099.
PR   18-JUL-2002; 2002US-00197942.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Eaton DL,  Filvaroff E,  Goddard A,  Grimaldi JC;
PI   Gurney AL,  Smith V,  Stephan JP,  Watanabe CK,  Wood WI,  Zhang Z;
PI   Fong S;
XX
DR   WPI; 2003-625487/59.
DR   P-PSDB; ADA01232.
XX
PT   Novel isolated PRO polypeptides e.g. PRO281 and PRO1560, useful in the
PT   preparation of a medicament for treating a condition responsive to PRO
PT   polypeptide, and as therapeutic agents e.g. vaccines.
XX
PS   Claim 2; Fig 91; 308pp; English.
XX
CC   The invention relates to isolated human PRO polypeptides (secreted and
CC   transmembrane polypeptides) and the polynucleotides encoding them. The
CC   invention also relates to an antibody which specifically binds to a PRO
CC   polypeptide, a method for stimulating the release of tumour necrosis
CC   factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC   proliferation or differentiation of chondrocyte cells and a method for
CC   detecting the presence of a tumour in a mammal (e.g. lung, colon, breast,
CC   prostate, rectal, kidney and liver tumours). The polynucleotides are
CC   useful in molecular biology, including uses as hybridisation probes, in
CC   chromosome and gene mapping, in generating antisense RNA and DNA and in
CC   gene therapy. The polynucleotides may also be used in preparing PRO
CC   polypeptides by recombinant techniques and in generating either
CC   transgenic animals or knock-out animals which are useful in the
CC   development and screening of therapeutically useful reagents. The PRO
CC   polypeptides or antibodies are used in preparing a medicament for
CC   treating a condition responsive to the polypeptides or antibodies, such
CC   as tumours, for stimulating and inhibiting proliferation of human
CC   microvascular endothelial cells and for inducing endothelial cell tube
CC   formation. This sequence represents a human PRO polynucleotide of the
CC   invention.
XX
SQ   Sequence 2597 BP; 688 A; 570 C; 642 G; 697 T; 0 U; 0 Other;

  Query Match             13.9%;  Score 793;  DB 8;  Length 2597;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  793;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        579 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 60

Qy        639 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 120

Qy        699 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 180

Qy        759 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        181 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 240

Qy        819 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 300

Qy        879 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 938
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 360

Qy        939 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 420

Qy        999 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 480

Qy       1059 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 540

Qy       1119 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 1178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 600

Qy       1179 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 1238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 660

Qy       1239 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 1298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 720

Qy       1299 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 1358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 780

Qy       1359 CAAGCTGAAGAAG 1371
              |||||||||||||
Db        781 CAAGCTGAAGAAG 793
```

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RESULT 8
ADA01115
ID   ADA01115 standard; cDNA; 2597 BP.
XX
AC   ADA01115;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Human cDNA encoding secreted/transmembrane polypeptide PRO34003.
XX
KW   ss; gene; human; PRO; secreted protein; transmembrane protein;
KW   endothelial cell tube formation; chondrocyte cell differentiation;
KW   microvascular endothelial cell; tumour; lung tumour; colon tumour;
KW   breast tumour; prostate tumour; rectal tumour; kidney tumour;
KW   liver tumour; cytostatic; vaccine.
XX
OS   Homo sapiens.
XX
PN   US2003068780-A1.
XX
PD   10-APR-2003.
XX
PF   16-SEP-2002; 2002US-00245143.
XX
PR   02-AUG-2000; 2000US-0222695P.
PR   20-JUN-2001; 2001WO-US019692.
PR   29-AUG-2001; 2001WO-US027099.
PR   18-JUL-2002; 2002US-00197942.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Eaton DL,  Filvaroff E,  Goddard A,  Grimaldi JC;
PI   Gurney AL,  Smith V,  Stephan JP,  Watanabe CK,  Wood WI,  Zhang Z;
PI   Fong S;
XX
DR   WPI; 2003-625485/59.
DR   P-PSDB; ADA01116.
XX
PT   Novel isolated PRO polypeptides e.g. PRO281 and PRO1560, useful in the
PT   preparation of a medicament for treating a condition responsive to PRO
PT   polypeptide, and as therapeutic agents e.g. vaccines.
XX
PS   Claim 2; Fig 91; 307pp; English.
XX
CC   The invention relates to an isolated secreted/transmembrane (PRO)
CC   polypeptide, having at least 80% sequence identity to a sequence selected
CC   from any one of the 57 amino acid sequences given in specification, or to
CC   a sequence encoded by a nucleic acid molecule selected from any one of
CC   the nucleic acids deposited under any of the ATCC accession numbers given
CC   in specification, or a sequence having at least 80% identity to PRO
CC   lacking its associated signal peptide, an extracellular domain of PRO
CC   with or without its associated signal peptide. Also included are vectors,
CC   transformed host cells, anti-PRO antibodies, the nucleic acids encoding
CC   PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
CC   administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
CC   PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
CC   an oligonucleotide probe derived from any one of the above nucleotide
CC   sequences. PRO6018 polypeptide is useful for stimulating the
CC   proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
CC   and PRO21383 polypeptides are useful for stimulating the proliferation of
CC   human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
CC   polypeptides are useful for inhibiting the proliferation of human
CC   microvascular endothelial cells. PRO polypeptides are useful for
CC   detecting the presence of tumour in a mammal, including tumours of lung,
CC   colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
CC   PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
CC   PRO34274 polypeptides are useful for inducing endothelial cell tube
CC   formation. PRO or the antibody are useful in the preparation of a
CC   medicament for treating a condition responsive to PRO polypeptide. The
CC   oligonucleotide probes are useful for isolating genomic and cDNA
CC   nucleotide sequences, for measuring or detecting the expression of an
CC   associated gene, and as antisense probes. PRO nucleic acid is useful as a
CC   hybridisation probe, in chromosome and gene mapping, in the generation of
CC   antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
CC   PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
CC   present sequence encodes a PRO protein.
XX
SQ   Sequence 2597 BP; 688 A; 570 C; 642 G; 697 T; 0 U; 0 Other;
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  Query Match           13.9%;  Score 793;  DB 8;  Length 2597;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  793;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        579 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 60

Qy        639 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 120

Qy        699 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 180

Qy        759 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 240

Qy        819 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 300
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Qy        879 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 938
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 360

Qy        939 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 420

Qy        999 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 480

Qy       1059 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 540

Qy       1119 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 1178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 600

Qy       1179 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 1238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 660

Qy       1239 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 1298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 720

Qy       1299 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 1358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 780

Qy       1359 CAAGCTGAAGAAG 1371
              |||||||||||||
Db        781 CAAGCTGAAGAAG 793
```

RESULT 9
ADA43672
ID ADA43672 standard; cDNA; 2597 BP.
XX
AC ADA43672;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human cDNA encoding secreted/transmembrane polypeptide PRO34003.
XX
KW ss; gene; human; PRO; secreted protein; transmembrane protein;
KW endothelial cell tube formation; chondrocyte cell differentiation;
KW microvascular endothelial cell; tumour; lung tumour; colon tumour;
KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
KW liver tumour; cytostatic; vaccine.
XX
OS Homo sapiens.
XX
PN US2003073190-A1.
XX
PD 17-APR-2003.
XX
PF 09-SEP-2002; 2002US-00238283.
XX
PR 01-JUL-1998; 98US-0091358P.
PR 02-JUN-1999; 99WO-US012252.
PR 20-JUL-1999; 99US-0144758P.
PR 28-JUL-1999; 99US-0146222P.
PR 25-AUG-1999; 99US-00380137.
PR 30-MAR-2000; 2000WO-US008439.
PR 02-JUN-2000; 2000WO-US015264.
PR 29-AUG-2001; 2001WO-US027099.
PR 18-JUL-2002; 2002US-00197942.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX
DR WPI; 2003-585304/55.
DR P-PSDB; ADA43673.
XX
PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
PT PRO21383, useful in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and in gene therapy.
XX
PS Claim 2; Fig 91; 352pp; English.
XX
CC The invention relates to an isolated secreted/transmembrane (PRO)
CC polypeptide, having at least 80% sequence identity to a sequence selected
CC from any one of the 57 amino acid sequences given in specification, or to
CC a sequence encoded by a nucleic acid molecule selected from any one of
CC the nucleic acids deposited under any of the ATCC accession numbers given
CC in specification, or a sequence having at least 80% identity to PRO
CC lacking its associated signal peptide, an extracellular domain of PRO
CC with or without its associated signal peptide. Also included are vectors,
CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
CC administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
CC an oligonucleotide probe derived from any one of the above nucleotide
CC sequences. PRO6018 polypeptide is useful for stimulating the
CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
CC and PRO21383 polypeptides are useful for stimulating the proliferation of
CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
CC polypeptides are useful for inhibiting the proliferation of human
CC microvascular endothelial cells. PRO polypeptides are useful for
CC detecting the presence of tumour in a mammal, including tumours of lung,
CC colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
CC PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
CC PRO34274 polypeptides are useful for inducing endothelial cell tube
CC formation. PRO or the antibody are useful in the preparation of a
CC medicament for treating a condition responsive to PRO polypeptide. The
CC oligonucleotide probes are useful for isolating genomic and cDNA
CC nucleotide sequences, for measuring or detecting the expression of an
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
CC hybridisation probe, in chromosome and gene mapping, in the generation of
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
CC present sequence encodes a PRO protein.
XX
SQ Sequence 2597 BP; 688 A; 570 C; 642 G; 697 T; 0 U; 0 Other;

Query Match 13.9%; Score 793; DB 8; Length 2597;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        579 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 60

Qy        639 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 120

Qy        699 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 180

Qy        759 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 240

Qy        819 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 300

Qy        879 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 938
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             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 360

Qy       939 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 998
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 420

Qy       999 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 1058
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 480

Qy      1059 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 1118
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 540

Qy      1119 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 1178
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 600

Qy      1179 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 1238
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 660

Qy      1239 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 1298
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 720

Qy      1299 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 1358
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 780

Qy      1359 CAAGCTGAAGAAG 1371
             |||||||||||||
Db       781 CAAGCTGAAGAAG 793
```

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RESULT 10
ADA06934
ID   ADA06934 standard; cDNA; 2597 BP.
XX
AC   ADA06934;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Human PRO polynucleotide #46.
XX
KW   Human; PRO; gene; ss; secreted polypeptide; transmembrane polypeptide;
KW   tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
KW   adrenal; lung; colon; breast; prostate; rectum; cervix; liver;
KW   microvascular endothelial cell; endothelial cell tube formation;
KW   bone disorder; cartilage disorder; sports injury; proteoglycan;
KW   cartilage; sports-related joint problem; articular cartilage defect;
KW   osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder;
KW   thalassaemia; immune system cell infiltration; cancer; vulnerary;
KW   antianaemic; osteopathic; antirheumatic; antiarthritic.
XX
OS   Homo sapiens.
XX
PN   US2003068781-A1.
XX
PD   10-APR-2003.
XX
PF   16-SEP-2002; 2002US-00245771.
XX
PR   03-AUG-1999;   99US-0146843P.
PR   15-MAY-2000; 2000WO-US013358.
PR   29-AUG-2001; 2001WO-US027099.
PR   18-JUL-2002; 2002US-00197942.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Eaton DL,  Filvaroff E,  Goddard A,  Grimaldi JC;
PI   Gurney AL,  Smith V,  Stephan JP,  Watanabe CK,  Wood WI,  Zhang Z;
PI   Fong S;
XX
DR   WPI; 2003-625486/59.
DR   P-PSDB; ADA06935.
XX
PT   Novel secreted and transmembrane polypeptides, PRO polypeptides useful
PT   for stimulating proliferation or differentiation of chondrocyte cells and
PT   inducing endothelial cell tube formation.
XX
PS   Claim 2; Fig 91; 307pp; English.
XX
CC   The invention relates to isolated human PRO polypeptides (secreted and
CC   transmembrane polypeptides) and the polynucleotides encoding them. The
CC   invention also relates to an antibody which specifically binds to a PRO
CC   polypeptide, a method for stimulating the release of tumour necrosis
CC   factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC   proliferation or differentiation of chondrocyte cells and a method for
CC   detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
CC   colon, breast, prostate, rectal, cervical and liver tumours). The
CC   polynucleotides are useful in molecular biology, including uses as
CC   hybridisation probes, in chromosome and gene mapping, in generating
CC   antisense RNA and DNA and in gene therapy. The polynucleotides may also
CC   be used in preparing PRO polypeptides by recombinant techniques and in
CC   generating either transgenic animals or knock-out animals which are
CC   useful in the development and screening of therapeutically useful
CC   reagents. The PRO polypeptides or antibodies are used in preparing a
CC   medicament for treating a condition responsive to the polypeptides or
CC   antibodies, such as tumours, for stimulating and inhibiting proliferation
CC   of human microvascular endothelial cells, for inducing endothelial cell
CC   tube formation and for treating various bone and/or cartilage disorders
CC   such as sports injuries and arthritis. PRO polypeptides which stimulate
CC   the release of proteoglycans from cartilage are useful for treating
CC   sports-related joint problems, articular cartilage defects,
CC   osteoarthritis and rheumatoid arthritis. PRO polypeptides are also useful
CC   for treating various mammalian haemoglobin-associated disorders such as
CC   various thalassaemias and conditions which may benefit from enhanced
CC   local immune system cell infiltration. This sequence represents a human
CC   PRO polynucleotide of the invention.
XX
SQ   Sequence 2597 BP; 688 A; 570 C; 642 G; 697 T; 0 U; 0 Other;

  Query Match             13.9%;  Score 793;  DB 8;  Length 2597;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  793;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       579 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 638
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 60

Qy       639 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 698
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 120

Qy       699 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 758
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 180

Qy       759 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 818
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 240

Qy       819 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 878
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 300

Qy       879 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 938
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 360

Qy       939 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 998
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 420
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Qy        999 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 480

Qy       1059 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 540

Qy       1119 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 1178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 600

Qy       1179 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 1238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 660

Qy       1239 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 1298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 720

Qy       1299 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 1358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 780

Qy       1359 CAAGCTGAAGAAG 1371
              |||||||||||||
Db        781 CAAGCTGAAGAAG 793
```

RESULT 11
ADA08422
ID ADA08422 standard; cDNA; 2597 BP.
XX
AC ADA08422;
XX
DT 06-NOV-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO34003 cDNA.
XX
KW ss; gene; osteopathic; antirheumatic; antiarthritic; gene therapy;
KW cell proliferation stimulator;
KW chondrocyte cell differentiation stimulator;
KW secreted and transmembrane protein; PRO; human; PRO1313; PRO20080;
KW PRO21383; human microvascular endothelial cell proliferation; PRO6071;
KW PRO4487; PRO6006; PRO240; PRO256; PRO698; PRO1002; PRO4316; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour;
KW sports-related joint problem; articular cartilage defect; osteoarthritis;
KW rheumatoid arthritis; tissue typing.
XX
OS Homo sapiens.
XX
PN US2003068783-A1.
XX
PD 10-APR-2003.
XX
PF 16-SEP-2002; 2002US-00245883.
XX
PR 09-MAY-2001; 2001US-0290589P.
PR 29-AUG-2001; 2001WO-US027099.
PR 18-JUL-2002; 2002US-00197942.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX
DR WPI; 2003-625488/59.
DR P-PSDB; ADA08423.
XX
PT Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for
PT stimulating proliferation of human microvascular endothelial cells, and
PT PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
PT cells.
XX
PS Claim 2; Fig 91; 308pp; English.
XX
CC The invention describes an isolated PRO (secreted and transmembrane)
CC polypeptide (I). PRO6018 polypeptide is useful for stimulating the
CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080,
CC or PRO21383 polypeptide is useful for stimulating the proliferation of
CC human microvascular endothelial cells. PRO6071, PRO4487, or PRO6006
CC polypeptide is useful for inhibiting the proliferation of human
CC microvascular endothelial cells. PRO polypeptides such as PRO240, PRO256,
CC PRO698, PRO1002, PRO4316, etc., are useful for detecting the presence of
CC tumour in a mammal which involves comparing the level of expression of
CC the above mentioned polypeptides in a test sample of cells taken from the
CC mammal, and a control sample of normal cells of the same cell type, where
CC a higher level of expression of the PRO polypeptide in the test sample as
CC compared to the control sample is indicative of the presence of tumour in
CC the mammal, the tumour being adrenal tumour, lung tumour, colon tumour,
CC breast tumour, prostate tumour, rectal tumour, cervical tumour or liver
CC tumour. PRO6018 polypeptide is useful for treating sports-related joint
CC problems, articular cartilage defects, osteoarthritis, or rheumatoid
CC arthritis. PRO polypeptides are useful as molecular weight markers for
CC protein electrophoresis. (I) is also useful for screening compounds to
CC identify those that mimic the PRO polypeptide (agonists) or prevent the
CC effect of the PRO polypeptide (antagonists). The polynulceotide (II)
CC encoding (I) is useful as hybridisation probes, in chromosome and gene
CC mapping and in the generation of anti-sense RNA and DNA. PRO nucleic acid
CC is also be useful for the preparation of PRO polypeptides. The full-
CC length native sequence of PRO gene or its portions may be used as
CC hybridisation probes for a cDNA library to isolate the full-length PRO
CC cDNA or to isolate still other cDNAs. Nucleotide sequences encoding PRO
CC can also be used to construct hybridisation probes for mapping the gene
CC which encodes that PRO and for the genetic analysis of individuals with
CC genetic disorders. (II) encoding (I) or its modified forms can also be
CC used to generate either transgenic animals or knockout animals which in
CC turn are useful in the development and screening of therapeutically
CC useful reagents. (II) encoding PRO polypeptides are also useful in gene
CC therapy techniques to treat conditions associated with aberrant
CC expression or activity of (I). The PRO polypeptides and nucleic acid
CC molecules are useful for tissue typing. This sequence encodes a novel
CC human secreted and transmembrane PRO polypeptide.
XX
SQ Sequence 2597 BP; 688 A; 570 C; 642 G; 697 T; 0 U; 0 Other;

Query Match 13.9%; Score 793; DB 8; Length 2597;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        579 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 60

Qy        639 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 120

Qy        699 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 180

Qy        759 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 240

Qy        819 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 300

Qy        879 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 938
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 360
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Qy        939 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 420

Qy        999 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 480

Qy       1059 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 540

Qy       1119 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 1178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 600

Qy       1179 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 1238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 660

Qy       1239 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 1298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 720

Qy       1299 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 1358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 780

Qy       1359 CAAGCTGAAGAAG 1371
              |||||||||||||
Db        781 CAAGCTGAAGAAG 793
```

RESULT 12
ADB99715
ID ADB99715 standard; cDNA; 2597 BP.
XX
AC ADB99715;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human PRO polynucleotide SEQ ID 91.
XX
KW Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide;
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
KW adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;
KW microvascular endothelial cell; endothelial cell tube formation;
KW sports-related joint problem; articular cartilage defect; osteoarthritis;
KW rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.
XX
OS Homo sapiens.
XX
PN US2003082728-A1.
XX
PD 01-MAY-2003.
XX
PF 16-SEP-2002; 2002US-00245185.
XX
PR 07-JUL-1998; 98US-0091978P.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 29-AUG-2001; 2001WO-US027099.
PR 18-JUL-2002; 2002US-00197942.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX
DR WPI; 2003-743898/70.
DR P-PSDB; ADB99716.
XX

PT New isolated, secreted and transmembrane PRO polypeptides and nucleic
PT acids, useful for diagnosing, preventing and/or treating tumors, such as
PT lung, colon, breast, prostate, rectal, kidney or liver tumors.
XX
PS Claim 2; Fig 91; 308pp; English.
XX
CC The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
CC colon, breast, prostate, rectal, cervical and liver tumours). The
CC polynucleotides are useful in molecular biology, including uses as
CC hybridisation probes, in chromosome and gene mapping, in generating
CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
CC be used in preparing PRO polypeptides by recombinant techniques and in
CC generating either transgenic animals or knock-out animals which are
CC useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides or antibodies are used in preparing a
CC medicament for treating a condition responsive to the polypeptides or
CC antibodies, such as tumours, for stimulating and inhibiting proliferation
CC of human microvascular endothelial cells, for inducing endothelial cell
CC tube formation and for treating sports-related joint problems, articular
CC cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence
CC represents a human PRO polynucleotide of the invention.
XX
SQ Sequence 2597 BP; 688 A; 570 C; 642 G; 697 T; 0 U; 0 Other;

Query Match 13.9%; Score 793; DB 8; Length 2597;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        579 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 60

Qy        639 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 120

Qy        699 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 180

Qy        759 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 240

Qy        819 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 300

Qy        879 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 938
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 360

Qy        939 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 420

Qy        999 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 480

Qy       1059 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 540

Qy       1119 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 1178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 600
```

```
Qy       1179 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 1238
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 660

Qy       1239 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 1298
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 720

Qy       1299 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 1358
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 780

Qy       1359 CAAGCTGAAGAAG 1371
             |||||||||||||
Db        781 CAAGCTGAAGAAG 793
```

RESULT 13
ADB86998
ID ADB86998 standard; cDNA; 2597 BP.
XX
AC ADB86998;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human PRO polynucleotide #46.
XX
KW Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide;
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
KW adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;
KW microvascular endothelial cell; endothelial cell tube formation;
KW sports-related joint problem; articular cartilage defect; osteoarthritis;
KW rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.
XX
OS Homo sapiens.
XX
PN US2003082726-A1.
XX
PD 01-MAY-2003.
XX
PF 12-SEP-2002; 2002US-00243095.
XX
PR 29-AUG-2001; 2001WO-US027099.
PR 18-JUL-2002; 2002US-00197942.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX
DR WPI; 2003-743897/70.
DR P-PSDB; ADB86999.
XX
PT New isolated, secreted and transmembrane PRO polypeptides and nucleic
PT acids, useful for diagnosing, preventing and/or treating tumors, such as
PT lung, colon, breast, prostate, rectal, kidney or liver tumors.
XX
PS Claim 2; Fig 91; 308pp; English.
XX
CC The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
CC colon, breast, prostate, rectal, cervical and liver tumours). The
CC polynucleotides are useful in molecular biology, including uses as
CC hybridisation probes, in chromosome and gene mapping, in generating
CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
CC be used in preparing PRO polypeptides by recombinant techniques and in
CC generating either transgenic animals or knock-out animals which are
CC useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides or antibodies are used in preparing a
CC medicament for treating a condition responsive to the polypeptides or
CC antibodies, such as tumours, for stimulating and inhibiting proliferation
CC of human microvascular endothelial cells, for inducing endothelial cell
CC tube formation and for treating sports-related joint problems, articular
CC cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence
CC represents a human PRO polynucleotide of the invention.
XX
SQ Sequence 2597 BP; 688 A; 570 C; 642 G; 697 T; 0 U; 0 Other;

Query Match   13.9%; Score 793; DB 8; Length 2597;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 793; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy        579 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 60

Qy        639 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 120

Qy        699 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 180

Qy        759 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 240

Qy        819 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 300

Qy        879 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 938
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 360

Qy        939 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 420

Qy        999 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 480

Qy       1059 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 540

Qy       1119 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 1178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 600

Qy       1179 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 1238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 660

Qy       1239 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 1298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 720

Qy       1299 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 1358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 780

Qy       1359 CAAGCTGAAGAAG 1371
              |||||||||||||
Db        781 CAAGCTGAAGAAG 793
```

```
RESULT 14
ADB66153
ID   ADB66153 standard; cDNA; 2597 BP.
XX
AC   ADB66153;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Human cDNA encoding secreted/transmembrane polypeptide PRO34003.
XX
KW   ss; gene; human; PRO; secreted protein; transmembrane protein;
KW   endothelial cell tube formation; chondrocyte cell differentiation;
KW   microvascular endothelial cell; tumour; lung tumour; colon tumour;
KW   breast tumour; prostate tumour; rectal tumour; kidney tumour;
KW   liver tumour; cytostatic; vaccine.
XX
OS   Homo sapiens.
XX
PN   US2003082729-A1.
XX
PD   01-MAY-2003.
XX
PF   16-SEP-2002; 2002US-00245427.
XX
PR   02-FEB-2001; 2001US-0266421P.
PR   09-FEB-2001; 2001US-0267623P.
PR   29-AUG-2001; 2001WO-US027099.
PR   18-JUL-2002; 2002US-00197942.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Eaton DL,  Filvaroff E,  Goddard A,  Grimaldi JC;
PI   Gurney AL,  Smith V,  Stephan JP,  Watanabe CK,  Wood WI,  Zhang Z;
PI   Fong S;
XX
DR   WPI; 2003-786917/74.
DR   P-PSDB; ADB66154.
XX
PT   New isolated, secreted and transmembrane PRO polypeptides and nucleic
PT   acids, useful for diagnosing, preventing and/or treating tumors, such as
PT   lung, colon, breast, prostate, rectal, kidney or liver tumors.
XX
PS   Claim 2; Fig 91; 308pp; English.
XX
CC   The invention relates to an isolated secreted/transmembrane (PRO)
CC   polypeptide, having at least 80% sequence identity to a sequence selected
CC   from any one of the 57 amino acid sequences given in specification, or to
CC   a sequence encoded by a nucleic acid molecule selected from any one of
CC   the nucleic acids deposited under any of the ATCC accession numbers given
CC   in specification, or a sequence having at least 80% identity to PRO
CC   lacking its associated signal peptide, an extracellular domain of PRO
CC   with or without its associated signal peptide. Also included are vectors,
CC   transformed host cells, anti-PRO antibodies, the nucleic acids encoding
CC   PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
CC   administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,
CC   PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
CC   an oligonucleotide probe derived from any one of the above nucleotide
CC   sequences. PRO6018 polypeptide is useful for stimulating the
CC   proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
CC   and PRO21383 polypeptides are useful for stimulating the proliferation of
CC   human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
CC   polypeptides are useful for inhibiting the proliferation of human
CC   microvascular endothelial cells. PRO polypeptides are useful for
CC   detecting the presence of tumour in a mammal, including tumours of lung,
CC   colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560,
CC   PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and
CC   PRO34274 polypeptides are useful for inducing endothelial cell tube
CC   formation. PRO or the antibody are useful in the preparation of a
CC   medicament for treating a condition responsive to PRO polypeptide. The
CC   oligonucleotide probes are useful for isolating genomic and cDNA
CC   nucleotide sequences, for measuring or detecting the expression of an
CC   associated gene, and as antisense probes. PRO nucleic acid is useful as a
CC   hybridisation probe, in chromosome and gene mapping, in the generation of
CC   antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
CC   PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
CC   present sequence encodes a PRO protein.
XX
SQ   Sequence 2597 BP; 688 A; 570 C; 642 G; 697 T; 0 U; 0 Other;

  Query Match             13.9%;  Score 793;  DB 8;  Length 2597;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  793;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        579 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 60

Qy        639 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 120

Qy        699 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 180

Qy        759 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 240

Qy        819 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 300

Qy        879 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 938
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 360

Qy        939 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 420

Qy        999 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 480

Qy       1059 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 540

Qy       1119 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 1178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 600

Qy       1179 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 1238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 660

Qy       1239 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 1298
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 720

Qy       1299 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 1358
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 780

Qy       1359 CAAGCTGAAGAAG 1371
              |||||||||||||
Db        781 CAAGCTGAAGAAG 793


RESULT 15
ADB99831
ID   ADB99831 standard; cDNA; 2597 BP.
XX
AC   ADB99831;
XX
```

DT 04-DEC-2003 (first entry)
XX
DE Human PRO polynucleotide SEQ ID 91.
XX
KW Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide;
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
KW adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;
KW microvascular endothelial cell; endothelial cell tube formation;
KW sports-related joint problem; articular cartilage defect; osteoarthritis;
KW rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.
XX
OS Homo sapiens.
XX
PN US2003073192-A1.
XX
PD 17-APR-2003.
XX
PF 16-SEP-2002; 2002US-00245055.
XX
PR 20-JUL-1999; 99US-0144758P.
PR 28-JUL-1999; 99US-0146222P.
PR 30-MAR-2000; 2000WO-US008439.
PR 02-JUN-2000; 2000WO-US015264.
PR 29-AUG-2001; 2001WO-US027099.
PR 18-JUL-2002; 2002US-00197942.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX
DR WPI; 2003-743813/70.
DR P-PSDB; ADB99832.
XX
PT New isolated secreted and transmembrane PRO polypeptides, e.g. PRO20080
PT or PRO21383, useful in stimulating the proliferation or differentiation
PT of chondrocyte cells and detecting the presence of a tumor in a mammal.
XX
PS Claim 2; Fig 91; 308pp; English.
XX
CC The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
CC colon, breast, prostate, rectal, cervical and liver tumours). The
CC polynucleotides are useful in molecular biology, including uses as
CC hybridisation probes, in chromosome and gene mapping, in generating
CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
CC be used in preparing PRO polypeptides by recombinant techniques and in
CC generating either transgenic animals or knock-out animals which are
CC useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides or antibodies are used in preparing a
CC medicament for treating a condition responsive to the polypeptides or
CC antibodies, such as tumours, for stimulating and inhibiting proliferation
CC of human microvascular endothelial cells, for inducing endothelial cell
CC tube formation and for treating sports-related joint problems, articular
CC cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence
CC represents a human PRO polynucleotide of the invention.
XX
SQ Sequence 2597 BP; 688 A; 570 C; 642 G; 697 T; 0 U; 0 Other;

Query Match 13.9%; Score 793; DB 9; Length 2597;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        579 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 638
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Qy        639 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 698
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Qy        759 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 818
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Qy        819 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 878
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Qy        879 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 938
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Qy        939 CTACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGA 998
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Qy       1119 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 1178
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Search completed: February 20, 2004, 03:12:05
Job time : 1381 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 20, 2004, 02:26:30 ; Search time 260 Seconds
(without alignments)
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Title: US-09-964-956-12
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	20	0.4	249	4	US-09-252-991A-3017	Sequence 3017, Ap
c	2	20	0.4	311	4	US-09-313-294A-7021	Sequence 7021, Ap
c	3	20	0.4	462	4	US-09-401-064-165	Sequence 165, App
c	4	20	0.4	616	3	US-09-385-982-238	Sequence 238, App
	5	20	0.4	894	4	US-09-252-991A-2754	Sequence 2754, Ap
	6	20	0.4	1029	4	US-09-252-991A-2651	Sequence 2651, Ap
c	7	20	0.4	1455	4	US-09-252-991A-3212	Sequence 3212, Ap
c	8	20	0.4	1456	4	US-09-976-594-779	Sequence 779, App
	9	20	0.4	1636	4	US-08-630-915A-31	Sequence 31, Appl
c	10	20	0.4	2522	4	US-09-620-312D-702	Sequence 702, App
c	11	20	0.4	13842	3	US-09-105-537-30	Sequence 30, Appl
c	12	20	0.4	36778	3	US-09-105-537-5	Sequence 5, Appli
c	13	20	0.4	38506	3	US-09-320-878-19	Sequence 19, Appl
c	14	20	0.4	38506	4	US-09-141-908-1	Sequence 1, Appli
c	15	20	0.4	38506	4	US-09-657-440-19	Sequence 19, Appl
	16	19	0.3	531	5	PCT-US95-04583-1	Sequence 1, Appli
c	17	19	0.3	588	2	US-08-924-695A-3	Sequence 3, Appli
c	18	19	0.3	791	4	US-09-657-346A-10	Sequence 10, Appl
	19	19	0.3	900	1	US-07-955-041-1	Sequence 1, Appli
	20	19	0.3	900	1	US-08-227-455-1	Sequence 1, Appli
	21	19	0.3	900	1	US-08-472-482-1	Sequence 1, Appli
	22	19	0.3	900	1	US-08-487-069-1	Sequence 1, Appli
c	23	19	0.3	1236	4	US-09-328-352-3326	Sequence 3326, Ap
	24	19	0.3	1407	4	US-09-894-844-35	Sequence 35, Appl
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	26	19	0.3	2477	4	US-09-907-794A-169	Sequence 169, App
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	33	19	0.3	4474	3	US-08-464-410A-9	Sequence 9, Appli
	34	19	0.3	4474	5	PCT-US94-06066-9	Sequence 9, Appli
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	37	19	0.3	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	38	19	0.3	4411529	3	US-09-103-840A-1	Sequence 1, Appli
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	51	18	0.3	1040	2	US-08-798-744-91	Sequence 91, Appl
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	58	18	0.3	1461	3	US-08-913-441B-1	Sequence 1, Appli
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c	76	18	0.3	13930	4	US-09-976-594-1011	Sequence 1011, Ap
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	168	17	0.3	1245	4	US-09-023-655-1412	Sequence 1412, Ap
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	183	17	0.3	1539	4	US-09-059-584-55	Sequence 55, Appl
	184	17	0.3	1569	2	US-08-901-306-3	Sequence 3, Appli
	185	17	0.3	1569	3	US-09-180-271-3	Sequence 3, Appli
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c	187	17	0.3	1622	4	US-09-599-360B-43	Sequence 43, Appl
	188	17	0.3	1643	4	US-09-023-655-753	Sequence 753, App
	189	17	0.3	1656	4	US-09-489-039A-3878	Sequence 3878, Ap
c	190	17	0.3	1669	4	US-09-591-466C-1	Sequence 1, Appli
	191	17	0.3	1671	4	US-09-795-691-3	Sequence 3, Appli
c	192	17	0.3	1737	4	US-09-591-466C-3	Sequence 3, Appli
c	193	17	0.3	1747	1	US-08-176-620A-1	Sequence 1, Appli
c	194	17	0.3	1747	1	US-08-463-862-1	Sequence 1, Appli
c	195	17	0.3	1747	2	US-08-461-985-1	Sequence 1, Appli
c	196	17	0.3	1747	2	US-08-458-887-1	Sequence 1, Appli
c	197	17	0.3	1747	3	US-08-932-787B-1	Sequence 1, Appli
c	198	17	0.3	1747	3	US-08-932-012C-1	Sequence 1, Appli
c	199	17	0.3	1747	4	US-08-888-818C-1	Sequence 1, Appli
	200	17	0.3	1872	4	US-09-280-116-110	Sequence 110, App
	201	17	0.3	1875	4	US-09-252-991A-5054	Sequence 5054, Ap
c	202	17	0.3	1904	1	US-08-212-375A-5	Sequence 5, Appli
	203	17	0.3	1926	3	US-09-117-250-4	Sequence 4, Appli
	204	17	0.3	1962	4	US-09-252-991A-5020	Sequence 5020, Ap
	205	17	0.3	1981	4	US-09-620-312D-715	Sequence 715, App
	206	17	0.3	1990	1	US-08-454-720A-35	Sequence 35, Appl
c	207	17	0.3	1997	4	US-09-620-312D-932	Sequence 932, App
c	208	17	0.3	1999	4	US-09-167-109-4	Sequence 4, Appli
c	209	17	0.3	1999	4	US-09-921-099A-12	Sequence 12, Appl
c	210	17	0.3	2004	2	US-08-691-814B-1	Sequence 1, Appli
c	211	17	0.3	2043	4	US-09-149-476-231	Sequence 231, App
	212	17	0.3	2086	3	US-08-724-586-1	Sequence 1, Appli
	213	17	0.3	2086	3	US-09-421-632-1	Sequence 1, Appli
	214	17	0.3	2086	4	US-09-932-190-1	Sequence 1, Appli
	215	17	0.3	2091	4	US-09-813-818-1	Sequence 1, Appli
	216	17	0.3	2117	2	US-08-655-640-1	Sequence 1, Appli
	217	17	0.3	2124	2	US-08-655-640-3	Sequence 3, Appli
	218	17	0.3	2165	3	US-09-366-257-1	Sequence 1, Appli
	219	17	0.3	2165	4	US-09-220-132-61	Sequence 61, Appl
c	220	17	0.3	2177	4	US-09-016-434-1084	Sequence 1084, Ap
c	221	17	0.3	2229	4	US-09-252-991A-7718	Sequence 7718, Ap
c	222	17	0.3	2295	4	US-09-252-991A-5162	Sequence 5162, Ap
	223	17	0.3	2319	1	US-08-154-019-1	Sequence 1, Appli
	224	17	0.3	2319	1	US-08-461-333-1	Sequence 1, Appli
	225	17	0.3	2319	3	US-08-464-167-1	Sequence 1, Appli
	226	17	0.3	2319	3	US-09-158-313-1	Sequence 1, Appli
	227	17	0.3	2319	3	US-08-476-798-1	Sequence 1, Appli
	228	17	0.3	2360	1	US-08-145-681-1	Sequence 1, Appli
	229	17	0.3	2360	1	US-08-250-308-1	Sequence 1, Appli
	230	17	0.3	2360	1	US-08-453-703-1	Sequence 1, Appli
	231	17	0.3	2360	2	US-08-456-106-1	Sequence 1, Appli
	232	17	0.3	2360	3	US-08-456-108-1	Sequence 1, Appli
	233	17	0.3	2360	3	US-09-265-577-1	Sequence 1, Appli
	234	17	0.3	2360	4	US-09-633-739-1	Sequence 1, Appli
	235	17	0.3	2360	5	PCT-US93-03614-1	Sequence 1, Appli
	236	17	0.3	2376	4	US-09-976-594-496	Sequence 496, App
	237	17	0.3	2493	1	US-07-977-434-5	Sequence 5, Appli
	238	17	0.3	2493	1	US-08-458-819-5	Sequence 5, Appli
	239	17	0.3	2493	5	PCT-US91-07035-5	Sequence 5, Appli
c	240	17	0.3	2540	3	US-08-838-151A-18	Sequence 18, Appl
c	241	17	0.3	2609	4	US-09-976-594-943	Sequence 943, App
	242	17	0.3	2619	1	US-08-154-019-3	Sequence 3, Appli
	243	17	0.3	2619	1	US-08-461-333-3	Sequence 3, Appli
	244	17	0.3	2619	3	US-08-464-167-3	Sequence 3, Appli
	245	17	0.3	2619	3	US-09-158-313-3	Sequence 3, Appli
	246	17	0.3	2619	3	US-08-476-798-3	Sequence 3, Appli

	247	17	0.3	2619	4	US-09-377-497-14	Sequence 14, Appl
	248	17	0.3	2686	4	US-09-795-691-1	Sequence 1, Appli
c	249	17	0.3	3015	4	US-09-489-039A-2544	Sequence 2544, Ap
c	250	17	0.3	3024	2	US-08-836-943-1	Sequence 1, Appli
c	251	17	0.3	3034	4	US-09-976-594-636	Sequence 636, App
	252	17	0.3	3060	4	US-09-252-991A-7846	Sequence 7846, Ap
	253	17	0.3	3366	4	US-09-345-650-2	Sequence 2, Appli
	254	17	0.3	3458	4	US-09-023-655-603	Sequence 603, App
	255	17	0.3	3505	1	US-08-454-097-34	Sequence 34, Appl
	256	17	0.3	3505	1	US-08-468-036-43	Sequence 43, Appl
	257	17	0.3	3505	2	US-08-376-843-43	Sequence 43, Appl
	258	17	0.3	3505	3	US-08-185-359-34	Sequence 34, Appl
	259	17	0.3	3601	3	US-09-017-631-23	Sequence 23, Appl
	260	17	0.3	3602	2	US-08-883-795A-33	Sequence 33, Appl
	261	17	0.3	3602	3	US-09-018-138-1	Sequence 1, Appli
	262	17	0.3	3900	4	US-09-023-655-1420	Sequence 1420, Ap
	263	17	0.3	3984	4	US-09-016-434-1199	Sequence 1199, Ap
	264	17	0.3	4307	4	US-09-552-950-2	Sequence 2, Appli
	265	17	0.3	4348	2	US-08-915-868-1	Sequence 1, Appli
c	266	17	0.3	4530	4	US-09-566-921-134	Sequence 134, App
	267	17	0.3	4559	4	US-09-919-172-61	Sequence 61, Appl
c	268	17	0.3	4643	4	US-09-453-702B-22	Sequence 22, Appl
	269	17	0.3	4672	4	US-09-221-017B-846	Sequence 846, App
	270	17	0.3	5124	4	US-09-534-638-2	Sequence 2, Appli
	271	17	0.3	5129	4	US-09-976-594-964	Sequence 964, App
	272	17	0.3	5330	4	US-09-023-905A-1	Sequence 1, Appli
	273	17	0.3	5889	1	US-08-463-092B-5	Sequence 5, Appli
	274	17	0.3	5889	2	US-08-462-109A-5	Sequence 5, Appli
	275	17	0.3	5889	2	US-08-460-907B-5	Sequence 5, Appli
	276	17	0.3	5889	3	US-08-463-179A-5	Sequence 5, Appli
	277	17	0.3	5889	3	US-08-461-384B-5	Sequence 5, Appli
	278	17	0.3	6002	1	US-08-698-551-15	Sequence 15, Appl
	279	17	0.3	6002	2	US-08-602-228-15	Sequence 15, Appl
	280	17	0.3	6002	2	US-08-839-032A-15	Sequence 15, Appl
	281	17	0.3	6002	4	US-09-185-258C-15	Sequence 15, Appl
c	282	17	0.3	6827	4	US-08-961-527-60	Sequence 60, Appl
c	283	17	0.3	6976	4	US-09-636-215-705	Sequence 705, App
c	284	17	0.3	6976	4	US-09-685-166A-705	Sequence 705, App
c	285	17	0.3	7063	4	US-09-485-632B-5	Sequence 5, Appli
c	286	17	0.3	7812	4	US-09-485-632B-9	Sequence 9, Appli
	287	17	0.3	8266	4	US-09-059-584-54	Sequence 54, Appl
	288	17	0.3	9772	4	US-09-552-950-5	Sequence 5, Appli
	289	17	0.3	14707	4	US-09-312-762A-3	Sequence 3, Appli
c	290	17	0.3	30001	1	US-08-125-468-1	Sequence 1, Appli
c	291	17	0.3	30001	2	US-08-474-933-1	Sequence 1, Appli
c	292	17	0.3	34001	4	US-09-596-002-18	Sequence 18, Appl
c	293	17	0.3	47981	4	US-09-679-279-1	Sequence 1, Appli
	294	17	0.3	58909	4	US-09-596-002-30	Sequence 30, Appl
	295	17	0.3	75395	4	US-09-984-890-3	Sequence 3, Appli
	296	17	0.3	77536	4	US-09-410-551B-1	Sequence 1, Appli
	297	17	0.3	98844	4	US-09-791-211-10	Sequence 10, Appl
	298	17	0.3	118067	4	US-09-497-855A-32	Sequence 32, Appl
c	299	17	0.3	161652	4	US-09-497-855A-40	Sequence 40, Appl
c	300	17	0.3	169998	4	US-09-676-610B-24	Sequence 24, Appl
	301	17	0.3	176373	3	US-09-128-155-17	Sequence 17, Appl
c	302	17	0.3	197496	4	US-09-877-177A-10	Sequence 10, Appl
c	303	17	0.3	580073	4	US-08-545-528D-1	Sequence 1, Appli
c	304	17	0.3	786431	4	US-09-751-389-3	Sequence 3, Appli
c	305	16	0.3	24	4	US-09-653-754-3	Sequence 3, Appli
	306	16	0.3	25	4	US-09-599-287A-16	Sequence 16, Appl
c	307	16	0.3	65	4	US-09-363-939A-164	Sequence 164, App
c	308	16	0.3	65	4	US-09-363-939A-168	Sequence 168, App
	309	16	0.3	78	3	US-08-479-744A-36	Sequence 36, Appl
	310	16	0.3	78	3	US-08-280-757B-36	Sequence 36, Appl
	311	16	0.3	78	4	US-09-227-595-5	Sequence 5, Appli
	312	16	0.3	78	4	US-09-425-762-36	Sequence 36, Appl
	313	16	0.3	80	3	US-09-133-321-9	Sequence 9, Appli
	314	16	0.3	129	4	US-09-209-676-88	Sequence 88, Appl
	315	16	0.3	131	1	US-07-998-003A-62	Sequence 62, Appl
	316	16	0.3	131	1	US-08-453-274B-62	Sequence 62, Appl
	317	16	0.3	131	1	US-08-453-695A-62	Sequence 62, Appl
	318	16	0.3	131	1	US-08-268-161A-62	Sequence 62, Appl
	319	16	0.3	131	2	US-08-453-702A-62	Sequence 62, Appl
	320	16	0.3	131	3	US-09-099-639-62	Sequence 62, Appl
	321	16	0.3	131	5	PCT-US93-12588-62	Sequence 62, Appl
	322	16	0.3	131	5	PCT-US95-08071-62	Sequence 62, Appl
c	323	16	0.3	149	4	US-09-621-976-15276	Sequence 15276, A
c	324	16	0.3	155	4	US-09-621-976-15275	Sequence 15275, A
c	325	16	0.3	157	4	US-09-621-976-15278	Sequence 15278, A
	326	16	0.3	182	4	US-09-313-294A-4709	Sequence 4709, Ap
	327	16	0.3	186	4	US-09-705-448-5	Sequence 5, Appli
c	328	16	0.3	210	4	US-09-134-001C-2749	Sequence 2749, Ap
	329	16	0.3	215	4	US-09-621-976-13270	Sequence 13270, A
c	330	16	0.3	224	4	US-09-621-976-15277	Sequence 15277, A
c	331	16	0.3	226	4	US-09-621-976-15272	Sequence 15272, A
	332	16	0.3	227	4	US-09-705-448-6	Sequence 6, Appli
	333	16	0.3	229	4	US-09-833-381-18	Sequence 18, Appl
c	334	16	0.3	247	4	US-09-016-434-436	Sequence 436, App
c	335	16	0.3	248	4	US-09-016-434-968	Sequence 968, App
c	336	16	0.3	258	4	US-09-252-991A-7356	Sequence 7356, Ap
	337	16	0.3	270	4	US-09-252-991A-5174	Sequence 5174, Ap
	338	16	0.3	280	4	US-09-313-294A-6796	Sequence 6796, Ap
	339	16	0.3	283	2	US-08-332-766A-21	Sequence 21, Appl
	340	16	0.3	289	4	US-09-313-294A-7265	Sequence 7265, Ap
	341	16	0.3	292	4	US-09-382-552-56	Sequence 56, Appl
	342	16	0.3	295	4	US-09-621-976-8492	Sequence 8492, Ap
	343	16	0.3	315	4	US-09-313-294A-5804	Sequence 5804, Ap
	344	16	0.3	354	4	US-09-489-039A-2664	Sequence 2664, Ap
c	345	16	0.3	360	4	US-09-621-976-2422	Sequence 2422, Ap
	346	16	0.3	368	4	US-09-397-787-143	Sequence 143, App
	347	16	0.3	384	4	US-09-134-000C-1544	Sequence 1544, Ap
c	348	16	0.3	396	4	US-09-640-173-147	Sequence 147, App
c	349	16	0.3	396	4	US-09-713-550-147	Sequence 147, App
	350	16	0.3	411	4	US-09-489-039A-712	Sequence 712, App
c	351	16	0.3	414	4	US-09-621-976-11049	Sequence 11049, A
c	352	16	0.3	420	3	US-09-532-803-5	Sequence 5, Appli
	353	16	0.3	420	4	US-09-252-991A-756	Sequence 756, App
c	354	16	0.3	421	3	US-09-211-631-12	Sequence 12, Appl
c	355	16	0.3	421	3	US-09-265-628-12	Sequence 12, Appl
c	356	16	0.3	421	3	US-09-001-141-10	Sequence 10, Appl
c	357	16	0.3	421	4	US-09-653-403-13	Sequence 13, Appl
c	358	16	0.3	421	4	US-09-643-597-321	Sequence 321, App
c	359	16	0.3	421	4	US-10-013-784-13	Sequence 13, Appl
c	360	16	0.3	421	4	US-09-480-884A-321	Sequence 321, App
c	361	16	0.3	421	4	US-09-542-615A-321	Sequence 321, App
c	362	16	0.3	421	4	US-09-606-421B-321	Sequence 321, App
c	363	16	0.3	421	4	US-09-786-606-11	Sequence 11, Appl
c	364	16	0.3	421	4	US-09-621-976-8508	Sequence 8508, Ap
	365	16	0.3	423	4	US-09-252-991A-11873	Sequence 11873, A
	366	16	0.3	423	4	US-09-489-039A-382	Sequence 382, App
c	367	16	0.3	423	4	US-09-489-039A-1140	Sequence 1140, Ap
	368	16	0.3	429	4	US-09-976-594-765	Sequence 765, App
	369	16	0.3	431	4	US-09-621-976-18939	Sequence 18939, A
	370	16	0.3	437	4	US-09-621-976-18230	Sequence 18230, A
	371	16	0.3	446	4	US-09-621-976-15600	Sequence 15600, A
	372	16	0.3	450	4	US-09-669-751-59	Sequence 59, Appl
	373	16	0.3	451	4	US-09-621-976-18938	Sequence 18938, A
c	374	16	0.3	457	4	US-09-621-976-17249	Sequence 17249, A
	375	16	0.3	462	4	US-09-621-976-11757	Sequence 11757, A
	376	16	0.3	470	4	US-09-621-976-3838	Sequence 3838, Ap
c	377	16	0.3	478	4	US-09-280-116-174	Sequence 174, App
	378	16	0.3	479	4	US-09-621-976-893	Sequence 893, App
c	379	16	0.3	480	4	US-09-621-976-1337	Sequence 1337, Ap
c	380	16	0.3	481	4	US-09-621-976-564	Sequence 564, App
	381	16	0.3	489	1	US-08-081-072-9	Sequence 9, Appli
	382	16	0.3	489	1	US-08-449-093A-9	Sequence 9, Appli
c	383	16	0.3	492	4	US-09-621-976-565	Sequence 565, App
	384	16	0.3	495	4	US-09-280-116-153	Sequence 153, App
	385	16	0.3	498	4	US-09-489-039A-6543	Sequence 6543, Ap
	386	16	0.3	501	4	US-09-328-352-3245	Sequence 3245, Ap
c	387	16	0.3	510	4	US-09-489-039A-1541	Sequence 1541, Ap
c	388	16	0.3	534	4	US-09-252-991A-14895	Sequence 14895, A
	389	16	0.3	540	4	US-09-252-991A-8727	Sequence 8727, Ap
c	390	16	0.3	546	3	US-08-331-625A-44	Sequence 44, Appl
c	391	16	0.3	546	4	US-09-494-151-44	Sequence 44, Appl
c	392	16	0.3	546	4	US-09-972-484-44	Sequence 44, Appl

c 393	16	0.3	552	4	US-09-489-039A-3494	Sequence 3494, Ap
c 394	16	0.3	571	4	US-09-404-879A-48	Sequence 48, Appl
c 395	16	0.3	571	4	US-09-338-933-48	Sequence 48, Appl
c 396	16	0.3	571	4	US-09-215-681-48	Sequence 48, Appl
c 397	16	0.3	571	4	US-09-216-003A-48	Sequence 48, Appl
c 398	16	0.3	576	1	US-08-086-428B-2	Sequence 2, Appli
c 399	16	0.3	576	2	US-08-468-570-2	Sequence 2, Appli
c 400	16	0.3	576	2	US-08-290-665A-2	Sequence 2, Appli
c 401	16	0.3	576	4	US-08-466-601A-2	Sequence 2, Appli
c 402	16	0.3	576	5	PCT-US95-10398-2	Sequence 2, Appli
403	16	0.3	579	4	US-09-252-991A-8637	Sequence 8637, Ap
404	16	0.3	582	4	US-09-621-976-18934	Sequence 18934, A
c 405	16	0.3	603	3	US-09-385-982-233	Sequence 233, App
406	16	0.3	605	4	US-09-643-597-207	Sequence 207, App
407	16	0.3	605	4	US-09-480-884A-207	Sequence 207, App
408	16	0.3	605	4	US-09-542-615A-207	Sequence 207, App
409	16	0.3	605	4	US-09-606-421B-207	Sequence 207, App
c 410	16	0.3	615	1	US-08-539-304A-1	Sequence 1, Appli
411	16	0.3	627	4	US-09-134-001C-2763	Sequence 2763, Ap
c 412	16	0.3	630	4	US-09-252-991A-656	Sequence 656, App
c 413	16	0.3	631	3	US-08-545-809A-31	Sequence 31, Appl
414	16	0.3	631	3	US-08-943-731-187	Sequence 187, App
415	16	0.3	651	4	US-09-489-039A-957	Sequence 957, App
c 416	16	0.3	654	4	US-09-252-991A-11814	Sequence 11814, A
c 417	16	0.3	669	4	US-09-221-017B-61	Sequence 61, Appl
418	16	0.3	672	4	US-09-489-039A-6264	Sequence 6264, Ap
c 419	16	0.3	688	3	US-09-328-111-453	Sequence 453, App
420	16	0.3	696	1	US-07-656-566-4	Sequence 4, Appli
421	16	0.3	697	6	5171843-10	Patent No. 5171843
c 422	16	0.3	701	3	US-08-331-625A-55	Sequence 55, Appl
423	16	0.3	701	3	US-09-133-321-1	Sequence 1, Appli
c 424	16	0.3	701	4	US-09-494-151-55	Sequence 55, Appl
c 425	16	0.3	701	4	US-09-972-484-55	Sequence 55, Appl
426	16	0.3	701	4	US-09-621-976-206	Sequence 206, App
427	16	0.3	703	4	US-09-023-655-1097	Sequence 1097, Ap
428	16	0.3	710	3	US-08-998-416-603	Sequence 603, App
429	16	0.3	715	4	US-09-247-155-139	Sequence 139, App
430	16	0.3	726	4	US-09-621-976-1875	Sequence 1875, Ap
c 431	16	0.3	729	4	US-09-252-991A-11877	Sequence 11877, A
432	16	0.3	730	3	US-09-352-990-3	Sequence 3, Appli
433	16	0.3	738	2	US-08-604-989A-8	Sequence 8, Appli
434	16	0.3	741	4	US-09-149-476-202	Sequence 202, App
435	16	0.3	741	4	US-09-252-991A-12066	Sequence 12066, A
436	16	0.3	741	4	US-09-489-039A-5512	Sequence 5512, Ap
c 437	16	0.3	742	2	US-08-966-316-2	Sequence 2, Appli
c 438	16	0.3	765	3	US-08-331-625A-40	Sequence 40, Appl
c 439	16	0.3	765	4	US-09-494-151-40	Sequence 40, Appl
440	16	0.3	765	4	US-09-252-991A-7969	Sequence 7969, Ap
c 441	16	0.3	765	4	US-09-972-484-40	Sequence 40, Appl
c 442	16	0.3	768	4	US-09-252-991A-9221	Sequence 9221, Ap
443	16	0.3	780	4	US-09-651-656-26	Sequence 26, Appl
444	16	0.3	780	4	US-09-650-855-26	Sequence 26, Appl
445	16	0.3	783	4	US-09-252-991A-11569	Sequence 11569, A
446	16	0.3	795	4	US-09-252-991A-3048	Sequence 3048, Ap
447	16	0.3	813	4	US-09-252-991A-12621	Sequence 12621, A
448	16	0.3	826	4	US-09-071-035-287	Sequence 287, App
449	16	0.3	835	3	US-08-957-302A-9	Sequence 9, Appli
450	16	0.3	835	3	US-09-542-403-9	Sequence 9, Appli
c 451	16	0.3	836	3	US-08-998-416-322	Sequence 322, App
452	16	0.3	840	4	US-09-252-991A-10789	Sequence 10789, A
453	16	0.3	840	4	US-09-252-991A-14967	Sequence 14967, A
454	16	0.3	843	4	US-09-252-991A-2744	Sequence 2744, Ap
455	16	0.3	858	4	US-09-172-952-8	Sequence 8, Appli
c 456	16	0.3	870	4	US-09-489-039A-764	Sequence 764, App
c 457	16	0.3	876	4	US-09-513-783A-9	Sequence 9, Appli
458	16	0.3	876	4	US-09-252-991A-8946	Sequence 8946, Ap
459	16	0.3	876	4	US-09-252-991A-14476	Sequence 14476, A
460	16	0.3	891	4	US-09-489-039A-360	Sequence 360, App
c 461	16	0.3	897	5	PCT-US96-05320A-303	Sequence 303, App
462	16	0.3	915	3	US-08-557-614-1	Sequence 1, Appli
463	16	0.3	915	4	US-09-252-991A-14968	Sequence 14968, A
464	16	0.3	918	4	US-09-252-991A-12009	Sequence 12009, A
c 465	16	0.3	933	4	US-09-252-991A-8606	Sequence 8606, Ap
c 466	16	0.3	954	4	US-10-043-238-2	Sequence 2, Appli
467	16	0.3	963	4	US-09-071-035-285	Sequence 285, App
468	16	0.3	963	4	US-09-134-000C-2132	Sequence 2132, Ap
c 469	16	0.3	966	4	US-09-252-991A-7439	Sequence 7439, Ap
470	16	0.3	972	4	US-09-252-991A-2956	Sequence 2956, Ap
c 471	16	0.3	987	4	US-09-489-039A-2674	Sequence 2674, Ap
c 472	16	0.3	990	4	US-09-252-991A-11517	Sequence 11517, A
c 473	16	0.3	1001	4	US-09-641-638-270	Sequence 270, App
c 474	16	0.3	1001	4	US-09-641-638-446	Sequence 446, App
c 475	16	0.3	1001	4	US-09-671-317-290	Sequence 290, App
c 476	16	0.3	1007	4	US-09-328-475C-106	Sequence 106, App
c 477	16	0.3	1011	4	US-09-641-806-3	Sequence 3, Appli
c 478	16	0.3	1011	4	US-09-723-129-3	Sequence 3, Appli
c 479	16	0.3	1011	4	US-09-252-991A-14782	Sequence 14782, A
c 480	16	0.3	1011	4	US-09-722-862-3	Sequence 3, Appli
481	16	0.3	1020	4	US-09-252-991A-6229	Sequence 6229, Ap
c 482	16	0.3	1026	4	US-09-641-806-1	Sequence 1, Appli
c 483	16	0.3	1026	4	US-09-723-129-1	Sequence 1, Appli
c 484	16	0.3	1026	4	US-09-722-862-1	Sequence 1, Appli
c 485	16	0.3	1029	4	US-09-252-991A-15460	Sequence 15460, A
486	16	0.3	1041	4	US-09-489-039A-194	Sequence 194, App
c 487	16	0.3	1044	1	US-07-975-526-1	Sequence 1, Appli
c 488	16	0.3	1044	4	US-07-974-409C-422	Sequence 422, App
c 489	16	0.3	1044	4	US-07-974-409C-423	Sequence 423, App
490	16	0.3	1047	4	US-09-252-991A-9034	Sequence 9034, Ap
c 491	16	0.3	1065	3	US-09-325-897-1	Sequence 1, Appli
c 492	16	0.3	1065	4	US-09-837-726-1	Sequence 1, Appli
493	16	0.3	1071	4	US-09-543-681A-3985	Sequence 3985, Ap
494	16	0.3	1086	3	US-09-280-409-3	Sequence 3, Appli
c 495	16	0.3	1088	4	US-09-755-665-61	Sequence 61, Appl
c 496	16	0.3	1090	4	US-09-755-665-59	Sequence 59, Appl
c 497	16	0.3	1090	4	US-09-755-665-60	Sequence 60, Appl
c 498	16	0.3	1091	4	US-09-755-665-62	Sequence 62, Appl
c 499	16	0.3	1098	4	US-09-252-991A-15400	Sequence 15400, A
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501	16	0.3	1103	4	US-09-424-712-2	Sequence 2, Appli
c 502	16	0.3	1110	4	US-09-543-681A-3342	Sequence 3342, Ap
c 503	16	0.3	1123	4	US-09-755-665-15	Sequence 15, Appl
504	16	0.3	1137	6	5171843-8	Patent No. 5171843
505	16	0.3	1139	4	US-09-690-454-13	Sequence 13, Appl
506	16	0.3	1140	4	US-09-252-991A-14999	Sequence 14999, A
507	16	0.3	1140	4	US-09-328-352-4089	Sequence 4089, Ap
c 508	16	0.3	1149	4	US-09-252-991A-14783	Sequence 14783, A
509	16	0.3	1176	4	US-09-543-681A-3917	Sequence 3917, Ap
510	16	0.3	1176	4	US-09-489-039A-5553	Sequence 5553, Ap
511	16	0.3	1179	2	US-08-465-794-4	Sequence 4, Appli
512	16	0.3	1179	3	US-09-049-813-4	Sequence 4, Appli
513	16	0.3	1182	1	US-07-640-476-4	Sequence 4, Appli
514	16	0.3	1182	4	US-09-252-991A-6534	Sequence 6534, Ap
515	16	0.3	1185	6	5290690-1	Patent No. 5290690
c 516	16	0.3	1194	4	US-09-252-991A-10197	Sequence 10197, A
517	16	0.3	1197	4	US-09-891-641-43	Sequence 43, Appl
c 518	16	0.3	1203	4	US-09-540-236-1433	Sequence 1433, Ap
519	16	0.3	1206	4	US-09-489-039A-823	Sequence 823, App
520	16	0.3	1212	4	US-09-252-991A-12510	Sequence 12510, A
c 521	16	0.3	1215	4	US-09-252-991A-16442	Sequence 16442, A
522	16	0.3	1218	4	US-09-543-681A-3574	Sequence 3574, Ap
523	16	0.3	1236	4	US-09-328-352-1841	Sequence 1841, Ap
524	16	0.3	1236	4	US-09-540-236-1436	Sequence 1436, Ap
c 525	16	0.3	1242	4	US-09-252-991A-14749	Sequence 14749, A
526	16	0.3	1245	1	US-07-887-072B-1	Sequence 1, Appli
527	16	0.3	1245	1	US-08-466-444-1	Sequence 1, Appli
c 528	16	0.3	1248	4	US-09-252-991A-6318	Sequence 6318, Ap
529	16	0.3	1248	4	US-09-252-991A-9872	Sequence 9872, Ap
c 530	16	0.3	1251	4	US-09-540-236-295	Sequence 295, App
531	16	0.3	1252	4	US-09-673-395A-73	Sequence 73, Appl
c 532	16	0.3	1257	4	US-09-489-039A-6981	Sequence 6981, Ap
c 533	16	0.3	1284	3	US-08-331-625A-42	Sequence 42, Appl
c 534	16	0.3	1284	4	US-09-494-151-42	Sequence 42, Appl
c 535	16	0.3	1284	4	US-09-972-484-42	Sequence 42, Appl
c 536	16	0.3	1287	4	US-09-489-039A-394	Sequence 394, App
537	16	0.3	1299	1	US-08-723-938-4	Sequence 4, Appli
538	16	0.3	1299	2	US-09-080-538-4	Sequence 4, Appli